

Db	557	TCGTGCCACAGACAAAGAGGCCCGGTACAGCGCGAGCTCTATCCGTACATCGCTGATACCAT	616
OY	1993	GGTGTCTTCGTACAGCGCGGCTTGTATGAAGGTTGGATTCACCGTGGTTGAAGCCATG	2052
Db	617	GGTGTCTTCGTACAGCGCGGCTTGTATGAAGGTTGGATTCACCGTGGTTGAAGCCATG	676
OY	2053	ACCTGTGGCTTCTACTTTTGGCAGCGCTCCATGGAGGTTCCAGCTGAGTACATAGAGCAT	2112
Db	677	ACCTGTGACCTTCTACTTTTGGCAGCGCTCCATGGAGGTTCCAGCTGAGTACATAGAGCAT	736
OY	2113	GGCGCTCGGGGCTTCCATTTGAGCCCGTACACCCCGGAACAGGCTGTTAATCTGATGGCC	2172
Db	737	GGCGCTCGGGGCTTCCATTTGAGCCCGTACACCCCGGAAGGCTGCTAATCTGATGGCC	796
OY	2173	GACTTCTTCCAGCCGGTGCAGACAGACCAGATCACTGGTGAATATTTCTGAGCAGGG	2232
Db	797	GACTTCTTCCAGCCGGTGCAGACAGACCAGATCACTGGTGAATATTTCTGAGCAGGG	856
OY	2233	CTGACAGCGCATATACAGAAATACATGGAAGATATCTCAGAGAGGTTGATGACACTG	2292
Db	857	CTGACAGCGCATATACAGAAATACATGGAAGATATCTCAGAGAGGTTGATGACACTG	916
OY	2293	GCCGGGGCTACGGCTTTCTGGAAGTACGTTCGAAAGCTCCAGAGGCTGGAACAGAGGCGC	2352
Db	917	GCCGGGGCTACGGCTTTCTGGAAGTACGTTCGAAAGCTCCAGAGGCTGGAACAGAGGCGC	976
OY	2353	TACCTTGAATGTTCTATACATCTGAAGTTCGCGAGCTGGGAAACCGTGCCTTGGCA	2412
Db	977	TACCTTGAATGTTCTATACATCTGAAGTTCGCGAGCTGGGAAACCGTGCCTTGGCA	1036
OY	2413	ATTGACCAACCGGAGTAGCTTGGCGCAATGGGACTGGCTAGCACTTGGTACAGACTGAA	2472
Db	1037	ATTGACCAACCGGAGTAGCTTGGCGCAATGGGACTGGCTAGCACTTGGTACAGACTGAA	1096
OY	2473	ACCTGAAGACCTTCAGTATTTAGCGCGGACAGACGGTACCAATATAATGTCCGGAG	2532
Db	1097	ACCTGAAGACCTTCAGTATTTAGCGCGGACAGACGGTACCAATATAATGTCCGGAG	1156
OY	2533	CTGAACAGGTTTTT 2546	
Db	1157	CTGAACAGGTTTTT 1170	

RESULT 6

US-09-237-183A-1015
Sequence 1015, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
TITLE OF INVENTION: Sucrose Pathway
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 1015
LENGTH: 428
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-1015

Query Match	10.1%	Score 278;	DB 10;	Length 428;
Best Local Similarity	99.7%;	Pred. No. 5.1e-133;		
Matches 328;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

O_Y^a 2218 ATATCTGAGCAGGAGCTGTGACGGCATATATGAGAAAGTACCATGGAAGTATATCTCAGAG 2277
 Db 63 ATATCTGAGCAGGAGCTGTGACGGCATATATGAGAAAGTACCATGGAAGTATATCTCAGAG 122

QY	2278	AGGTGATGACACATGGCGCGGGGTCTACGGTTCTGGAAGTACGCTGGAAGCTGAGG	2337
Db	123	AGGTTANTGACATCGGCCGGGGCTACGGTTCTGGAAGTACGCTGGAAGCTGAGG	182
QY	2338	CTGAGACACGAGCGGCTTACCTTGAGATGTTCTACACTGAAATTCCGCGAAGCTGGCGAG	2397
Db	183	CGGAGACACGAGCGGCTTACCTTGAGATGTTCTACACTGAAATTCCGCGAAGCTGGCGAG	242
QY	2398	ACCGTGCCGGCTTGAAATTGACCAACCGAGAGCTTGGCGAAGCTGCGGATGAGCACT	245
Db	243	ACCGTGCCGGCTTGAAATTGACCAACCGGAGAGCTTGGCGAAGCTGCGGATGAGCACT	302
QY	2458	TGGTACAAAGACTGAACCTGAAAGACCTTCAGTAATTTAAGCGCGGCGAGACGATAGCCAA	2517
Db	303	TGGTACAAAGACTGAACCTGAAAGACCTTCAGTAATTTAAGCGCGGCGAGACGATAGCCAA	362
QY	2518	TAAATGTCGCGAGCTGAAGCTGTTT	2546
Db	363	TAAATGTCGCGAGCTGAAGCTGTTT	391

RESULT 7

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US-09-237-183A-533
; Sequence 533, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, No. K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With Thea
; TITLE OF INVENTION: Sucrose Pathway
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 533
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-533

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Query Match	9.2%;	Score 255;	DB 10;	Length 303;
Best Local Similarity	100.0%;	Pred. No. 4.3e-121;		
Matches 255	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1761	GCTGTGGAAGCTTTTCTAAGTCGCTAAGCTAGGGAGCTGGTAAACCTTGTGTCGT	1820
Db	1	GCTGTGGAAGCTTTTCTAAGTCGCTAAGCTAGGGAGCTGGTAAACCTTGTGTCGT	60
QY	1821	TGCGGGGTCAATGATGTCAA CAAGTCCAAGACAGGGAGAGATGCGGAGATAGAGA	1880
Db	61	TGCGGGGTCAATGATGTCAA CAAGTCCAAGACAGGGAGAGATGCGGAGATAGAGA	120
QY	1881	GATCATGAACTCATCAAGACCCACAACTTGTGGGCAAGTTCGCTGGATCTCTGCCA	1940
Db	121	GATCATGAACTCATCAAGACCCACAACTTGTGGGCAAGTTCGCTGGATCTCTGCCA	180
QY	1941	GACAAACAGGACCCGTAACGCGAGCTCTATGCTACATGCTGATACCCATGGTGCTTT	2000
Db	181	GACAAACAGGACCCGTAACGCGAGCTCTATGCTACATGCTGATACCCATGGTGCTTT	240
QY	2001	CGTACAGCCGCGCTT 2015	
Db	241	CGTACAGCCGCGCTT 255	

RESULT 8

US-10-080-114A-13
; Sequence 13, Application US/10080114A
; Publication No. US20030005482A1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 06:46:08 ; Search time 976.542 Seconds
(without alignments)
12830.798 Million cell updates/sec

Title: US-10-080-114a-11
Perfect score: 2757
Sequence: 1 atgtctgcccgaagctga.....aaaaaaaaagggcgccgc 2757

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2953838 seqs, 2272363821 residues

Word size : 58

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Published Applications_NA.*
2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2757	100.0	2757	US-10-080-114a-11	Sequence 11, Appl
2	2571	93.3	2737	US-10-080-114a-1	Sequence 1, Appl
3	990	35.9	1874	US-10-425-114-6561	Sequence 6561, Ap
4	963	34.9	2275	US-10-425-114-6036	Sequence 6036, Ap
5	695	25.2	1340	US-10-425-114-5285	Sequence 5285, Ap
6	278	10.1	428	US-09-237-183A-1015	Sequence 1015, Ap
7	255	9.2	303	US-09-237-183A-533	Sequence 533, Ap
8	246	8.9	347	US-10-080-114a-13	Sequence 13, Appl
9	209	7.6	283	US-09-237-183A-526	Sequence 526, Ap
10	159	5.8	285	US-09-237-183A-513	Sequence 513, Ap
11	158	5.7	297	US-09-237-183A-516	Sequence 516, Ap
12	150	5.4	150	US-09-237-183A-527	Sequence 527, Ap
13	143	5.2	411	US-09-237-183A-1018	Sequence 1018, Ap
14	134	4.9	253	US-09-237-183A-528	Sequence 528, Ap

15	130	4.7	181	10	US-09-237-183A-524	Sequence 524, Ap
16	114	4.1	310	10	US-09-237-183A-523	Sequence 523, Ap
17	99	3.6	148	10	US-09-237-183A-525	Sequence 525, Ap
18	83	3.0	137	10	US-09-237-183A-529	Sequence 529, Ap
19	63	2.3	264	10	US-09-237-183A-522	Sequence 522, Ap

ALIGNMENTS

RESULT 1
US-10-080-114a-11
; Sequence 11, Application US/10080114A
; Publication No. US20030005482A1
; GENERAL INFORMATION:
; APPLICANT: Dhuqga, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; TITLE OF INVENTION: to Improve Stalk and Grain Quality
; FILE REFERENCE: 1301P
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2757
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2430)
; FEATURE:
; NAME/KEY: source
; LOCATION: (1) ... (39)
; OTHER INFORMATION: Sorghum pronguinum
; NAME/KEY: source
; LOCATION: (40) ... (2757)
; OTHER INFORMATION: Zea mays
US-10-080-114a-11

Query Match 100.0%; Score 2757; DB 15; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTTCGCCGGAAGCTGGAACCGGACGAGCATCCGGAACCGGCTGAGAGACCCCTC	60
DB	1	ATGCTTCGCCGGAAGCTGGAACCGGACGAGCATCCGGAACCGGCTGAGAGACCCCTC	60
QY	61	CACGCGACCGCAACGAGCTGTCCTCTCTCAAGTACTGAAACAGGGAAGGAC	120
DB	61	CACGCGACCGCAACGAGCTGTCCTCTCTCAAGTACTGAAACAGGGAAGGAC	120
QY	121	ATCTTGAGGCGGACCAATCTCTGAGCGCTGACGAGGTCGAGGCTCGGAGTCCGC	180
DB	121	ATCTTGAGGCGGACCAATCTCTGAGCGCTGACGAGGTCGAGGCTCGGAGTCCGC	180
QY	181	GCGCTCCGCGGAGGACCTTCTCTGAGCTCTCCGCTCCGCGAGAGAGCGATGCTG	240
DB	181	GCGCTCCGCGGAGGACCTTCTCTGAGCTCTCCGCTCCGCGAGAGAGCGATGCTG	240
QY	241	CCGCGCTGCTGTCGCAATCGCGGTGCGCGCGCGCGGAGATTTGGAGATAGTCCGCTC	300
DB	241	CCGCGCTGCTGTCGCAATCGCGGTGCGCGCGCGCGGAGATTTGGAGATAGTCCGCTC	300
QY	301	AACGTTCACGAGCTCAAGGTGAGAGCTCAAGTTCAGTACCTCGCTCAAGAG	360
DB	301	AACGTTCACGAGCTCAAGGTGAGAGCTCAAGTTCAGTACCTCGCTCAAGAG	360
QY	361	GAGCTTGACGAGCGGACGACCAATGATCCCTAGCTTCTGAGCTTGACCTGAGCGCTTC	420
DB	361	GAGCTTGACGAGCGGACGACCAATGATCCCTAGCTTCTGAGCTTGACCTGAGCGCTTC	420

QY	421	AATGTCACGTC	CCAAAGCCCAATCGGTCATCATCTTTGGAAACGGGTGGACGTTCTG	480
Db	421	AATGTCACGTC	CCAAAGCCCAATCGGTCATCATCTTTGGAAACGGGTGGACGTTCTG	480
QY	481	AACCGACACTGT	CTCTCAATCATGTTCGCGACAGGAGATTGCTTGAGACCCCTGTGGAT	540
Db	481	AACCGACACTGT	CTCTCAATCATGTTCGCGACAGGAGATTGCTTGAGACCCCTGTGGAT	540
QY	541	TTCCTCGCTG	CCACCGGCAACAGGGGCGATGTTATGATGCTTAATGATAGAAATCAAAAGC	600
Db	541	TTCCTCGCTG	CCACCGGCAACAGGGGCGATGTTATGATGCTTAATGATAGAAATCAAAAGC	600
QY	601	TTGGGAGAGGCT	TTCAGTCTGTGCTGTACCAAAAGCTGAGAGACCTGTCAAAGCTCCCTGCT	660
Db	601	TTGGGAGAGGCT	TTCAGTCTGTGCTGTACCAAAAGCTGAGAGACCTGTCAAAGCTCCCTGCT	660
QY	661	GACACACCATCT	CACAAATTTGCTTATTAATTTCAAGATGAGGGGCTGAGAAAGGTGG	720
Db	661	GACACACCATCT	CACAAATTTGCTTATTAATTTCAAGATGAGGGGCTGAGAAAGGTGG	720
QY	721	GGTGATACAG	GAGACATGTTTTGGAAATGATCATCTCTTTCAGACATCATTCAGGCG	780
Db	721	GGTGATACAG	GAGACATGTTTTGGAAATGATCATCTCTTTCAGACATCATTCAGGCG	780
QY	781	CCAGACCCAT	TACCCCTAGAGAAATTTCTGGGGAGAGATCCCAAGATTTTAAAGTGTG	840
Db	781	CCAGACCCAT	TACCCCTAGAGAAATTTCTGGGGAGAGATCCCAAGATTTTAAAGTGTG	840
QY	841	GTGGTATCCCT	CATGAGATCTTTGGTTCAAAGCTATGATTTAGGCTTGCCAGACACAGA	900
Db	841	GTGGTATCCCT	CATGAGATCTTTGGTTCAAAGCTATGATTTAGGCTTGCCAGACACAGA	900
QY	901	GGACAGATCG	TCTATATATCTGAGCAACAGTCCGTGCACCTAGAGAAATGAGATGGTTCGCT	960
Db	901	GGACAGATCG	TCTATATATCTGAGCAACAGTCCGTGCACCTAGAGAAATGAGATGGTTCGCT	960
QY	961	TTTAAAGAAA	CAAGGGCTTGATGTTTTCCCAAGATTTCTCATTTGTACTCGGTGATACCA	1020
Db	961	TTTAAAGAAA	CAAGGGCTTGATGTTTTCCCAAGATTTCTCATTTGTACTCGGTGATACCA	1020
QY	1021	GATGCAAAAG	AAACATCATGCAATCAGCGGCTTGAGAGAAATTAGTGGAAACACACATACT	1080
Db	1021	GATGCAAAAG	AAACATCATGCAATCAGCGGCTTGAGAGAAATTAGTGGAAACACACATACT	1080
QY	1081	TACATATTTA	CGAGTCCCTTCAGAAATGAAAATGGGATCTTAAAGAAATGGATATCAAGA	1140
Db	1081	TACATATTTA	CGAGTCCCTTCAGAAATGAAAATGGGATCTTAAAGAAATGGATATCAAGA	1140
QY	1141	TTTGAATGTG	GGCCATATCTGGAAAACATTTGCTGAGAGATGCTGCTGGTGAATTTGCTGCT	1200
Db	1141	TTTGAATGTG	GGCCATATCTGGAAAACATTTGCTGAGAGATGCTGCTGGTGAATTTGCTGCT	1200
QY	1201	GAATTACAA	GATCTCCAGACTCTCAATTAATTTGSAACATCACTGATGAGAAATCTTGTGGCG	1260
Db	1201	GAATTACAA	GATCTCCAGACTCTCAATTAATTTGSAACATCACTGATGAGAAATCTTGTGGCG	1260
QY	1261	TCATGCTAT	CTTACAGATGGGAATTAACCAAGTGCACATTTGCTCATGCTCTGGAANAAG	1320
Db	1261	TCATGCTAT	CTTACAGATGGGAATTAACCAAGTGCACATTTGCTCATGCTCTGGAANAAG	1320
QY	1321	ACTAAGATTA	CCAGATTCAGACATTAATTTGGAGAAATTTGAGTAGAGAGATACATTTCTCC	1380
Db	1321	ACTAAGATTA	CCAGATTCAGACATTAATTTGGAGAAATTTGAGTAGAGAGATACATTTCTCC	1380
QY	1381	TGCCAGTTC	ACGTCGATATATGCTATGGAACATGCTGATTTTATCATCAACAGACACA	1440
Db	1381	TGCCAGTTC	ACGTCGATATATGCTATGGAACATGCTGATTTTATCATCAACAGACACA	1440
QY	1441	TACCAAGAA	ATTGCTGGAAGCAAAATATCTGTGGACAGTATGAGAGTCAATCTGCCCTTT	1500
Db	1441	TACCAAGAA	ATTGCTGGAAGCAAAATATCTGTGGACAGTATGAGAGTCAATCTGCCCTTT	1500

QY	1501	ACTCTGCTGGTCTCTATCCGAGTTGTCATGGGATGCAATCTCTGATCCAAAGTTCAAT	1560
Db	1501	ACTCTGCTGGTCTCTATCCGAGTTGTCATGGGATGCAATCTCTGATCCAAAGTTCAAT	1560
QY	1561	ATTATCTCTCTGGAGCTGCATGTCTCATTTACATTCACGAGAGGCCAAGCCGA	1620
Db	1561	ATTATCTCTCTGGAGCTGCATGTCTCATTTACATTCACGAGAGGCCAAGCCGA	1620
QY	1621	CTCACTCTCTTCATGGTTCAATCGAAAATTGATTTATGACCCGGAGCAAAACGATGAA	1680
Db	1621	CTCACTCTCTTCATGGTTCAATCGAAAATTGATTTATGACCCGGAGCAAAACGATGAA	1680
QY	1681	CACATGGGACATCGAATGACCGGTCAAAGCCCATCTCTTCCTCCATGGCAAGCTCGAC	1740
Db	1681	CACATGGGACATCGAATGACCGGTCAAAGCCCATCTCTTCCTCCATGGCAAGCTCGAC	1740
QY	1741	AGGGTGAAAGACATTAACAGGCGCTGGTGAAGCTTTGCTAAGTTCGCGTAAAGCTGAGGAG	1800
Db	1741	AGGGTGAAAGACATTAACAGGCGCTGGTGAAGCTTTGCTAAGTTCGCGTAAAGCTGAGGAG	1800
QY	1801	CTGGTAAACCTTGTCTGTGTGTCGGGCTGCAATGATGTCAACAAAGTCAAGGACAGGGAA	1860
Db	1801	CTGGTAAACCTTGTCTGTGTGTCGGGCTGCAATGATGTCAACAAAGTCAAGGACAGGGAA	1860
QY	1861	GAGATCGCGAGATAGAGAAATGATCATGAATCTATCAAGAACCAACCTTGTTCGGGACG	1920
Db	1861	GAGATCGCGAGATAGAGAAATGATCATGAATCTATCAAGAACCAACCTTGTTCGGGACG	1920
QY	1921	TTTCGCTGGATCTCTGCCGACACAAACAGGCGCCGTATACGCGAGCTTATCGCTACATC	1980
Db	1921	TTTCGCTGGATCTCTGCCGACACAAACAGGCGCCGTATATCGCTACATC	1980
QY	1981	GCTGATACCCAAAGGAGCTTGTCTACACCGGAGCTCTGATTAAGAGCTTCAGCTCACCGTC	2040
Db	1981	GCTGATACCCATGAGTGTCTTGTCTACACCGGAGCTCTGATTAAGAGCTTCAGCTCACCGTC	2040
QY	2041	GTTGAGGCGATGACCTGTGAGCTTCTCTACTTTGCGCAGCTCCATGAGGTTCCAGCTGAG	2100
Db	2041	GTTGAGGCGATGACCTGTGAGGCTTCTCTACTTTGCGCAGCTCCATGAGGTTCCAGCTGAG	2100
QY	2101	ATCATTAAGAGCATGGGCTGTGGGCTTCCACATTTGACCCGATACACCCCGAAAGGCTGTT	2160
Db	2101	ATCATTAAGAGCATGGGCTGTGGGCTTCCACATTTGACCCGATACACCCCGAAAGGCTGTT	2160
QY	2161	AATCTGATGGCGGACTTCTTGACCGGCTGCAGAGAACCCGAGTCACTGGGTGAATATA	2220
Db	2161	AATCTGATGGCGGACTTCTTGACCGGCTGCAGAGAACCCGAGTCACTGGGTGAATATA	2220
QY	2221	TCTGAGAGAGGCTGTGACGCGCATATTAAGAAAGTACATGAAAGATATCTCGAAGAGG	2280
Db	2221	TCTGAGAGAGGCTGTGACGCGCATATTAAGAAAGTACATGAAAGATATCTCGAAGAGG	2280
QY	2281	TGATATGACATCGGCGGAGTCTACGGTTCTCGAAGTACGTGTGCAAGCTGCGAAGGCTG	2340
Db	2281	TGATATGACATCGGCGGAGTCTACGGTTCTCGAAGTACGTGTGCAAGCTGCGAAGGCTG	2340
QY	2341	GAGACGAGGCGCTACCTTGAGATGTTCTACATACTGAAGTTCCGCGAGCTGGGGAAACC	2400
Db	2341	GAGACGAGGCGCTACCTTGAGATGTTCTACATACTGAAGTTCCGCGAGCTGGGGAAACC	2400
QY	2401	GAGCGGCTTGCAATTGACCAACCGGAGTAGTTCCGCAACTGCGACATGCTACACTTGG	2460
Db	2401	GAGCGGCTTGCAATTGACCAACCGGAGTAGTTCCGCAACTGCGACATGCTGAGTACTGG	2460
QY	2461	TACAAAGCTGAACCTGAAAGACCTTCAATATTAGGCGCGGACAGCCGTAACCAATAA	2520
Db	2461	TACAAAGCTGAACCTGAAAGACCTTCAATATTAGGCGCGGACAGCCGTAACCAATAA	2520
QY	2521	AATGTGCGGAGGCTGAACCTGTGTTTTATTAATGATCAATAAGGACAGATAAACAAATAC	2580
Db	2521	AATGTGCGGAGGCTGAACCTGTGTTTTATTAATGATCAATAAGGACAGATTAACAAATAC	2580
QY	2581	TGAAAGCAGGTGGGTTGCAATGTGTGTGTCTGTAAGTATTAAGTATTAATGTAAGCTGT	2640

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Db 2581 TGAAGGACAGTGGTGCAGTGTGTGTTGCTTACTGTATATGTCACACCTG 2640
QY 2641 CGGCTGCATTTCTTTCGTGGGAGCGGACGACGTCGTGATTAATACATCA 2700
Db 2641 CGGCTGCATTTCTTTCGTGGGAGCGGACGACGTCGTGATTAATACATCA 2700
QY 2701 TATTCGTGACCTGTGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2757
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RESULT 2
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; Sequence 1, Application US/10080114A
; Publication No. US20030005482A1
; GENERAL INFORMATION:
; APPLICANT: Duquesa, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080,114A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Zea mays
US-10-080-114A-1
Query Match 93.3%; Score 2571; DB 15; Length 2737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 GCCGAGGAGCCCTTCCTCGACGTCCTCCGCTCCGCGACGAGGCGATGCTGCCGCG 246
Db 167 GCCGAGGAGCCCTTCCTCGACGTCCTCCGCTCCGCGACGAGGCGATGCTGCCGCG 226
QY 247 TTCGTGGCCATCGCGGTGGGCGCCCGCGCGGAGTTTGGAGATACGTCGCGCAAGTT 306
Db 227 TTCGTGGCCATCGCGGTGGGCGCCCGCGCGGAGTTTGGAGATACGTCGCGCAAGTT 286
QY 307 CACGAGCTCAGGCTCGAGCAGCTCAGAGTCTCGAGTACTCCGCTTCAAGAGAGACT 366
Db 287 CACGAGCTCAGGCTCGAGCAGCTCAGAGTCTCGAGTACTCCGCTTCAAGAGAGACT 346
QY 367 GTTCGAGGCGACGACATGATGCTTCTGAGCTTGACTTTCGAGCCGTTCAATGTC 426
Db 347 GTTCGAGGCGACGACATGATGCTTCTGAGCTTGACTTTCGAGCCGTTCAATGTC 406
QY 427 TCAGTCCCGACGCCCAATCGGTATATCTATGTAAGAAAGGTGCGATCTTCAACGCA 486
Db 407 TCAGTCCCGACGCCCAATCGGTATATCTATGTAAGAAAGGTGCGATCTTCAACGCA 466
QY 487 CAATTGCTCATCATGTTCCGCAACAGGAGTTGTTGAGCCCGTTGGAATTTCTC 546
Db 467 CAATTGCTCATCATGTTCCGCAACAGGAGTTGTTGAGCCCGTTGGAATTTCTC 526
QY 547 CGTGGCCACCGGACCAAGGGGCAATGTTATGATGTTATGATAGATTAAGAGTTGAGG 606
Db 527 CGTGGCCACCGGACCAAGGGGCAATGTTATGATGTTATGATAGATTAAGAGTTGAGG 586
QY 607 AGGCTTCAGTCTGTGTCGACCAAGGCTGAGAGAGACTTTCGAAAGCTCCCTGCTGACACA 666
Db 587 AGGCTTCAGTCTGTGTCGACCAAGGCTGAGAGAGACTTTCGAAAGCTCCCTGCTGACACA 646
QY 667 CCATACCTCAATTTGCTTAAATTTCAAGAGTGGGGCTTGGAGAAAGGTTGGGGTAT 726
Db 647 CCATACCTCAATTTGCTTAAATTTCAAGAGTGGGGCTTGGAGAAAGGTTGGGGTAT 706

QY 727 AAGGACGACATGTTTGGAAATGATTCATCTCCTCTGACATCAATGAGGGCCAGAC 786
Db 707 AAGGACGACATGTTTGGAAATGATTCATCTCCTCTGACATCAATGAGGGCCAGAC 766
QY 787 CCATCACTCAGAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGTGTGTTGAT 846
Db 767 CCATCACTCAGAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGTGTGTTGAT 826
QY 847 TCCCTCATGATATCTTGTGTCAGAGTATGATGATGAGCTTGGCAGACACAGAGAGAG 906
Db 827 TCCCTCATGATATCTTGTGTCAGAGTATGATGATGAGCTTGGCAGACACAGAGAGAG 886
QY 907 ATGCTCTATATCTGACCAAGTCCGTGACCTGAGAAATGAGATGATGCTCCGTTTAAAG 966
Db 887 ATGCTCTATATCTGACCAAGTCCGTGACCTGAGAAATGAGATGATGCTCCGTTTAAAG 946
QY 967 AAGCAAGGCTGATGTTTCCCAAGATTCGATTTACTGGCTGATACAGATGCA 1026
Db 947 AAGCAAGGCTGATGTTTCCCAAGATTCGATTTACTGGCTGATACAGATGCA 1006
QY 1027 AAGGAAACATCATGCAATCGCGCTTGAGAGATTAAGGAAACAGCATATCTTACATA 1086
Db 1007 AAGGAAACATCATGCAATCGCGCTTGAGAGATTAAGGAAACAGCATATCTTACATA 1066
QY 1087 TTAAGAGTCCCTTCAAGAAATGAAATGGGACCTTAAGAAATGAGATTAAGATTTGAT 1146
Db 1067 TTAAGAGTCCCTTCAAGAAATGAAATGGGACCTTAAGAAATGAGATTAAGATTTGAT 1126
QY 1147 GTGAGCATATCTGAAACATTTGCTGAGAGTCTGCTGTAATTTGCTGTAATTA 1206
Db 1127 GTGAGCATATCTGAAACATTTGCTGAGAGTCTGCTGTAATTTGCTGTAATTA 1186
QY 1207 CAAGGATCTCAGACTTCAATATTTGAAATTTGAGATGAGATTTCTTGGGCTCATTTG 1266
Db 1187 CAAGGATCTCAGACTTCAATATTTGAAATTTGAGATGAGATTTCTTGGGCTCATTTG 1246
QY 1267 CTATCTTCAAGATGAGAAATTAACCGCTGAGCACTGCTATGCTGAAAGAGCTAAG 1326
Db 1247 CTATCTTCAAGATGAGAAATTAACCGCTGAGCACTGCTATGCTGAAAGAGCTAAG 1306
QY 1327 TATCAGATTCAGACATATTTTGGAGAAATTTGAGATGAGATTTCTTCTGCGAG 1386
Db 1307 TATCAGATTCAGACATATTTTGGAGAAATTTGAGATGAGATTTCTTCTGCGAG 1366
QY 1387 TTCAGTCTGATATATTTGCTATGACATGCTGATTTTATCATCAACGACATACCA 1446
Db 1367 TTCAGTCTGATATATTTGCTATGACATGCTGATTTTATCATCAACGACATACCA 1426
QY 1447 GAAATGCTGAGAGCAAAATATCTGAGACAGATGAGAGTATGCTGCTTACTCTG 1506
Db 1427 GAAATGCTGAGAGCAAAATATCTGAGACAGATGAGAGTATGCTGCTTACTCTG 1486
QY 1507 CTTGATCTGATACGAGTTGTCATGAGATGATGCTTCTCATCCAAAGTTCAATATGTC 1566
Db 1487 CTTGATCTGATACGAGTTGTCATGAGATGATGCTTCTCATCCAAAGTTCAATATGTC 1546
QY 1567 TCTCTGAGCTGACATGTCATATTACTTTTCAATACAGAGAGGCTCAAGCTCACCC 1626
Db 1547 TCTCTGAGCTGACATGTCATATTACTTTTCAATACAGAGAGGCTCAAGCTCACCC 1606
QY 1627 TCTCTGATAGTTTAAATGCAAAATTTGATTTTATACCGAGGCAAAACATGAAACATTT 1686
Db 1607 TCTCTGATAGTTTAAATGCAAAATTTGATTTTATACCGAGGCAAAACATGAAACATTT 1666
QY 1687 GGGCATCTGATGACCGGTCAGAGCCATCTTCTTCTCATGAGCAAGCTGACAGGATG 1746
Db 1667 GGGCATCTGATGACCGGTCAGAGCCATCTTCTTCTCATGAGCAAGCTGACAGGATG 1726
QY 1747 AAGAACATTAACAGGCTGCTGAGGCTTTTGTATGAGGCTTATGCTGAGGAGACTGCTA 1806
Db 1727 AAGAACATTAACAGGCTGCTGAGGCTTTTGTATGAGGCTTATGCTGAGGAGACTGCTA 1786
QY 1807 AACCTTGCTGCTGTCGCGGATCAATGATGTCAAAGTCCAGAGACAGGGAAGAGATC 1866

|||||
Db 781 TGGGACATCGTGTGATCTTACAGAGATGGGAATTACCCAGGCAACATGGCTCATGCTCT 840
|||
Qy 1314 GGAAGAAACATTAAGTATCCAGATTGACATATTTTGGAGAAATTCGATGGAGTACCA 1373
|||
Db 841 GGAAGAAACATTAAGTATCCAGATTGACATATTTTGGAGAAATTCGATGGAGTACCA 903
|||
Qy 1374 TTTCTCCGCACTGCTGCTGATATATATGCTATGAGCAATGCTGATTTTATCATCAC 1433
|||
Db 931 TTTCTCCGCACTGCTGCTGATATATATGCTATGAGCAATGCTGATTTTATCATCAC 966
|||
Qy 1434 CAGCAATACCAAGAAATGCTGGAGCAAAAATATCTGTTGAGCAATGAGTCAATAC 1493
|||
Db 961 CAGCAATACCAAGAAATGCTGGAGCAAAAATATCTGTTGAGCAATGAGTCAATAC 1020
|||
Qy 1494 TGCCTTACTGCTGCTGCTGATATATGCTGATGCTGATGCTGATGCTGATGCTGAT 1553
|||
Db 1021 TGCCTTACTGCTGCTGCTGATATATGCTGATGCTGATGCTGATGCTGATGCTGAT 1080
|||
Qy 1554 GTTCAATATAGTCTCTCTGAGGCTGACATGTCATATATCTTCCACATACCGAAGGC 1613
|||
Db 1081 GTTCAATATAGTCTCTCTGAGGCTGACATGTCATATATCTTCCACATACCGAAGGC 1140
|||
Qy 1614 CAGGCACTGCTGCTGCTGATATATGCTGATGCTGATGCTGATGCTGATGCTGAT 1673
|||
Db 1141 CAGGCACTGCTGCTGCTGATATATGCTGATGCTGATGCTGATGCTGATGCTGAT 1200
|||
Qy 1674 CGATGACATATGAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1733
|||
Db 1201 CGATGACATATGAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1260
|||
Qy 1734 ACTGCAAGGCTGAGAAACATATACAGGCTGCTGAGAACTTTTGTATGAGTGGTACCT 1793
|||
Db 1261 ACTGCAAGGCTGAGAAACATATACAGGCTGCTGAGAACTTTTGTATGAGTGGTACCT 1320
|||
Qy 1794 GAGGAGCTGCTGATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853
|||
Db 1321 GAGGAGCTGCTGATATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
|||
Qy 1854 CAGGAGAGAGATGCGGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATG 1913
|||
Db 1381 CAGGAGAGAGATGCGGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATG 1440
|||
Qy 1914 CCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1973
|||
Db 1441 CCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
|||
Qy 1974 CTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2033
|||
Db 1501 CTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
|||
Qy 2034 CACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2093
|||
Db 1561 CACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
|||
Qy 2094 AGCTGAGATCATAGAGATGAGGCTGCTGCGGCTTCCACATTTGACCCGTCACCCGAGACA 2153
|||
Db 1621 AGCTGAGATCATAGAGATGAGGCTGCTGCGGCTTCCACATTTGACCCGTCACCCGAGACA 1680
|||
Qy 2154 GCTCTTATATCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2213
|||
Db 1681 GCTCTTATATCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
|||
Qy 2214 GAAATATCTGAGAGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 2273
|||
Db 1741 GAAATATCTGAGAGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 1800
|||
Qy 2274 AGAGAGGCTGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333
|||
Db 1801 AGAGAGGCTGATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
|||
Qy 2334 GAGGCTGAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2393
|||

Db 1861 GAGGCTGAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy 2394 GAGAGCCGTGCTC 2405
Db 1921 GAGAGCCGTGCTC 1932
|||
RESULT 5
US-10-425-114-5285
; Sequence 5285, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5285
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454567_F11
US-10-425-114-5285
Query Match 25.2%; Score 695; DB 13; Length 1340;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1145; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1393 GCTGATATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1452
Db 17 GCTGATATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 76
Qy 1453 GCTGAGCAAAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
Db 77 GCTGAGCAAAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 136
Qy 1513 CTGTAACGAGTGTCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1572
Db 137 CTGTAACGAGTGTCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
Qy 1573 GAGAGTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1632
Db 197 GAGAGTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 256
Qy 1633 CATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
Db 257 CATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
Qy 1693 CTGATGAGCCGTCAGAAAGCCCATCTCTTCCATGAGCAAGCTGCAAGGCTGAGAAAC 1752
Db 317 CTGATGAGCCGTCAGAAAGCCCATCTCTTCCATGAGCAAGCTGCAAGGCTGAGAAAC 376
Qy 1753 ATTAAGAGGCTGCTGAGAGCTTCTGCTGATGAGCAAGCTGCAAGGCTGAGAAAC 1812
Db 377 ATTAAGAGGCTGCTGAGAGCTTCTGCTGATGAGCAAGCTGCAAGGCTGAGAAAC 436
Qy 1813 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1872
Db 437 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
Qy 1873 ATTAAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
Db 497 ATTAAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
Qy 1933 TCTGCCCAAGCAAAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1992
|||

|||||
Db TCTGCCAGACAAAGAGGCCCCGTAACGGCGAGCTCTATCGCTACATGCTATACCAT 616
QY GGTGCTTTCTGACACCGCGCTTGTATGAAAGCTTGGGTCTACCGCTGAGGCAATG 2052
1993
|||||
Db GGTGCTTTCTGACACCGCGCTTGTATGAAAGCTTGGGTCTACCGCTGAGGCAATG 676
QY 2053 ACCTGTGGGCTTCTACTTTCCGACGCTCCATGAGGCTCCAGTGAATCATAGACAT 2112
677 ACCTGTGACATTTCTACTTTCCGACGCTCCATGAGGCTCCAGTGAATCATAGACAT 736
Db 2113 GCGCTCTGCGGCTTCCACATTTGACCCGTAACCCCGAAGAGGCTTTATCTGATGCGC 2172
737 GCGCTCTGCGGCTTCCACATTTGACCCGTAACCCCGAAGAGGCTTTATCTGATGCGC 796
QY 2173 GACTTCTCGACCGGCTGACAGACCCAGATCACTGGGTGAATATCTGAGAGGG 2232
797 GACTTCTCGACCGGCTGACAGACCCAGATCACTGGGTGAATATCTGAGAGGG 856
Db 2233 CTGACGCCATATACGAGAGTACATGGAAGATTAATCTGAGAGGTTGATGACATG 2232
857 CTGACGCCATATACGAGAGTACATGGAAGATTAATCTGAGAGGTTGATGACATG 916
QY 2233 GCGCGGCTCTACGCTTTCTGAAAGTACGTGTGAAAGCTTGAAGGCTGAGAGGCGC 2352
917 GCGCGGCTCTACGCTTTCTGAAAGTACGTGTGAAAGCTTGAAGGCTGAGAGGCGC 976
QY 2353 TACCTTGAGATGTTCTACATACGAGAGTCCGCGAGCTGCGGAGACCGTCCGCTTGA 2412
977 TACCTTGAGATGTTCTACATACGAGAGTCCGCGAGCTGCGGAGACCGTCCGCTTGA 1036
Db 2413 ATTGACCAACCGCAGTAGCTTCCGCACTGCGACTGCGTAGCACTTGTATCAAGACTGA 2472
1037 ATTGACCAACCGCAGTAGCTTCCGCACTGCGACTGCGTAGCACTTGTATCAAGACTGA 1096
QY 2473 ACCTGAGGACCTTCAATATTTAGCGCGGCGAGACGTGATGCAATTAATGTCCGGAG 2532
1097 ACCTGAGGACCTTCAATATTTAGCGCGGCGAGACGTGATGCAATTAATGTCCGGAG 1156
Db 2533 CTGAACTGCTTTT 2546
QY 1157 CTGAACTGCTTTT 1170
Db

RESULT 6

US-09-237-183A-1015
; Sequence 1015, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 1015
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-1015

Query Match 10.1%; Score 278; DB 10; Length 428;
Best Local Similarity 99.7%; Pred. No. 5.1e-133;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2218 AATTCGAGAGCGGCTGACGCGCATATACGAGAGTACATGAGATATCTGAGAG 2277
Db 63 AATTCGAGAGCGGCTGACGCGCATATACGAGAGTACATGAGATATCTGAGAG 122

QY 2278 AGTTGATACACTGCGCGGCTTCTACCGTTTCTGAAATAGTGTGAAAGCTTCGAGAG 2337
Db 123 AGTTGATACACTGCGCGGCTTCTACCGTTTCTGAAATAGTGTGAAAGCTTCGAGAG 182
QY 2338 CTGAGAGAGCGGCTTACCTTGAAGATTTCTCATATACATGAAAGTCCGCGAGCTGGCGAG 2397
Db 183 CTGAGAGAGCGGCTTACCTTGAAGATTTCTCATATACATGAAAGTCCGCGAGCTGGCGAG 242
QY 2398 ACCGTGCGCTTGAATTAACCAACCGCAGTAGCTTGCACCACTGCGACTGCTAGCACT 2457
243 ACCGTGCGCTTGAATTAACCAACCGCAGTAGCTTGCACCACTGCGACTGCTAGCACT 302
Db 2458 TGGTACAGAGCTGAAAACCTGAAAGACCTTCAATTTAGGCGCGGCAAGCGTATGCA 2517
303 TGGTACAGAGCTGAAAACCTGAAAGACCTTCAATTTAGGCGCGGCAAGCGTATGCA 362
QY 2518 TAAATGTCGCGAGAGCTGAACTGCTTTT 2546
Db 363 TAAATGTCGCGAGCTGAACTGCTTTT 391

RESULT 7

US-09-237-183A-533
; Sequence 533, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 533
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-533

Query Match 9.2%; Score 255; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1761 GCTGTGCAAGCTTTGCTTAAGTGGCTTAAGCTGAGGAGCTGGTAAACCTTGTGCTG 1820
Db 1 1 GCTGTGCAAGCTTTGCTTAAGTGGCTTAAGCTGAGGAGCTGGTAAACCTTGTGCTG 60
QY 1821 TGCCTGGTATCATGATGTCAACAAGTCCAGAGACAGGAGAGATGCGAGATAGAGA 1880
Db 61 TGCCTGGTATCATGATGTCAACAAGTCCAGAGACAGGAGAGATGCGAGATAGAGA 120
QY 1881 GATGATGAATCTATCAAGACCAACTTGTGGGCACTTCCGCTGATCTTGTGCCA 1940
Db 121 GATGATGAATCTATCAAGACCAACTTGTGGGCACTTCCGCTGATCTTGTGCCA 180
QY 1941 GACAAACAGGCGCGTAAAGCGGAGCTTATGCTATCATGAGATGCAATGCTGCTT 2000
Db 181 GACAAACAGGCGCGTAAAGCGGAGCTTATGCTATCATGAGATGCAATGCTGCTT 240
QY 2001 CGTACAGCGGCTT 2015
Db 241 CGTACAGCGGCTT 255

RESULT 8

US-10-080-114A-13
; Sequence 13, Application US/10080114A
; Publication No. US20030005482A1


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GENERAL INFORMATION:
APPLICANT: Dhingra, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080,114A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/270,777
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 347
TYPE: DNA
ORGANISM: Sorghum proproquum
US-10-080-114a-13

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Query Match
Best Local Similarity 100.0%; Score 246; DB 15; Length 347;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTCTCCCGGAGCTGAAACCGCAAGCGCATCCGGACCGGCTCGAGAACCTTC 60
DB 102 ATGCTCTCCCGGAGCTGAAACCGCAAGCGCATCCGGACCGGCTCGAGAACCTTC 161
QY 61 CAGCGGACCGGCAACGAGCTGTCGCTCTCTCTCAAGTACGTGAACAAGGGAGAGG 120
DB 162 CAGCGGACCGGCAACGAGCTGTCGCTCTCTCTCAAGTACGTGAACAAGGGAGAGG 221
QY 121 ATCTGAGCGCGCAACCAATCTTGAAGCGCTGACGAGGTCCAGGGCTCCGGCTCCG 180
DB 222 ATCTGAGCGCGCAACCAATCTTGAAGCGCTGACGAGGTCCAGGGCTCCGGCTCCG 281
QY 181 GCGCTCGCGGAGGAGACCTTCTCTGAGCTCTCGGCTTCGGCGAGGAGGCGATGTGCTG 240
DB 282 GCGCTCGCGGAGGAGACCTTCTCTGAGCTCTCGGCTTCGGCGAGGAGGCGATGTGCTG 341
QY 241 CCGCGG 246
DB 342 CCGCGG 347

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RESULT 9
US-09-237-183A-526
Sequence 526, Application US/09237183A
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 526
LENGTH: 283
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-526

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Query Match
Best Local Similarity 100.0%; Score 209; DB 10; Length 283;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1549 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTTCACATACCGAG 1608
DB 9 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTTCACATACCGAG 68
QY 1609 AAGGCAAGCACTCACTCTCTTCAATGATGCAATGAAAAATTGATTTATATACCGAG 1668

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DB 69 AAGGCAAGCACTCACTCTCTTCAATGATGCAATGAAAAATTGATTTATATACCGAG 128
QY 1669 CAAAGCATTAACATTTGGGCACTCTGATGACCGGCAAGCCCATCTCTTCATG 1728
DB 129 CAAAGCATTAACATTTGGGCACTCTGATGACCGGCAAGCCCATCTCTTCATG 188
QY 1729 GCAAGCTGACAGGAGTGAACATTAAC 1757
DB 189 GCAAGCTGACAGGAGTGAACATTAAC 217

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RESULT 10
US-09-237-183A-513
Sequence 513, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 513
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-513

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Query Match
Best Local Similarity 100.0%; Score 159; DB 10; Length 285;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1857 GAAAGATCCGCGAGATGAGAGATGATGAACTCATCAAGACCCCACTTGTTCG 1916
DB 1 GAAAGATCCGCGAGATGAGAGATGATGAACTCATCAAGACCCCACTTGTTCG 60
QY 1917 GCAAGTCCGCTGATCTCTGCGGACCAACAGGGCCCGGTAAAGGCTTATGCTA 1976
DB 61 GCAAGTCCGCTGATCTCTGCGGACCAACAGGGCCCGGTAAAGGCTTATGCTA 120
QY 1977 CATGCTGATTAACCATGCTGCTTTCGTCACAGCCGACCTT 2015
DB 121 CATGCTGATTAACCATGCTGCTTTCGTCACAGCCGACCTT 159

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RESULT 11
US-09-237-183A-516
Sequence 516, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 516
LENGTH: 297
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-516

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Query Match          5.7%; Score 158; DB 10; Length 297;
Best Local Similarity 99.2%; Pred. No. 8,2e-71;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1122 TAAGAAATGATATCAAGATTGATGTGGCCATATCTGGAAACATTGCTGAGATGC 1181
DB 2 TAAGAAATGATATCAAGATTGATGTGGCCATATCTGGAAACATTGCTGAGATGC 61

QY 1182 TGCTGTGAATTTGCTGGCAATTAAGAATCTCAGACTTCATTAATGGAACTACAG 1241
DB 62 TGCTGTGAATTTGCTGGCAATTAAGAATCTCAGACTTCATTAATGGAACTACAG 121

QY 1242 TGATGAATATCTTGGGCTCATGCTATCTTAACAAGATGGAAATTAACCACTGCAACAT 1301
DB 122 TGATGAATATCTTGGGCTCATGCTATCTTAACAAGATGGAAATTAACCACTGCAACAT 181

QY 1302 TGCTCATGCTCTGGAAGAAAGACTTAAGTATCCAGATTGACATATTTTGGAAATTTGCA 1361
DB 182 TGCTCATGCTCTGGAAGAAAGACTTAAGTATCCAGATTGACATATTTTGGAAATTTGCA 241

QY 1362 TGAGAAATACCATTTCTCTCT 1381
DB 242 TGAGAAATACCATTTCTCTCT 261

RESULT 12
US-09-237-183A-527
; Sequence 527, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 527
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-527

Query Match          5.4%; Score 150; DB 10; Length 150;
Best Local Similarity 100.0%; Pred. No. 1,2e-66;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 ACCGATGTCATCGGATGAGTCTTCATCCAAAGTTCAATATAGTCTCTCGGAG 1576
DB 1 ACCGATGTCATCGGATGAGTCTTCATCCAAAGTTCAATATAGTCTCTCGGAG 60

QY 1577 CTGACATGTCATATCTTCCACATACCGAAGGCCAAGCGACTACCTCTCTCAAG 1636
DB 61 CTGACATGTCATATCTTCCACATACCGAAGGCCAAGCGACTACCTCTCTCTCAAG 126

QY 1637 GTTCAATCGAAATTTGATTTATGACCCCG 1666
DB 121 GTTCAATCGAAATTTGATTTATGACCCCG 150

RESULT 13
US-09-237-183A-1018
; Sequence 1018, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The

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; TITLE OF INVENTION: Sucrose Pathway
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 1018
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(411)
; OTHER INFORMATION: unsure at all n locations
US-09-237-183A-1018

Query Match          5.2%; Score 143; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 4,8e-63;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 GGGCTGATCGAAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAACTTGTCTC 1818
DB 88 GGGCTGATCGAAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAACTTGTCTC 147

QY 1819 GTTCCGGGTGACATATGATGTCACACAGTCCACAGGACAGGATCGGGAGATGAG 1878
DB 148 GTTCCGGGTGACATATGATGTCACACAGTCCACAGGACAGGATCGGGAGATGAG 207

QY 1879 AAGATGATGATCACTCATCAAGAC 1501
DB 208 AAGATGATGATCACTCATCAAGAC 230

RESULT 14
US-09-237-183A-528
; Sequence 528, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 528
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-528

Query Match          4.9%; Score 134; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 2,3e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 ATGATAGAAATCAAAAGCTTGGGAGGCTTGAAGTGTGCTGACCAAGCTGAGAGCACT 643
DB 110 ATGATAGAAATCAAAAGCTTGGGAGGCTTGAAGTGTGCTGACCAAGCTGAGAGCACT 169

QY 644 TGTCAAAGCTCCCTGCTGACACACCATATCTCAATTTGCTATTAATTTCAAGAGTGG 703
DB 170 TGTCAAAGCTCCCTGCTGACACACCATATCTCAATTTGCTATTAATTTCAAGAGTGG 229

QY 704 GCTTGAGAAAGCT 717
DB 230 GCTTGAGAAAGCT 243

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RESULT 15
US-09-237-183A-524
; Sequence 524; Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 524
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-524

Query Match 4.7%; Score 130; DB 10; Length 181;
Best Local Similarity 99.4%; Pred. No. 2.7e-56;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1408 ATGAACATGCTGATTATCATCCAGACATACCAAGAAATGCTGAAAGCAAAAT 1467
DB 1 ATGAACATGCTGATTATCATCCAGACATACCAAGAAATGCTGAAAGCAAAAT 60
QY 1468 ACTGTTGACAGTATGAGAGTCATACGCTTTACTGCTGCTGTGTGACCGAGTTGTC 1527
DB 61 ACTGTTGACAGTATGAGAGTCATACGCTTTACTGCTGCTGTGTGACCGAGTTGTC 120
QY 1528 CATGGATGATGCTTGTGATCCAAAGTTCAATATAGTCTCTCGAGCTGACATGTCC 1587
DB 121 CATGGATGATGCTTGTGATCCAAAGTTCAATATAGTCTCTCGAGCTGACATGTCC 180
QY 1588 A 1588
DB 181 A 181

Search completed: May 26, 2004, 13:23:01
Job time : 978.542 secs

INDIVIDUAL ISOLATE: Saccharosynhase
IMMEDIATE SOURCE:
LIBRARY: phage lambda zap
FEATURE:
NAME/KEY: CDS
LOCATION: 3..2303
US-08-553-436A-7

Query Match 43.0% Score 1177.8; DB 2; Length 2563;
Bseq Local Similarity 70.9% Pred. No. 2.2e-295;
Matches 1592; Conservative 0; Mismatches 647; Indels 6; Gaps 2;

164 CTAGCCGAGGAGACCTTCTCTGACGCTCTCCGCTCCGCGACAGAGCGATCGCTGCGG 223
21 CTAGCGATGAGCCGCTTAGGAGATTTCTAGAGCTGCGTCAAGAGGACATAGTGTCTCT 80
224 CCGTTCGTCGATCGCGGTGCGCCCGGCGCCGAGATTGGAGATGAGTCCGCTCAAC 283
81 CCGTTGTGCTATAGCAGTCCGTCCAGACCTGAGATTGGAAATATGTTGTATAT 140
284 GTTCACGAGCTCAGGCTGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAGAG 343
141 GTCTGTGACTGATGATGAGAGAGCTTACTGTGTGAGTATCTTCATTTCAAGAGAG 200
344 CTGTGAGAGCGCCAGACAGATATCCCTAGCTTCTGAGCTTGACTTGCAGCCGTTCA 403
201 CTGTGATGAGAAAGGCTGATGACCATATGCTTGAAGCTTGAATTCAGAGCTTTAT 260
404 GTCTGAGTCCAGCGCCAAATGCTGTCTATCTATTGAAACGGTGTAGTCTCCAG 463
261 GAATAGTTCACGTCACGCTCTTCTCATATGATGATGATGATGATGATGATGATG 320
464 CGACCTTGTCTCTCATATGTTCCGCAACAGGATGCTTGGAGCCCTGTGATTTTC 523
321 CGGACCTGTCTCATAGATGTTCTGCAACAAAGATGCTTGGAGCCGTTACTGATTT 383
524 CTCCGTGCGCACCGGACAGAGGAGGATGTTATGATGCTTAAATGATGATGATGAT 583
381 CTTAAGTGCACAAACATTAAGAGATGTTGATGATGATGATGATGATGATGATGAT 440
584 GGGAGGCTTCAATCTGTCTGACCAAGCTGAGAGAGCTTGTCAAGCTCCCTGTGAC 643
441 CAGGCTTCTCACTGCTGATTTCTAAAGCTGAGATTTCTTAATCAACTCTCCAGAG 500
644 ACACCACTCACAATTTGCTTAAATTTCAAGAGTGGGCTGAGAGAAAGGTTGGGT 703
501 ACACCTTACTTGAATTTGATTTGATTCAGAGATGATGATGATGATGATGATGATG 560
704 GATACGAGAGACATGTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 763
561 GATACGCTGAGAAAGGTTCTAGAAATGATGATGATGATGATGATGATGATGATGAT 623
764 GACCCATCTACCCCTAGAGAAATTTCTGGGAGAGATCCCATGATTTTAAAGTGTG 823
823 GATCGCTTCACTTGAAGACATTTCTGGAGAGCTTCCATGATGATTTATGTTGAT 880
824 GTATCCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 883
681 TGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 740
884 CAGATGCTTATATCTGAGACAGAGTCCGTGCACTAGAAATGATGATGATGATGAT 943
741 CAGATGCTTATATCTGAGACAGAGTCCGTGCACTAGAAATGATGATGATGATGAT 803
944 AAGAAACAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
801 AAGAAACAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
1004 GCAAAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
861 GCAAAAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
1064 ATTTATGAGGTTCCCTTCAAGAAATGAAATGAGATCTTAAAGAAATGATGATGAT 1123

921 ATCTGAGAGTTCCTTTCCGATCAGAGAAAGAAATCTCCGAAATGATGATGATGAT 980
1124 GATGTGCGCAATCTGAGAAACATTTGCTGAGAGTCTGTGAAATTCGCTGAA 1183
981 GATGATGCGCTTATTTAGAGCTTCACTGAGATGAGTGTGAAATTTATGGCAG 1040
1184 TTACAGGATCTCCAGCTTCTATATTTGAAACCTACATGATGAGAAATCTTGTG 1243
1041 TTGAGGCTGCTGAGATCTGATATTTGCACTACAGAGATGAGAAATGATGATGAT 1100
1244 TTGCTATCTTCAAGATGAGAAATTTACCGAGTCACTTGTGATGCTTGGAAAG 1303
1101 TTATGCTCCAGAAATGAGTGTCAACGAGCAATATGACCATGATGAGAAAG 1160
1304 AAGTATCCAGATTCAGACATATTTTGAAGATTTGATGAGAAATGATGATGATGAT 1363
1161 AAGTATCCAGATTCAGACATATTTTGAAGATTTGATGAGAAATGATGATGATGAT 1220
1364 CAGTCACTGCTGATATATTTGCTATATGAAATGCTGATTTATCATGACGACAT 1423
1221 CAATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1280
1424 CAGAAATTTGCTGAGAGCAAAATCTGTTGACAGATGAGAGTCACTGCTTACT 1483
1281 CAGAGATGCTGAGAGAGAGATACGTTGTGATATGAAAGCATTAGGCTTACT 1340
1484 CTGCTGCTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1543
1341 TTTCGAGGCTGATATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1400
1544 GTCTCTCTGAGCTGACATGTCATATCTTTCCATACAGAGAG--GCCAGCA 1600
1401 GTCTGCGCAGGCGACAGATGCGCATCTTCCATTTCCAGAGAGAGATGATGATGAT 1460
1601 CTACCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660
1461 CTACCTGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1520
1521 CACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
1721 AAGGTAAGAAATTAACAGGCTGCTGAAAGCTTGTGATGATGATGATGATGATGAT 1780
1581 CGTGTGAAATTAACAGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1640
1781 CTGTTAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1840
1641 CTGCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1700
1841 GAGATGCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
1701 GAATTTGCGAAATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1760
1901 TTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1960
1761 TTTCGCTGATGCTTCTCAACAACTGATGATGATGATGATGATGATGATGATGATGAT 1820
1961 GCTGATACCATGCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2020
1821 TGTGACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1880
2021 GTTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2080
1881 GTTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1940
2081 ATCATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2140
1941 ATTTATGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
2141 ATCTGATGCGCATCTTCTTCAAGGCTGAGAGCAAGCATGATGATGATGATGATGAT 2200

Db 2201 AA---AATGACTGAATCTTTGTCAAGTGACAGAGAGATCCAACTACTGACCTAAATTC 2057
 QY 2201 TCTGAGAGAGGCTGACAGGATATACAGAGATACATGAGAGATATCTCAGAGAG 2260
 Db 2058 TCTGAGAGAGGCTTCTAAGATCAAGAGATATCTCTGCAAAATATGCTCTAACTAGAGAGAG 2117
 QY 2261 TTGATGACACTGACGCGGCTTACGCTTCTGGAAGTACGTGTGAAAGCTGAGAGGCTG 2320
 Db 2118 TTAAAGATATGAGAGAGGCTGATGCTTCTGAAATATGCTCTAACTAGAGAGAGAG 2177
 QY 2321 GAGAGAGGCTTACCTTGAAGATTTCTACATCTGAGAGTCCGAGAGCTGCGAGAGAGC 2380
 Db 2178 GAGAGACACCTTATCTTGAAGATTTCTCAATTTGAAAGTCCGATCTGCGCACTT 2237
 QY 2381 GTCGCGCTTGAATGACCAACGC 2405
 Db 2238 GTTCGCTGACCAAGATGAGAGC 2262

RESULT 2

US-09-598-401C-57
 / Sequence 57, Application US/09598401C
 / Patent No. 6596925
 / GENERAL INFORMATION:
 / APPLICANT: Perera, J. Ranjan
 / APPLICANT: Eagleton, Clare
 / APPLICANT: Rice, Stephen J.
 / TITLE OF INVENTION: Compositions and Methods for the
 / FILE REFERENCE: 11000.10362
 / CURRENT FILING DATE: 2000-06-20
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,539
 / PRIOR FILING DATE: 1999-03-25
 / NUMBER OF SEQ ID NOS: 120
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO: 57
 / LENGTH: 3103
 / TYPE: DNA
 / ORGANISM: Eucalyptus grandis
 US-09-598-401C-57

Query Match 41.0%; Score 1123; DB 4; Length 3103;
 Best Local Similarity 67.0%; Pred. No. 4e-281;
 Matches 1610; Conservative 0; Mismatches 790; Indels 3; Gaps 1;

QY 5 ACCCAAGCGCTCCGCGAGCGCTGAGAGACACCTTCACGCGAGCAAGAGCTGCTC 64
 Db 471 AGCCACAGCGCTTGCAGAGCTTTGAGAGAGACCTCTCTGCTCAACGCAACGATTTG 530
 QY 65 GCGCTCTCTCAAGTACGTGAACAAAGGAGGAGGATCTGCAAGCGCAACATCTC 124
 Db 531 GCGTCTCTTCAAGGCTTGAAGCCAAAGGCAAGGATCTTGAAGCGCAACGATTTT 530
 QY 125 GAGCGCTGAGAGAGTCTCAAGGCTCCGCGGCGCGCGCTAGCCAGAGGAGACCTTCTC 184
 Db 591 GCTGAATTTGAGGCTCTCTGAGAGAGAGCAAGCAAGGCTCTTGAATGAGGCTTTG 650
 QY 185 GAGCTCTCTCGCTCCGCGAGAGAGGAGATGCTGCTCCGCGCTTCTGCTGCTGCTG 244
 Db 651 GAGATCTCTCAATCTCACTGAGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTG 710
 QY 245 GCGCGCGCGCGAGGCTTTGAGAGTACGCTCCGCTCAAGTTCAGAGAGCTCAGCTGAG 304
 Db 711 GCTCCAAAGCGCGCGCTGCTGAGAGCAATCTGCTGAGAGCTTCATGAGGCTTTGAG 770
 QY 305 GAGCTCAAGCTCTCGAGAGTACCTCCGCTTCAAGAGAGAGCTTGTGAGAGCGCAAG 364
 Db 771 CAATGAGAGTGTCTGAGTATCTGCACTTCAAGAGAGGCTTGTCTGATGAGAGTGAAT 830

QY 365 GATCCCTAGCTTCTGAGCTTGAATTCGAGCCCTTCAATGTCTAGTCCCAAGCCCAAT 424
 Db 831 GGTAACTTGTCTGAGCTTGAATTCGAGCCCTTCAATGTCTAGTCCCAAGCCCAAT 890
 QY 425 CGGTATATCTATTTGAGAAAGGCTGCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCT 484
 Db 891 CTTTCAAGCTTATTTGAGAAAGGCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCT 950
 QY 485 TTCCGCAAGAGGATTTGAGAGGCTTGTGATTTCTCCGCTGAGAGAGAGAGAG 544
 Db 951 TTCCATGAGAGAGAAAGCTTGAACCTCTGCTGATTTCTCCAGAGAGAGAGAG 1010
 QY 545 GCGCATGTTATGAGCTTATATGAGAGATGAGAGAGCTTGGAGAGCTTCAAGTGTGCTG 604
 Db 1011 GCGAAGAGATGAGTGAATGAGAGATGAGAGAGCTTCCCTCCAGAGAGAGAG 1070
 QY 605 ACCAAGCTGAGAGAGAGCTTGTCAAGGCTTCCGCTGAGAGAGAGAGAGAGAGAG 664
 Db 1071 AGAAGAGAGAGAGAGATGAGCTTGAACCTCTGAGAGAGAGAGAGAGAGAGAGAG 1130
 QY 665 TATTAATTTCAAG 724
 Db 1131 CACAAGTTCAG 1190
 QY 725 GAAATATCTATCTCTTCTGAGAGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 784
 Db 1191 GAGATATCTATCTCTTCTGAGAGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1250
 QY 785 TTCTGAG 844
 Db 1251 TTCTGAG 1310
 QY 845 GGTCAAGCTATATGATTAAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
 Db 1311 GGTCAAG 1370
 QY 905 CAAAGCTGAG 964
 Db 1371 CAAAGCTGAG 1430
 QY 965 TCCCAAG 1024
 Db 1431 ACTCTGAG 1490
 QY 1025 CAGCGCTTGAAG 1084
 Db 1491 CAGCGCTTGAAG 1550
 QY 1085 AATGAG 1144
 Db 1551 AATGAG 1610
 QY 1145 ACATTTGAG 1204
 Db 1611 AGATACATGAG 1670
 QY 1205 ATAAATGAG 1264
 Db 1671 ATCAATGAG 1730
 QY 1265 ATTAACAG 1324
 Db 1731 GTTACAG 1790
 QY 1325 TTTTGAAG 1384
 Db 1791 TACTGAG 1850
 QY 1385 GCTATGAACAG 1444
 Db 1851 GCTATGAACAG 1910

Db 180 CCTGCTGACACACACTACTACAACTTGTATTAATTAAGAGTGCGGC--TGAGCA 237
Qy 694 AGTTGGGGTATACAGAGGACATGTT 721
Db 238 AAGTGGGGTATACAGAGGACATGTT 265

RESULT 5
US-08-483-376-1
Sequence 1, Application US/08483376
Patent No. 5955330
GENERAL INFORMATION:
APPLICANT: Vasil, Vimala
APPLICANT: Clancy, Maureen A.
APPLICANT: Ferl, Robert J.
APPLICANT: Vasil, Indra K.
APPLICANT: Hannah, L. C.
TITLE OF INVENTION: No. 5955330a1 Means for Enhancing Gene
TITLE OF INVENTION: Expression
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,540
FILING DATE: 07-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,115
FILING DATE: 04-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/830,956
FILING DATE: 05-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,854
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fether, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 10-94B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6386 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
STRAIN: Black Sweet
FEATURE:
NAME/KEY: exon
LOCATION: 131..182
FEATURE:
NAME/KEY: exon

LOCATION: 1211..1324
FEATURE:
NAME/KEY: exon
LOCATION: 1828..1948
FEATURE:
NAME/KEY: exon
LOCATION: 2041..2187
FEATURE:
NAME/KEY: exon
LOCATION: 2269..2460
FEATURE:
NAME/KEY: exon
LOCATION: 2605..2728
FEATURE:
NAME/KEY: exon
LOCATION: 2822..3038
FEATURE:
NAME/KEY: exon
LOCATION: 3236..3351
FEATURE:
NAME/KEY: exon
LOCATION: 3447..3620
FEATURE:
NAME/KEY: exon
LOCATION: 3702..3818
FEATURE:
NAME/KEY: exon
LOCATION: 3912..4078
FEATURE:
NAME/KEY: exon
LOCATION: 4158..4381
FEATURE:
NAME/KEY: exon
LOCATION: 4517..4835
FEATURE:
NAME/KEY: exon
LOCATION: 4768..5212
FEATURE:
NAME/KEY: exon
LOCATION: 5372..5510
FEATURE:
NAME/KEY: exon
LOCATION: 5636..5917
US-08-483-376-1

Query Match 5.7%; Score .55; DB 2; Length 6386;
Best Local Similarity 70.5%; Pred. No. 6-9e-30;
Matches 222; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

Qy 1673 CTGATGACCGGTCAAGCCCATCTCTTTCATGCGCAAGACTGACAGGGTGAAGAC 1732
Db 4524 CTGAAGGACAGAAAGAGCCGATCATCTTCGATGGCGCGCTCGACCGGTGAAGAC 4583
Qy 1733 ATTAAGGGCTGTGCGAGCTTTTGCCTAAGTGGCTAGCTGAGGAGGCTGTAACCTT 1792
Db 4584 ATGACAGGCTGTGCGATGATGATGACGCAAGACGGCGCTTGAAGGAGCTGCGAACCCTC 4643
Qy 1793 GTGCTGTGCGGTACATGATGATGATCAAGATGCAAGAGCAAGGAGAGATGCGGAG 1852
Db 4644 GTGATGCTGCGGTGAC---CAGGCAAGAGATCCAGGACAGGAGGAGCGGAG 4700
Qy 1853 ATAGAGAGATGATGAACTCATCAAGCCCAACTTGTGGGAGAGTTCGCTGATC 1912
Db 4701 TTCAAGAGATGACGCTCATTCAGCAGATGCAAGTGAAGGCGCATATTCGGTGAATC 4760
Qy 1913 TCTGCCAGACAAACAGGGCCGTAACGGAGCTCTATCGTACATCGCTGACACCCAT 1972
Db 4761 TCGGCGAGATGACCGGCTCGCAACGGGAGCTGTACCGCTACATTCGATGAGAG 4820
Qy 1973 GATGCTTGTGACAG 1987
Db 4821 GGCGCATGTCAG 4835

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RESULT 6
US-09-598-401C-56
; Sequence 56, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Bagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.10362
; CURRENT APPLICATION NUMBER: US/09/598,401C
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-598-401C-56

Query Match          4.9%; Score 134; DB 4; Length 532;
Best Local Similarity 61.4%; Pred. No. 56-25;
Matches 215; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 5 ACCACGGCTCCGCGAGCGCTCGAGACACCTCTCAAGCGCAGCGAAGCTCTGC 64
DB 182 AGCCACAGCCTTCGGAGAGGTTTGACAGACGACCTCTCTGCTACCGCAGCATATTG 241
QY 65 GCCCTCTGTCAGTACGTAAACAGGAGGAGCATCTCTGACCGCAGCATCTCTC 124
DB 242 GCTTCTCTTCAAGGTTGAGAACCAAGGAGGATCTTTCAGGCGCAGCATTTT 301
QY 125 GACGGCTCGAGAGGTTCAGAGGCTCCGCGCGCGCGCTGACGAGGAGCATCTCTC 184
DB 302 GCTGAGTTGAGGCACTCTGAGAGAGACAGCAAGCTTCTTATGAGGCTTTTGT 361
QY 362 GAGTCTCTCCGCTCCGCGAGAGGAGCATCTCTGCGCGCTCTGCGCATCGCGGTG 244
DB 362 GAGTCTCTTAATTCATCAGAGAGGAGTGTGTGCTGCTCATGAGGTTGCTTGTG 421
QY 245 GCGCCGCGCGCGAGGAGTGTGAGATGTCGCGCTCAAGCTTCAAGAGCTCAGCGT 304
DB 422 CGTCCAGAGCGCGGCTGTGAGAGCAGATCCGTGTGAAGTCATCGCTTGTGTGAG 481
QY 305 GAGCTCAGCTCTCGAGTACCTCCGCTTCAAGAGAGAGGCTTGTGAGCG 354
DB 482 CAATTGAGAGTGTGATGATCTGCACTTCAAGAGAGAGCTTGTATG 531

RESULT 7
US-09-313-294A-1221
; Sequence 1221, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1221
; LENGTH: 272
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TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No. 6476212 700550572H1
US-09-313-294A-1221

Query Match          4.3%; Score 117.2; DB 4; Length 272;
Best Local Similarity 67.0%; Pred. No. 7.9e-21;
Matches 181; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 1446 ATACTGTGACAGATGAGATCATCTACTGCTTACTCTGCTGTGTAACCGATG 1505
DB 4 ACACGCTGGCGAGTACAGTCCCATCGCTTACTCTTCTGCGCTCTACCGGTG 63
QY 1506 TCCATGAGATGATGTCCTGATCCAAAGTTCATATATGCTCTCTGAGCTGATG 1565
DB 64 TCCATGAGATGATGTCCTGATCCAAAGTTCATATATGCTCTCTGAGCGATG 123
QY 1566 CCATATCTTTCATATACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1625
DB 124 GTGTTACTACCGGTATAGGA-AAAGACAGAGAGGAGGAGGAGGAGGAGGAGG 182
QY 1626 AAAATTGATTTATGACCGGAGCAAAACGATGAAACATTTGAGGAGGAGGAGG 1685
DB 183 AGAGCTCATCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 242
QY 1686 CAAGCGCATCTCTTCTCATGCGAAGC 1715
DB 243 AGAGCGCATCTCTTCTCATGCGCGCTC 272

RESULT 8
US-09-313-294A-1826
; Sequence 1826, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1826
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incycle ID No. 6476212 700551585H1
US-09-313-294A-1826

Query Match          4.1%; Score 111.8; DB 4; Length 271;
Best Local Similarity 65.7%; Pred. No. 2e-19;
Matches 175; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 869 CAGACAGAGAGAGAGATCTCTATATAGTACAGGAGGAGGAGGAGGAGGAGG 928
DB 2 CTTGACAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 61
QY 929 ATGCTTCCGTTTAAAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 988
DB 62 ATGCTTCCGTTTAAAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 121
QY 989 CGGCTGATACAGATGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1048
DB 122 AGGTTGCTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 181
QY 1049 ACAGAGATCTTATATATAGAGTCCCTTGAGAAATGAGGAGATCTTAAAGAA 1108
```

Db 182 AC-CGGCAGCTGCGATATCTTCGCGTCCATTCGAGAACAGAAAAGGAAATCGTTCGCAAG 240
QY 1109 TGGATATCAAGATTGATGTGGCCATATC 1139
Db 241 TGGATCTCGGATTGAAAGTGGCCGTAAC 271

RESULT 9
US-08-175-471-6

Sequence 6, Application US/08175471
Patent No. 565892
GENERAL INFORMATION:
APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J.M.
APPLICANT: Voelker, T.
TITLE OF INVENTION: Sucrose Phosphate Synthase (SPS), Its
TITLE OF INVENTION: Process for Preparation, Its CDNA, and Utilization of CDNA TO
TITLE OF INVENTION: Modify The Expression Of SPS In The Plant Cells
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,471
FILING DATE: 27-DEC-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/672,646
FILING DATE: 18 MAR 1991
APPLICATION NUMBER: EP 90402084.9
FILING DATE: 20 JUL 1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 72-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-08-175-471-6

Query Match 3.3%; Score 89.8; DB 1; Length 3509;
Best Local Similarity 51.0%; Pred. No. 4,1e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 1658 GAACACATTTGGGATCTGATGACCGGTCAAGCCCATCTCTTCATCGCAGAGACTC 1717
Db 1543 GAGAGTAGCGGCTTCTGACCACTTCAAGCCGATCTCTGCGTTATCAAGACCA 1602
QY 1718 GACAGGTTGAGACATTAACAGGCTGTGCAAGCTTTTCTTAAGTGGCTTAAGCTGAAG 1777
Db 1603 GACCCGAGAGAACATCACTACCTCTGCAAGCGTTTGAGAGGTGTGTCACATCAAG 1652
QY 1778 GAGCTGTAACTTGTCTGCTTCGCGGCTCAATGATGTAACAAGTCCAGGACAG 1837

Db 1663 GAATTCGAAACCTTACTCTGATCATGCGTAAAGAGATGATGATGACATGATCTGCT 1722
QY 1838 GAAGAGATCCGGAGATGAGAAAGATGCAATGATCTCAAGACCCCACTTTTCGGG 1897
Db 1723 GGCAATGCCAGTGTCTTACACACAGTTCTGAAGCTGAATGCAAGTATGATCTTAAGG- 1781
QY 1898 CAGTTCCGCTGATCTCTGCGCCAGCAAAACAGGCGCCGTAAAGGCGAGCTTATGCTAC 1957
Db 1782 --AAGCGTGGGCTTCCATACATGATCAATAGGCTGACGTCGGGATATTAAGCTTC 1839
QY 1958 ATCGCTATACCCATGATGCTGCTTTCGTAACGCGGCTTGAATGAAGCGTTGCTACCC 2017
Db 1840 GCGGCCAAATGAAGGCGCTTTCATCAACCTCTCTCGTTGAGCGGTTGATCTACCC 1899
QY 2018 GTCTGAGGCGCATACCTGTGAGCTTCTACTTTCCGAGGCTCCCATGAGAGTTCAGCT 2077
Db 1900 CTGATCAGGCTGCGGACACAGGACTCCGATAGTGTCTTACCAAGAAATGATGTCGGTTC 1959
QY 2078 GAGATCATAGCATGGGCTGCGGCTTCACATTAACCCGTACACC 2126
Db 1960 GACATTAACAATGATTAACAACGAGACTGCTGCTTGAACCCACAGACT 2008

RESULT 10

US-08-718-777-6
Sequence 6, Application US/08718777
Patent No. 5981852

GENERAL INFORMATION:
APPLICANT: Van Assche, C.
APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.
APPLICANT: Voelker, T.
APPLICANT: Gervais, M.
TITLE OF INVENTION: MODIFICATION OF SUCROSE
TITLE OF INVENTION: PHOSPHATE
TITLE OF INVENTION: SYNTHASE IN PLANTS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Law Offices of Barbara Rae-Venter
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3c
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter

REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 3509 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 112..3315

US-08-718-777-6

Query Match 3.3%; Score 89.8; DB 2; Length 3509;
Best Local Similarity 51.0%; Pred. No. 4.1e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1558 GAACACATTGGGACATCTGATGACCGGTCAAAAGCCCATCTCTTCTCCATGGCAAGACTC 1717
1543 GAAGTAGATGCGGTCTCTGACCAACCTCTCAAGCCCATATCTGCGGTATCCAGACCA 1602
1718 GACAGGATGAAGACATTAACAGGCGTGGCGAGCTTTGCTAAAGGCGCTAAGCTGAGG 1777
1603 GACCCGAAGAGAACATCACTACCTCTGCAAAAGCTTTGAGAGTGTCTGCACCTCAGG 1662
1778 GAGCTGTAAACCTTGTCTGCTGCGGCTTCAATGATGTCACAAAGTCCAGAGCAGG 1837
1663 GAACCTTGCAAACTTACTGTATCATGAGGTACAGAGATGACATGACGACATGCTGCT 1722
1838 GAAGAGATGCGGAGATGAGAGATGATGAACTTCATCAAGACCCCAACTTGTTCGGG 1897
1723 GGCATATGCGCATGTCTCTCAACAGTTCTGAAGCTTATGACAAAGTATGATCTGACGG- 1781
1898 CAGTTCGCTGATCTCTGCGCCAGACAAACAGGCGCCGTAAAGCGGCTTATGCTGCTAC 1957
1782 --AAGCGTGGCGTTCTCTTAAGCTACATCAATCAGGCTGAGCTCCCGAGATCTATCGCTC 1839
1958 ATGCTGTATACCATGATGCTTCTGTACAGCGCGCTTGTATGAGCGTTGCTGCTCACC 2017
1840 GCGGCAAAATGAAAGGCGCTCTTCATCAACCTGCTCTGTTGAGCGTTTGTGCTCACC 1899
2018 GTGCTGAGGCGCATGACCTGTGGGCTTCTTCTTGTGCGAGCTCCATGAGAGTCCAGCT 2077
1930 CTGATCGAGGCTGCGGACACAGGACTCCGATGATGCTGCTACCAAGATGTGTGCTCGGTC 1959
2078 GAGATCATGAGAGATGAGCGCTCTGCGCTTCAATGACCCGTACACC 2126
1960 GACATTACAAATGATTAAACAGGACTGCTGTTGACCCACACAGACC 2008

RESULT 11

US-09-078-862-2
Sequence 2, Application US/09078862
Patent No. 6091003

GENERAL INFORMATION:

APPLICANT: Nan, Guo-Jing

APPLICANT: Nagai, Chifumi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
TITLE OF INVENTION: TRANSFORMATION OF PINAPPLE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,862

FILING DATE: 14-MAY-1998

CLASSIFICATION: 80C

ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: US-03321

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3509 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-078-862-2

Query Match 3.3%; Score 89.8; DB 3; Length 3509;
Best Local Similarity 51.0%; Pred. No. 4.1e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1658 GAACACATTGGGACATCTGATGACCGGTCAAAAGCCCATCTCTTCTCCATGGCAAGACTC 1717
1543 GAAGTAGATGCGGTCTCTGACCAACCTCTCAAGCCCATATCTGCGGTATCCAGACCA 1602
1718 GACAGGATGAAGACATTAACAGGCGTGGCGAGCTTTGCTAAAGGCGCTAAGCTGAGG 1777
1603 GACCCGAAGAGAACATCACTACCTCTGCAAAAGCTTTGAGAGTGTCTGCACCTCAGG 1662
1778 GAGCTGTAAACCTTGTCTGCTGCGGCTTCAATGATGTCACAAAGTCCAGAGCAGG 1837
1663 GAACCTTGCAAACTTACTGTATCATGAGGTACAGAGATGACATGACGACATGCTGCT 1722
1838 GAAGAGATGCGGAGATGAGAGATGATGAACTTCATCAAGACCCCAACTTGTTCGGG 1897
1723 GGCATATGCGCATGTCTCTCAACAGTTCTGAAGCTTATGACAAAGTATGATCTGACGG- 1781
1898 CAGTTCGCTGATCTCTGCGCCAGACAAACAGGCGCCGTAAAGCGGCTTATGCTGCTAC 1957
1782 --AAGCGTGGCGTTCTCTTAAGCTACATCAATCAGGCTGAGCTCCCGAGATCTATCGCTC 1839
1958 ATGCTGTATACCATGATGCTTCTGTACAGCGCGCTTGTATGAGCGTTGCTGCTCACC 2017
1840 GCGGCAAAATGAAAGGCGCTCTTCATCAACCTGCTCTGTTGAGCGTTTGTGCTCACC 1899
2018 GTGCTGAGGCGCATGACCTGTGGGCTTCTTCTTGTGCGAGCTCCATGAGAGTCCAGCT 2077
1930 CTGATCGAGGCTGCGGACACAGGACTCCGATGATGCTGCTACCAAGATGTGTGCTCGGTC 1959
2078 GAGATCATGAGAGATGAGCGCTCTGCGCTTCAATGACCCGTACACC 2126
1960 GACATTACAAATGATTAAACAGGACTGCTGTTGACCCACACAGACC 2008

RESULT 12

US-09-051-341-6
Sequence 6, Application US/09051341
Patent No. 6124528

GENERAL INFORMATION:

APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Yenter Law Group, P.C.

STREET: 260 Sheridan Avenue, Suite 440

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341

FILING DATE: 25-OCT-1996

CLASSIFICATION: 80C

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/17351

FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
 FILING DATE: 27-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/372,200
 FILING DATE: 12-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara Rae-Venter, Ph.D.,
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGBE.110.02US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)328-4400
 TELEFAX: (415)328-4477
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3509 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 112..3315
 US-03-051-341-6

Query Match 3.3%; Score 89.8; DB 3; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps -;

1558 GAACACATTGGGCATCTGATGATGACCGGTCAAGGCCATCTCTTCCATGCGAAGACTC 1717
 1543 GAAGTATGCGGTTCTCTACCAACCTCAAGCCGATGATCTGGCTTATCAAGACCA 1602
 1718 GACAGGTTGAAGAAATATTAACAGGGGCTGTGCAAGCTTTGCTAAGTGGCTTAAGCGAGG 1777
 1603 GACCCGAAAGAAACATCACTACCTCTGCAAGGCTTTGAGAGTGTCTCACTCAGG 1662
 1778 GAGCTGTAAACCTTGTGCTGCTCCGCTTCCGCTTCAATGATGTCAAGTCAAGACAGG 1837
 1663 GAACCTGCAACCTTACTCTGATCATGAGGTACAGAGATGACATGACAGCATGTCTGCT 1722
 1838 GAAAGATGCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1897
 1723 GGCATGCGCAGTGTCTTCAACCAAGTCTGAGAGCTGATGACAGATGATGATGATGATG 1731
 1898 CAGTTCGGCTGATCTCTGCGCCAGCAACAGGGGCGCGGAGCTTATGCTATGCTATG 1957
 1782 --AAGCGTGGCGTTCCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1839
 1958 ATGCTGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2017
 1840 GGGGCCAAATGAAAGGGCGCTTTCATCAACCTGCTCTGTTGAGCGTTTGGTCTCACC 1899
 2018 GTGTTGAGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2077
 1900 CTGATCGAGGCTGCGGCAACGACATCCGATAGTGTGCTACCAAGATGTGTGTGCGGTC 1959
 2078 GAGATCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2126
 1960 GACATTACAAATGATTAACAAAGGACTGCTGTTGACCCACACACACC 2008

RESULT 13

US-09-866-153-12
 Sequence 12, Application US/09866153
 Patent No. 6638766
 GENERAL INFORMATION:
 APPLICANT: Albert, Henrik H.
 APPLICANT: Wei, Hairong
 TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
 FILE REFERENCE: US-03648
 CURRENT APPLICATION NUMBER: US/09/866,153
 CURRENT FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: 09/270,976

PRIOR FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 12
 LENGTH: 3509
 TYPE: DNA
 ORGANISM: Zea mays
 US-09-866-153-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1558 GAACACATTGGGCATCTGATGATGACCGGTCAAGGCCATCTCTTCCATGCGAAGACTC 1717
 1543 GAAGTATGCGGTTCTCTACCAACCTCAAGCCGATGATCTGGCTTATCAAGACCA 1602
 1718 GACAGGTTGAAGAAATATTAACAGGGGCTGTGCAAGCTTTGCTAAGTGGCTTAAGCGAGG 1777
 1603 GACCCGAAAGAAACATCACTACCTCTGCAAGGCTTTGAGAGTGTCTCACTCAGG 1662
 1778 GAGCTGTAAACCTTGTGCTGCTCCGCTTCCGCTTCAATGATGTCAAGTCAAGACAGG 1837
 1663 GAACCTGCAACCTTACTCTGATCATGAGGTACAGAGATGACATGACAGCATGTCTGCT 1722
 1838 GAAAGATGCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1897
 1723 GGCATGCGCAGTGTCTTCAACCAAGTCTGAGAGCTGATGACAGATGATGATGATGATG 1781
 1898 CAGTTCGGCTGATCTCTGCGCCAGCAACAGGGGCGCGGAGCTTATGCTATGCTATG 1957
 1782 --AAGCGTGGCGTTCCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1839
 1958 ATGCTGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2017
 1840 GGGGCCAAATGAAAGGGCGCTTTCATCAACCTGCTCTGTTGAGCGTTTGGTCTCACC 1899
 2018 GTGTTGAGCCATGACCTGTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2077
 1900 CTGATCGAGGCTGCGGCAACGACATCCGATAGTGTGCTACCAAGATGTGTGTGCGGTC 1959
 2078 GAGATCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2126
 1960 GACATTACAAATGATTAACAAAGGACTGCTGTTGACCCACACACACC 2008

RESULT 14

US-09-693-467A-12
 Sequence 12, Application US/09693467A
 Patent No. 6686513
 GENERAL INFORMATION:
 APPLICANT: Albert, Henrik H.
 APPLICANT: Wei, Hairong
 TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
 FILE REFERENCE: US-04331
 CURRENT APPLICATION NUMBER: US/09/693,467A
 CURRENT FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 09/270,976
 PRIOR FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 12
 LENGTH: 3509
 TYPE: DNA
 ORGANISM: Zea mays
 US-09-693-467A-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1558 GAACACATTGGGCATCTGATGATGACCGGTCAAGGCCATCTCTTCCATGCGAAGACTC 1717

1543 GAAGTATGCGGTTCTGACCAACCCCTCAACAAGCCGATGCTGCGCTTATCAAGACCA 1602
 1718 GACAGGAGGAGACATTAACAGGCGTGTGCAAGCTTTTGTAGTGCCTTAAGCTAGG 1777
 1603 GACCCGAGAGAACATCACTACCTCTGTCACAAAGCTTTGGAGAGTGTGTCCACTCAG 1662
 1778 GAGCTGTAAACCTTCTGCTGCTGCGGGTACAAATGATGTCAACAGTCCAGAGACAG 1837
 1663 GAACCTGCAACCTTACTCTGATCAAGGTAAACAGAGATGATGACATGACATGTCTGCT 1722
 1838 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1897
 1723 GGCATATGCGAGTGTCTTCAACAGCTTCTGAAAGCTGATGAGATGATGATGATGATGAT 1781
 1898 CAGTTCCGCTGATCTCTGCGCCCAACAACAGGCGCCGATGAGAGAGCTTATGCTAC 1957
 1782 --AAGCGTGGCTTCCCTTACAGATCAATCAAGCTGAGCTCCGAGATCTTATGCTCTC 1839
 1958 ATCGCTATACCATGATGCTTCTGTCACAGCCGCTTGTATGAGAGCTTCTGCTCACC 2017
 1840 GCGGCCAAATGAGAGGCGCTTCTTCAACCCCTGCTCTGTTGAGCGCTTGTCTCACC 1899
 2018 GTGCTTGAAGCCATGACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2077
 1900 CTGATCGAGGCTGCGGACACAGGACTCCGATAGTGTCTTCAACAGATGATGATGATGAT 1959
 2078 GAGATCATGAGATGAGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2126
 1960 GACATTACAAATGATTTAAACAGGAGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 2008

RESULT 15

US-08-429-054A-12
 Sequence 12, Application US/08429054A

GENERAL INFORMATION:
 APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
 APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
 TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
 TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERMAN AND MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,054A
 FILING DATE: 26-APR-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 842,337
 FILING DATE: 20-March-1992
 APPLICATION NUMBER: PCT/FR 91/00593
 FILING DATE: 18-July-1991
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: French 90402894.9
 FILING DATE: 20-July-1990
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Charles A. Musserlian
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 146.1137
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-9002
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3509
 TYPE: Nucleic acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 US-08-429-054A-12

Query Match 2.9%; Score 80.4; DB 2; Length 3509;
 Best Local Similarity 51.2%; Pred. No. 1.1e-10;
 Matches 214; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

1543 GAAGTATGCGGTTCTGACCAACCCCTCAACAAGCCGATGCTGCGCTTATCAAGACCA 1602
 1718 GACAGGAGGAGACATTAACAGGCGTGTGCAAGCTTTTGTAGTGCCTTAAGCTAGG 1777
 1603 GACCCGAGAGAACATCACTACCTCTGTCACAAAGCTTTGGAGAGTGTGTCCACTCAG 1662
 1778 GAGCTGTAAACCTTCTGCTGCTGCGGGTACAAATGATGTCAACAGTCCAGAGACAG 1837
 1663 GAACCTGCAACCTTACTCTGATCAAGGTAAACAGAGATGATGACATGACATGTCTGCT 1722
 1838 GAAGAGATCGCGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1897
 1723 GGCATATGCGAGTGTCTTCAACAGCTTCTGAAAGCTGATGAGATGATGATGATGATGAT 1781
 1898 CAGTTCCGCTGATCTCTGCGCCCAACAACAGGCGCCGATGAGAGAGCTTATGCTAC 1957
 1782 --AAGCGTGGCTTCCCTTACAGATCAATCAAGCTGAGCTCCGAGATCTTATGCTCTC 1839
 1958 ATCGCTATACCATGATGCTTCTGTCACAGCCGCTTGTATGAGAGCTTCTGCTCACC 2017
 1840 GCGGCCAAATGAGAGGCGCTTCTTCAACCCCTGCTCTGTTGAGCGCTTGTCTCACC 1899
 2018 GTGCTTGAAGCCATGACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2077
 1900 CTGATCGAGGCTGCGGACACAGGACTCCGATAGTGTCTTCAACAGATGATGATGATGAT 1959
 2078 GAGATCATGAGATGAGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2126
 1960 GACATTACAAATGATTTAAACAGGAGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 2008

Search completed: May 25, 2004, 22:35:39
 Job time: 135.516 secs

181 CCTGACGTCCTCCGCTCCGCGAGAGAGGCGATCGTGTCCGCGCTTGTGAGCCATGCG 240
181 CCTGACGTCCTCCGCTCCGCGAGAGAGGCGATCGTGTCCGCGCTTGTGAGCCATGCG 240
241 GGTGGCCGCGCGCGCGAGTGTGGAGATCGTCCGCGCTCAAGCTTCAAGAGCTAGCGCT 300
241 GGTGGCCGCGCGCGCGAGTGTGGAGATCGTCCGCGCTCAAGCTTCAAGAGCTAGCGCT 300
301 CGAGAGCTCAAGCTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGAGCGCGAGA 360
301 CGAGAGCTCAAGCTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGAGCGCGAGA 360
361 CAATATCCCTACGTTCTCGAGCTTGAATCGAGCCGTTCAATGTCTCAGTCCGCGCGC 420
361 CAATATCCCTACGTTCTCGAGCTTGAATCGAGCCGTTCAATGTCTCAGTCCGCGCGC 420
421 AATGCGTCATCATTTATTTGAAAGGAGTGTGAGTTCCTCAACCGACCTTGTCCCAT 480
421 AATGCGTCATCATTTATTTGAAAGGAGTGTGAGTTCCTCAACCGACCTTGTCCCAT 480
481 CATGTTCCGCAACAAGAGATGCTTGGAGCCCTGTTGATTTCTCCGCGCGAGCGCA 540
481 CATGTTCCGCAACAAGAGATGCTTGGAGCCCTGTTGATTTCTCCGCGCGAGCGCA 540
541 CAAGGCGCATGTATGATGCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 600
541 CAAGGCGCATGTATGATGCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 600
601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGTGACACAGCACTTCAAT 660
601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGTGACACAGCACTTCAAT 660
661 TGTCTTAATTAATTTCAAGAGTGGAGCTGTGAGAGAGTGTGGGTGATACAGCAGAG 720
661 TGTCTTAATTAATTTCAAGAGTGGAGCTGTGAGAGAGTGTGGGTGATACAGCAGAG 720
721 TTTGGAATGATCCATCT 780
721 TTTGGAATGATCCATCT 780
781 GAAATTTCTGGGAGAGATCCCATGATTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGT 840
781 GAAATTTCTGGGAGAGATCCCATGATTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGT 840
841 CTTGGTCAAGCTAATGATTAAGCTTTCGACAGACAGAGAGAGAGAGAGAGAGAGAGAG 900
841 CTTGGTCAAGCTAATGATTAAGCTTTCGACAGACAGAGAGAGAGAGAGAGAGAGAGAG 900
901 GGACCAAGCTCGGTCAGTAAAGAAATGAGATGCTTCTCCGTTTAAAGAAAGAGGCTTGA 960
901 GGACCAAGCTCGGTCAGTAAAGAAATGAGATGCTTCTCCGTTTAAAGAAAGAGGCTTGA 960
961 TGTTCCTCCCAAGATTTCTCATTTGTTACTGGCTGATACAGAGTGCAGAAAGAAATCATG 1020
961 TGTTCCTCCCAAGATTTCTCATTTGTTACTGGCTGATACAGAGTGCAGAAAGAAATCATG 1020
1021 CAATCAAGCGCTTGAAGATTAAGTGAACAAGACATCTTACATTTACAGAGTTCCTT 1080
1021 CAATCAAGCGCTTGAAGATTAAGTGAACAAGACATCTTACATTTACAGAGTTCCTT 1080
1081 CAGAAATGAAAATGGGATTTCTTAAAGATGATCAAGATTTGATGATGATGATGATGATGAT 1140
1081 CAGAAATGAAAATGGGATTTCTTAAAGATGATCAAGATTTGATGATGATGATGATGATGAT 1140
1141 GGAATCATTTGCTGAGAGTGTCTGTGTAATGCTGTGTAATTAAGAGTACTCCAGA 1200
1141 GGAATCATTTGCTGAGAGTGTCTGTGTAATGCTGTGTAATTAAGAGTACTCCAGA 1200
1201 CTTCAATTTGGAATCTACAGTATGAAATCTTGTGGGCTCATTTGATCTTAAAGAT 1260
1201 CTTCAATTTGGAATCTACAGTATGAAATCTTGTGGGCTCATTTGATCTTAAAGAT 1260
1261 GGAATTAACCAAGTCAACATTTGCTCATGCTGTGAAAAAGATTAAGATTCAGATTCAGA 1320

1261 GGAATTAACCAAGTCAACATTTGCTCATGCTGTGAAAAAGATTAAGATTCAGATTCAGA 1320
1321 CATATTTTGAAGATTTGATGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1380
1321 CATATTTTGAAGATTTGATGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1380
1381 AATTCATGAAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTCGAGAG 1440
1381 AATTCATGAAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTCGAGAG 1440
1441 CAAAAATCTGTTGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 CAAAAATCTGTTGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 AGTTGCTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1501 AGTTGCTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1561 CATGTCATATATCTTCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1561 CATGTCATATATCTTCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
1621 AATGCAAAATTTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1621 AATGCAAAATTTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
1681 CCGGTCAAGCCCATCT 1740
1681 CCGGTCAAGCCCATCT 1740
1741 GCTGTGAAAGCTTTTGTCTAAGTGGCTAAGTGTGAGAGAGTGTGAACTTGTGTCTGT 1800
1741 GCTGTGAAAGCTTTTGTCTAAGTGGCTAAGTGTGAGAGAGTGTGAACTTGTGTCTGT 1800
1801 TGGCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1801 TGGCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1801 TGGCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1801 TGGCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1861 GAT 1920
1861 GAT 1920
1921 GACAAACAGGCGCGGTAACGAGCTCTATGCTATGATGATGATGATGATGATGATGATGAT 1980
1921 GACAAACAGGCGCGGTAACGAGCTCTATGCTATGATGATGATGATGATGATGATGATGAT 1980
1981 GGTACAGCGCGCTTGTATGAGAGCTTGGCTCAACCGCTGAGAGAGAGAGAGAGAGAGAG 2040
1981 GGTACAGCGCGCTTGTATGAGAGCTTGGCTCAACCGCTGAGAGAGAGAGAGAGAGAGAG 2040
2041 GCTTCTACTTTCGAGAGCTTCATGAGAGTCAAGTGAATCATAGAGATGAGCTCTC 2100
2041 GCTTCTACTTTCGAGAGCTTCATGAGAGTCAAGTGAATCATAGAGATGAGCTCTC 2100
2101 GGGCTTCCATGATGAGAGCTTACCAACCGGAGAGCTGTTATCTGATGAGAGCTCTT 2160
2101 GGGCTTCCATGATGAGAGCTTACCAACCGGAGAGCTGTTATCTGATGAGAGCTCTT 2160
2161 GAGAGCGGTCAG 2220
2161 GAGAGCGGTCAG 2220
2221 CATATACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2221 CATATACGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2281 CTAAGCTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
2281 CTAAGCTTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
2341 GATGTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400

[illegible]

```

1 RESULT 2
2 US-10-080-114A-11
3 / Sequence 11, Application US/10080114A
4 / Publication No. US2003005482A1
5 /
6 / GENERAL INFORMATION:
7 / APPLICANT: Dhugra, Kamarpal S.
8 / TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
9 / TITLE OF INVENTION: to Improve Stalk and Grain Quality
10 /
11 / FILE REFERENCE: 1381P
12 / CURRENT FILING DATE: 2002-04-30
13 / PRIOR APPLICATION NUMBER: US 63/270,777
14 / PRIOR FILING DATE: 2001-02-22
15 / NUMBER OF SEQ ID NOS: 13
16 /
17 / SOFTWARE: FastSeq for Windows Version 4.0
18 /
19 / SEQ ID NO 11
20 /
21 / LENGTH: 2757
22 /
23 / TYPE: DNA
24 /
25 / ORGANISM: Zea mays
26 /
27 / FEATURES:
28 / NAME/KEY: CDS
29 / LOCATION: (1)...(2430)
30 /
31 / FEATURE:
32 / NAME/KEY: source
33 / LOCATION: (1)...(39)
34 /
35 / OTHER INFORMATION: Sorghum pronginum
36 /
37 / FEATURE:
38 / NAME/KEY: source
39 / LOCATION: (40)...(2757)
40 /
41 / OTHER INFORMATION: Zea mays
42 /
43 / US-10-080-114A-11

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	Query Match	Similarity	99.2%	Score 2714	DB 15	Length 2757	
	Best Local	Similarity	99.8%	Pred. No. 0			
	Match 2717	Conservative		Mismatches 5	Indels 0	Gaps 0	
QY	16	CGGCGACCGCGCTCGAGACACCTTCTCAACGCGACCGCAACGAGCTGTCGCTCTCTTC	75				
Db	36	CCGGACCCGCGTCGAGGACACCTTCCAAGCGACCGCAACGAGCTGTCGCTCTCTTC	95				
QY	76	CAAGTACGTGAACAAGGGGGAAGGCGATCCTGACGCGGACCAACATCTCGACGCGCTCGA	135				
Db	96	CAAGTACGTGAACAAGGGGGAAGGCGATCTTGCAGCGCGGACCAACATCTCGACGCGCTCGA	155				
QY	136	CGAGGTCAAGGAGCTTCGAGGAGCGCGCGCTAAGCGAGGAGACCTTCTCGACGTCTTCG	195				

Db	156	CGAGGCTCCAGGGAGCTCCGAGGAGCTCCGCGCGCTCCGACGGAACCCCTTCTCCACAGCTCCG	215
QY	196	CTCCGCGCAGAGAGGCGATTCGTCCTGCCCGCGCTTCGAGGCACTGGCGGTGGCGCGCGGCC	255
Db	216	CTCCGCGCAGAGAGGCGATTCGTCCTGCCCGCGCTTCGAGGCACTGGCGGTGGCGCGCGGCC	275
QY	256	GGAGATTGGAGATGACCTCCGCGCTCAACGTTCAAGACTAGCGTCCAGCAGCTACAGT	315
Db	276	GGAGATTGGAGATGACCTCCGCGCTCAACGTTCAAGACTAGCGTCCAGCAGCTACAGT	335
QY	316	CTCGAGACTCTCCGCTTCAAGAGAGCTTGTCCAGCGGCCACACAATGATCCTTACGT	375
Db	336	CTCGAGACTCTCCGCTTCAAGAGAGCTTGTCCAGCGGCCACACAATGATCCTTACGT	395
QY	376	TCTGAGCTTGACCTTCAGCGCGCTCAATGTCAGTCCCAAGGCCAATGGGTATCATC	435
Db	396	TCTGAGCTTGACCTTCAGCGCGCTCAATGTCAGTCCCAAGGCCAATGGGTATCATC	455
QY	436	TATTGAAACGGTGTGCAAGTTCCTCAACCGACCTTGCTCTCATGTTTCCGCAACG	495
Db	456	TATTGAAACGGTGTGCAAGTTCCTCAACCGACCTTGCTCTCATGTTTCCGCAACG	515
QY	496	GGATTGCTTGAAGCCCTGTTGATTTCTCCGCGGCAACGGACAAAGGGGCAATGAT	555
Db	516	GGATTGCTTGAAGCCCTGTTGATTTCTCCGCGGCAACGGACAAAGGGGCAATGAT	575
QY	556	GATGCTTAATGATAGAAATACAAAGCTTGGAGGCTTCACTGTGTGTCGACCAAGCTGA	615
Db	576	GATGCTTAATGATAGAAATACAAAGCTTGGAGGCTTCACTGTGTGTCGACCAAGCTGA	635
QY	616	GGAGCACTTGTCAAAGCTCCCTGCTGACACACGCTCAGCATTTGCTTATAATTTC	675
Db	636	GGAGCACTTGTCAAAGCTCCCTGCTGACACACGCTCAGCATTTGCTTATAATTTC	695
QY	676	AGAGTGGGGGCTGGAGGAAAGGTTGGGGGATGATAGCAGACATGTTTGGAAATGATCCA	735
Db	696	AGAGTGGGGGCTGGAGGAAAGGTTGGGGGATGATAGCAGACATGTTTGGAAATGATCCA	755
QY	736	TCTCCTTTAGACATCATTTCAAGGGCGCAAGCCATCTACCTTAGAAGAAATTTCTGGGAG	795
Db	756	TCTCCTTTAGACATCATTTCAAGGGCGCAAGCCATCTACCTTAGAAGAAATTTCTGGGAG	815
QY	796	GATCCCGCAGATTTTAAAGTGTGTGGAGTATCCCTCAAGAGATCTTGCTGCAAGCTAA	855
Db	816	GATCCCGCAGATTTTAAAGTGTGTGGAGTATCCCTCAAGAGATCTTGCTGCAAGCTAA	875
QY	856	TGTAATTAGGCTTGCACAGACAGAGAGGACAGATGCTATATACTGACCAAGTCCGTGC	915
Db	876	TGTAATTAGGCTTGCACAGACAGAGAGGACAGATGCTATATACTGACCAAGTCCGTGC	935
QY	916	ACTAGAAATGAGATGTTCTTCGTTTAAABAAACAAGGCTTGATGTTTCCCAAAAT	975
Db	936	ACTAGAAATGAGATGTTCTTCGTTTAAABAAACAAGGCTTGATGTTTCCCAAAAT	995
QY	976	TCTCATTTTACTCGGCTGATACAGAGATGCAAAAGGAACATCATGCAATCAGCGCTTGA	1035
Db	996	TCTCATTTTACTCGGCTGATACAGAGATGCAAAAGGAACATCATGCAATCAGCGCTTGA	1055
QY	1036	GAGAAATTAGAGAACACAGCACTACTTACATATTCAGAGTCCCTTCAGAAATGAAATG	1095
Db	1056	GAGAAATTAGAGAACACAGCACTACTTACATATTCAGAGTCCCTTCAGAAATGAAATG	1115
QY	1096	GATGCTTAAGAAATGAGATATCAAGATTTGATGAGTGGGCATATCGGAAACATTTGCTGA	1155
Db	1116	GATGCTTAAGAAATGAGATATCAAGATTTGATGAGTGGGCATATCGGAAACATTTGCTGA	1175
QY	1156	GGATGCTCTGTGAATTTGCTGCTGAAATTACAGAGTCTCCAGACTTCATATTTGAAA	1215
Db	1176	GGATGCTCTGTGAATTTGCTGCTGAAATTACAGAGTCTCCAGACTTCATATTTGAAA	1235
QY	1216	CTACAGATAGGAAATCTTGCGGCTCATTCGATCTTCAAGATGGGAATTAACCAAGT	1275
Db	1236	CTACAGATAGGAAATCTTGCGGCTCATTCGATCTTCAAGATGGGAATTAACCAAGT	1295

QY 1276 CAACATTGCTCATCTCTGAAAAAGACTAAGTATCCAGATTCCAGACATATTTTGGAGAA 1335
 Db 1296 CAACATTGCTCATCTCTGAAAAAGACTAAGTATCCAGATTCCAGACATATTTTGGAGAA 1355
 QY 1336 TTTCGATGAGAGTACCACTTTCTCTCTGCACTGCTGATATATTTGCTATGAGAA 1395
 Db 1356 TTTCGATGAGAGTACCACTTTCTCTCTGCACTGCTGATATATTTGCTATGAGAA 1415
 QY 1396 TTTCGATGAGAGTACCACTTTCTCTCTGCACTGCTGATATATTTGCTATGAGAA 1455
 Db 1416 TTTCGATGAGAGTACCACTTTCTCTCTGCACTGCTGATATATTTGCTATGAGAA 1475
 QY 1456 ACAGATGAGAGTACCTGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515
 Db 1476 ACAGATGAGAGTACCTGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1535
 QY 1516 CGATGCTTCTGATCCAAAGTTCAATATGATCTCTCTGCTGCTGCTGCTGCTGCTGCT 1575
 Db 1536 CGATGCTTCTGATCCAAAGTTCAATATGATCTCTCTGCTGCTGCTGCTGCTGCTGCT 1595
 QY 1576 TCCGATACCGAGAGGCGCAAGCACTCACCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1635
 Db 1596 TCCGATACCGAGAGGCGCAAGCACTCACCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1655
 QY 1636 TTATGACCCGAGAGCAAAAGATGAAACATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1695
 Db 1656 TTATGACCCGAGAGCAAAAGATGAAACATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1715
 QY 1696 CCTCTCTCTCCATGCGCAAGCTCGACAGGGTGAAGAACTAATACAGGGCTGCTGCTGCTGCT 1755
 Db 1716 CCTCTCTCTCCATGCGCAAGCTCGACAGGGTGAAGAACTAATACAGGGCTGCTGCTGCTGCT 1775
 QY 1756 TGTCAAGTCCCTAAGCTGAGGGAGCTGGTAAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1815
 Db 1776 TGTCAAGTCCCTAAGCTGAGGGAGCTGGTAAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1835
 QY 1816 TGTCAAGTCCCTAAGCTGAGGGAGCTGGTAAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1875
 Db 1836 TGTCAAGTCCCTAAGCTGAGGGAGCTGGTAAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1895
 QY 1876 CAAGACCCCAAACTTGTTCGGGCACTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1935
 Db 1896 CAAGACCCCAAACTTGTTCGGGCACTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1955
 QY 1936 TAAAGGCGAGCTCTATCGCTACATCGCTGATACCATGGTCTTCTGCTGCTGCTGCTGCTGCT 1995
 Db 1956 TAAAGGCGAGCTCTATCGCTACATCGCTGATACCATGGTCTTCTGCTGCTGCTGCTGCTGCT 2015
 QY 1996 GTATGAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2055
 Db 2016 GTATGAGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2075
 QY 2056 GAAGCTCCATGAGAGTCCAGCTGAGATGATAGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2115
 Db 2076 GAAGCTCCATGAGAGTCCAGCTGAGATGATAGAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2135
 QY 2116 CCCGTAACCAACCCGAAAGGCTGTTAATCTGATGCGCACTTCTTCTGCAACCGTGGCAAGCA 2175
 Db 2136 CCCGTAACCAACCCGAAAGGCTGTTAATCTGATGCGCACTTCTTCTGCAACCGTGGCAAGCA 2195
 QY 2176 AGACCCAGATGATCTGGTGAATATATCTGAGCAAGGCTGCAAGGCGATATATGAGAGT 2235
 Db 2196 AGACCCAGATGATCTGGTGAATATATCTGAGCAAGGCTGCAAGGCGATATATGAGAGT 2255
 QY 2236 CAAGTGAAGATATCTCAAGAGAGTTGATGCACTGAGCGGGGCTCTACCGTTCTGGA 2295
 Db 2256 CAAGTGAAGATATCTCAAGAGAGTTGATGCACTGAGCGGGGCTCTACCGTTCTGGA 2315
 QY 2296 GTACGCTGTCGAAGCTCGAGAGGCTGAGAGCGAGGCGCTACCTTGAAGATGTTCTACATCT 2355
 Db 2316 GTACGCTGTCGAAGCTCGAGAGGCTGAGAGCGAGGCGCTACCTTGAAGATGTTCTACATCT 2375

QY 2356 GAAGTCCGCGAGCTGCGGAAAGACCGCTGCTGCAATTTACCAACCGCAGTACCTTGC 2415
 Db 2376 GAAGTCCGCGAGCTGCGGAAAGACCGCTGCTGCAATTTACCAACCGCAGTACCTTGC 2435
 QY 2416 GCAACTGCGACTGGGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2475
 Db 2436 GCAACTGCGACTGGGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2495
 QY 2476 AGGCGCGCAGACGCTGACCAATTAATGTCGCGAGCTGCAATCTGTTTTTATATGTA 2535
 Db 2496 AGGCGCGCAGACGCTGACCAATTAATGTCGCGAGCTGCAATCTGTTTTTATATGTA 2555
 QY 2536 CATATGCGAGTATATACAAATCTACTGAGGCAAGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCT 2595
 Db 2556 CATATGCGAGTATATACAAATCTACTGAGGCAAGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCT 2615
 QY 2596 TGTTCATCTGATATATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2655
 Db 2616 TGTTCATCTGATATATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2675
 QY 2656 TGTTCATCTGATATATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2715
 Db 2676 TGTTCATCTGATATATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2735
 QY 2716 AAAAAAAAAAGGCGCGCGC 2737
 Db 2736 AAAAAAAAAAGGCGCGCGC 2757

RESULT 3

US-10-425-114-6036
 ; Sequence 6036, Application US/10425114
 ; Publication No. US2004003488A1
 GENERAL INFORMATION:
 APPLICANT: Zhou, Yinhua
 APPLICANT: Liu, Yindong
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53313)B
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6036
 ; LENGTH: 2275
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700551647_F11
 US-10-425-114-6036

Query Match 80.0%; Score 2189.2; DB 13; Length 2275;
 Best Local Similarity 98.9%; Ered No. 0;
 Matches 2225; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

QY 454 GTTCTCAACCGACACTTCTCTCAATCAATGTTCCGCAACAGGATGCTTGAAGCCCT 513
 Db 1 GTTCTCAACCGACACTTCTCTCAATCAATGTTCCGCAACAGGATGCTTGAAGCCCT 60
 QY 514 GTTGAATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
 Db 61 GCTGATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 574 ACAAGCTTGGGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633
 Db 121 ACAAGCTTGGGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 634 CCTGCTGACACACCATATCTCACAATTTGCTTATTAATTTCAAGATGAGGCTTGGAGAA 693
 Db 181 CCTGCTGACACACCATATCTCACAATTTGCTTATTAATTTCAAGATGAGGCTTGGAGAA 240

QY 694 AGGTGGGGGTGATACGACGACATGTTTGGAAATGATCCATCTCTTACACATCAT 753
 DB 241 AGGTGGGGGTGATACGACGACATGTTTGGAAATGATCCATCTCTTACATATATAT 300
 QY 754 TCAGGGCCGACAGCCCTTACCTTACGAAATCTTGGGAGGATCCCTGATTTTAA 813
 DB 301 TCAGGGCCGACAGCCCTTACCTTACGAAATCTTGGGAGGATCCCTGATTTTAA 360
 QY 814 CGTTGTTGTTATCCCTCATGATGATCTTGGTCAAGTATGATATAGCTTGCACA 873
 DB 361 CGTTGTTGTTATCCCTCATGATGATCTTGGTCAAGTATGATATAGCTTGCACA 420
 QY 874 CACAGGAGACAGATGCTATATACCTGACCAAGTCCGTGACCTAGAAAATGAGATGCT 933
 DB 421 CACAGGAGACAGATGCTATATATCTGACCAAGTCCGTGACCTAGAAAATGAGATGCT 480
 QY 934 TCTCCGTTTAAAGAAACAAGGGCTTATGTTTCCCAAGATCTGATGTTTCTGGCT 993
 DB 481 TCTCCGTTTAAAGAAACAAGGGCTTATGTTTCCCAAGATCTGATGTTTCTGGCT 540
 QY 994 GATACGAGATGCAAAAGAAACATCATCATACGCGCTTGAAGAAATAGTGAACACA 1053
 DB 541 GATACGAGATGCAAAAGAAACATCATCATACGCGCTTGAAGAAATAGTGAACACA 600
 QY 1054 GCATCTTACATATTCAGAGTTCCTTCAAGAAATGAAATGGATATCTTAAAGATGAT 1113
 DB 601 GCATCTTACATATTCAGAGTTCCTTCAAGAAATGAAATGGATATCTTAAAGATGAT 660
 QY 1114 ATCAAGATTTGATGTTGGGCTCATCTGAAACATTTGCGAGAGATGCTGGTGAAT 1173
 DB 661 ATCAAGATTTGATGTTGGGCTCATCTGAAACATTTGCGAGAGATGCTGGTGAAT 720
 QY 1174 TCTGCTGATTAACAAGTACTCAGACTTCATATTTGAAACTAGAGTATGAAATCT 1233
 DB 721 TCTGCTGATTAACAAGTACTCAGACTTCATATTTGAAACTAGAGTATGAAATCT 780
 QY 1234 TGTGGCGTATGCTATCTTACAGATGGAAATTAACCGAGTCAATGCTCATGCTCT 1293
 DB 781 TGTGGCGTATGCTATCTTACAGATGGAAATTAACCGAGTCAATGCTCATGCTCT 840
 QY 1294 GAAAAAGACTAAGTATCCAGATTCAGACATTTTGGAAATTTGATGAGAAATGACA 1353
 DB 841 GAAAAAGACTAAGTATCCAGATTCAGACATTTTGGAAATTTGATGAGAAATGACA 900
 QY 1354 TTCTCTGCTGCAAGTTCAGTCTGATATATTTGCTATGAAACATGCTGATTTTATCATC 1413
 DB 901 TTCTCTGCTGCAAGTTCAGTCTGATATATTTGCTATGAAACATGCTGATTTTATCATC 960
 QY 1414 CAGACATACCAAGAAATGCTGGAAGCAAAATTAATCTTGAACAGTATGAGTCAATAC 1473
 DB 961 CAGACATACCAAGAAATGCTGGAAGCAAAATTAATCTTGAACAGTATGAGTCAATAC 1020
 QY 1474 TGTCTTACTGCTGCGTCTGTTACAGAGTTCATGAGGATGATGCTTCCATCCAAA 1533
 DB 1021 TGTCTTACTGCTGCGTCTGTTACAGAGTTCATGAGGATGATGCTTCCATCCAAA 1080
 QY 1534 GTTCAATATAGTCTCTCTGAGACTGATGTCATATATCTTCCATATCCAGAAAGGC 1593
 DB 1081 GTTCAATATAGTCTCTCTGAGACTGATGTCATATATCTTCCATATCCAGAAAGGC 1140
 QY 1594 CAAAGCACTACCTCTCTTCAATGCTTCAATGAAATTTGATTTATGACCCGAGCAAAA 1653
 DB 1141 CAAAGCACTACCTCTCTTCAATGCTTCAATGAAATTTGATTTATGACCCGAGCAAAA 1200
 QY 1654 CGATGAACACATTTGGGCTATGATGACCGGTCAAAAGCCATCTCTTCCATGCGAAG 1713
 DB 1201 CGATGAACACATTTGGGCTATGATGACCGGTCAAAAGCCATCTCTTCCATGCGAAG 1260
 QY 1714 ACTCGACAGGGTGAAGAACATTAACAGGGCTGTGGAAGCTTTTGTAAAGTCCGTAACT 1773
 DB 1261 ACTCGACAGGGTGAAGAACATTAACAGGGCTGTGGAAGCTTTTGTAAAGTCCGTAACT 1320

QY 1774 GAGGAGCTGTGTAACCTTGTCTGCTGTCGCGGTACATAGATGTCAACAAAGTCCAAAGA 1833
 DB 1321 GAGGAGCTGTGTAACCTTGTCTGCTGTCGCGGTACAAAGATGTCAACAAAGTCCAAAGA 1380
 QY 1834 CAGGAAAGATGCGCGAGATAGAGAAAGATGATGAACTCATCAAGACCAAACTTGT 1893
 DB 1381 CAGGAAAGATGCGCGAGATAGAGAAAGATGATGAACTCATCAAGACCAAACTTGT 1440
 QY 1894 CCGGCAAGTTCGCTGATCTCTGCGCAACAACAGGCGCTTAAAGGCGAGCTCTATCG 1953
 DB 1441 CCGGCAAGTTCGCTGATCTCTGCGCAACAACAGGCGCTTAAAGGCGAGCTCTATCG 1500
 QY 1954 CTACATGCTGATACCATGATGCTTCTGACAGCGGCTTGTATGAAAGCTTGGTCT 2013
 DB 1501 CTACATGCTGATACCATGATGCTTCTGACAGCGGCTTGTATGAAAGCTTGGTCT 1560
 QY 2014 CACCGTGTGAGGCGCATGCTGTGAGCTTCTCTACTTTCGCGAGCGCTCCATGAGAGTCC 2073
 DB 1561 CACCGTGTGAGGCGCATGCTGTGAGCTTCTCTACTTTCGCGAGCGCTCCATGAGAGTCC 1620
 QY 2074 AGCTGAGATCATAGAGCATGCGTCTGCGCTTTCACATTTGACCCGTAACCCCGAACA 2133
 DB 1621 AGCTGAGATCATAGAGCATGCGTCTGCGCTTTCACATTTGACCCGTAACCCCGAACA 1680
 QY 2134 GCGTGTAAATCTGATGCGCGCATCTTCTTCAACCGGTGCAACCAAGACCATGCTGGGT 2193
 DB 1681 GCGTGTAAATCTGATGCGCGCATCTTCTTCAACCGGTGCAACCAAGACCATGCTGGGT 1740
 QY 2194 GAATATATCTGAGACAGGGCTGCAAGCATATGACAGAAATGACATAGAAATGACTC 2253
 DB 1741 GAATATATCTGAGACAGGGCTGCAAGCATATGACAGAAATGACATAGAAATGACTC 1800
 QY 2254 AGAGAGTTGATGACATGCGCGGGCTTACAGTTTCTGAAAGTACGTGTGAAAGCTCGA 2313
 DB 1801 AGAGAGTTGATGACATGCGCGGGCTTACAGTTTCTGAAAGTACGTGTGAAAGCTCGA 1860
 QY 2314 GAGGCTGAGAACAGAGCGCTACCTTGAAGTCTTCAATCTGAAAGTTCGCGAGCTGGC 2373
 DB 1861 GAGGCTGAGAACAGAGCGCTACCTTGAAGTCTTCAATCTGAAAGTTCGCGAGCTGGC 1920
 QY 2374 GAAAGCCGTCGCTTGCATATGACCAACCGAGTACCTTGCAGACCTGCACTGCTAG 2433
 DB 1921 GAAAGCCGTCGCTTGCATATGACCAACCGAGTACCTTGCAGACCTGCACTGCTAG 1980
 QY 2434 CACTGCTACAGACTGAAACCTGAAAGACCTTCAATTTAGCGCGGAGACGCTAG 2493
 DB 1981 CACTGCTACAGACTGAAACCTGAAAGACCTTCAATTTAGCGCGGAGACGCTAG 2040
 QY 2494 CCATTAATGATGCGCGAGCTGAACTGTTTTTATATGATGACATTAATGCAATGACA 2553
 DB 2041 CCATTAATGATGCGCGAGCTGAACTGG-TTTTATATGATGACATTAATGCAATGACA 2098
 QY 2554 AAATTAATGAGGAGGCTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATG 2613
 DB 2099 AAATTAATGAGGAGGCTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATG 2158
 QY 2614 AAGCTGTGCGCTGCAATTTCTTGTCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 2673
 DB 2159 AAGCTGTGCGCTGCAATTTCTTGTCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 2218
 QY 2674 TACATCATATCTGTTGACCTGTGAAAAA 2703
 DB 2219 TACATCATATCTGTTGACCTGTGAAAAA 2248

RESULT 4

US-10-425-114-6561
 ; Sequence 6561, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.

DB 1860 TTCTGTTGACCTGTG 1874

RESULT 5

US-10-425-114-15113
Sequence 15113, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15113
LENGTH: 2832
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3051-038-E10_FLI
US-10-425-114-15113

Query Match 49.0%; Score 1340.8; DB 13; Length 2832;

Best Local Similarity 72.7%; Pred. No. 0;
Matches 1748; Conservative 0; Mismatches 652; Indels 6; Gaps 1;

DB 16 CGGCGACCGCGTGAAGACACCTCCACGCGCACCGACGAGCTCGGCGCTCTGTC 75
DB 138 CAGAGACCGAGTTGAGACACTCTCTGCTCAACCGTACGAACTCATTTCTCTCTC 197
QY 76 CAGTACGTGAAGAGGAGGAGGATCTCTGACCGGACACACCTCTGACGCGCTCGA 135
DB 198 CAGGTATGTGGCTCAGGGGAGAGGAGTTTGCAACCCCATTAATTGATGAACTGA 257
QY 136 CGAGTTCAGAGG-----TCGCGGGGCGCGGCGCTAGCGAGGAGCCCTTCCTCGAGT 189
DB 258 CAGCATCTCGCGGATGATCAGACATATGATGATCTTAAATATGCTCTTGGTGAAT 317
QY 190 CCTCCGCTCCGCGAGAGGCGATGCTGCTGCGCGCGCTGCTGCGCATGCGGCTGCC 249
DB 318 CGTCAAGTCTGAAAGGAGGAGGAGGATTTGCTCTCTCTTGTGCAATGCAAGTCTGC 377
QY 250 GCGCGCGGAGTTTGGAGTACGTCGCGCTCAAGCTTCAAGCTTCAAGCTTCAAGCT 309
DB 378 AAGACCTGTGTTGGAAATATGTCGTTAAATGCTGAGCTCAGCTGAGCAATT 437
QY 310 CACAGTCTCGAGTACTCCGCTTCAAGAGAGAGCTTGCAGCGCGGACGACATGATCC 369
DB 438 AAGTGTCTCTGATATCTCAGCTTCAAGAGAGAGCTTGTAGATGAGAAAGATATAGCAA 497
QY 370 CTAGCTTCTGAGCTTGAAGCTGAGCGCTTCAATGCTCAGTCTCCAGCGGCAATCGCTC 429
DB 498 TTTGTAATGGAGCTGATTTTGAAGCATTTAATGCAATTTCTGTCGCAATCTGCTC 557
QY 430 ATATCTATTTGAAAGAGGTGTGAGTCTCTCAACCGACCTTGTCTCAATCATGTTCCG 489
DB 558 AGCATCATTTGGAGAGAGGTGTGCAATTTTCAATTCGACCTTTCATCTATATGTTGG 617
QY 490 CACAGGAGATTTGCTGAGCGCGCTGTGATTTTCTCGTGGCGACCGGAGCAAGGAGCA 549
DB 618 CACAGAGATTTCTTGAAGCGCTTGTCTGATTTCTCTCGAGCTCAAAATACAGGAGCA 677
QY 550 TGTATGATGCTTAATGATGAATACAAAGCTTGGGAGGCTTCAATGCTGCTGACCAA 609
DB 678 TGTCTGATGTTAAATGATGATACAAACATTTCCAAACTTCAGTCTGATTTGGCAA 737

QY 610 AGCTGAGAGACACTTGTCAAGCTCCCTGCTGACACACCACTACACTTGTCTTAA 669
DB 738 GCGTGAAGATTTATCTCTAAGCTTGACATGATACCTATTCAGGTTGATATGCT 797
QY 670 ATTTCAGAGTGGGCGCTGAGAGAAAGTTGGGATGATACAGACAGATGTTTGAAT 723
DB 798 ATTGCAGAGATGGGTTTGAAGAGGTTGGGATGATCTGATCAAGGATTTGAAT 857
QY 730 GATTCATCTCTCTTACATCATTCATTCAGGCGCCAGACCATCTACCTTGAAGAAATCTT 789
DB 858 GATCATCTCTATTTGATATTTCTTCAAGCTCCGATCTCTTCACTAGAGACTTCTCT 917
QY 790 GGGAGAGATCCCATATTTTAAAGCTGTGTGTGTATCCCTATGATGATCTTGTGCA 849
DB 918 TGGAGAGTACCAATGATTTCAATGTTGCTATATTTCTCTATGCTACTTGTGACA 977
QY 850 AGCTAATGTTAGGCTTGCAGACACAGAGAGACAGATCGTATATACAGCAAGT 909
DB 978 AGCCATCTCTTGGGTTTGTCTGACACTGAGGCGAGGTTTATATATCAATCAAGT 1037
QY 910 CCGTGACTGAGAAATGAGATGTTCTCCGTTTAAAGAACAGGCGCTTGAATTTCCC 969
DB 1038 GCGTCCCTTGAATATGAGATGCTCTTCGATCAGAAACAGGAGCTTGTATCACTCC 1097
QY 970 AAGATTCATTTGTTACTCGGCTGATACAGATGCAAAAGAAATCATGCAATCAGCG 1029
DB 1098 AAGATTTCAATTTGTTACAGGTTAATCCGATGCAAGGAGAAACATCAACAGCG 1157
QY 1030 GCTTGAAGATTTAGTGAACACAGACATATCATATTAAGAGTCTCTTCAAGATGA 1089
DB 1158 GCTAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
QY 1090 AATGGAATCTTAAAGATGATATCAAGATTTGATGATGATGATGATGATGATGATGAT 1149
DB 1218 GTCAGAGATCTCCGTTAAATGATTTCAAGGTTGATGATGATGATGATGATGATGATGAT 1277
QY 1150 TGTGAGAGATGCTGCTGATGAAATGCTGCTGATGAAATGCTGCTGATGAAATGCTGCTGAT 1209
DB 1278 TGCAGAGATGCTGCTGATGAAATGCTGCTGATGAAATGCTGCTGATGAAATGCTGCTGAT 1337
QY 1210 TGGAAATCTAGAGATGAAATCTTGGGCTGATGATGATGATGATGATGATGATGATGAT 1269
DB 1338 TGGAAATCTAGAGATGAAATCTTGGGCTGATGATGATGATGATGATGATGATGATGAT 1397
QY 1270 CAGTGAACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1329
DB 1398 AAGTGAACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1457
QY 1330 GAAATTTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1389
DB 1458 GAAATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1517
QY 1390 GAAATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
DB 1518 GAAATTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577
QY 1450 TGTGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
DB 1578 TGTGAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637
QY 1510 TGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
DB 1638 TGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1697
QY 1570 ATACTTTCATTCAG 1629
DB 1698 ATATTTTCCCTACCTGAAAG 1757
QY 1630 TTTGATTTTGAAG 1689
DB 1758 GCTATTTTGTCTCTGAG 1817
QY 1690 GCCATCTCTTCTCAG 1749

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Db 1818 GCGCAATATTCTCCATGCGAAGGCTACACAGAGTAAAAACATACCTGCAATTGGTACA 1877
Qy 1750 AGCTTTGCTAAGTGGCTAAGCTGAGGAGCTGGTAAACCTTGTGCTGCTGCGGCTA 1809
Db 1878 AAGCTTTGTAAGAACAGCAATTAAGGAACTGTGCAACTTGTATATAGTGTGCTTA 1937
Qy 1810 CATATATGCAACAAAGTCCAGAGCAAGGAGAGATCCGCGAGATAGAGAGATGCATGA 1869
Db 1938 TATTATATGTAAGAGAGTCCAGTGAACAGAGAAATTTGAGAAATGCATGA 1997
Qy 1870 ACTATCAAGACCCCACTGTGTGGGAGTCCGCTGATCTCTGCCCAACAAACG 1929
Db 1998 GCTCATGAAAAAGTAACTTAAGTGTGATTTGTGTGATTTGCTGCCAAACAAATG 2057
Qy 1930 GACCCGTAACGCGAGCTCTATCGCTACATCGCTGATACCCATGGTGTCTTGTACAGCC 1989
Db 2058 GGCACGTATAGGAGAGCTGTATCGCTACATGACACACACAAAGTGTCTTGTACAGCC 2117
Qy 1990 GACCTGTATGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2049
Db 2118 TGTCTTCTATGAGAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2177
Qy 2050 TTTGCGACGCTCCATGAGAGGTCAGCTAGATCATAGAGATGGCGTCTCGGGCTTCA 2109
Db 2178 TTTTGTCTATGCTGCGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2237
Qy 2110 CATGACCCGTAACACCCCGAAGAGCTGTATCTGATGTGCGGCTTGTGACCGGTG 2169
Db 2238 CATGATCTCTATGACCCCGATCAAGCTTCAAGCTATGATGTAATTTTCCAAAAGAG 2297
Qy 2170 CAAAGAAACCCAGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2229
Db 2298 CAAAGAGAGACCCAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2357
Qy 2230 GAAATGACATGAGAGATATATCTCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2289
Db 2358 AAGGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2417
Qy 2290 CTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2349
Db 2418 CTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2477
Qy 2350 CATCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2409
Db 2478 TATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2537
Qy 2410 GCTTGC 2415
Db 2538 ACTAGC 2543

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RESULT 6
US-10-424-599-98889
; Sequence 98889, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285884
; SEQ ID NO 98889
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (1)..(3191)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1
US-10-424-599-98889

Query Match      48.0%; Score 1314; DB 13; Length 3191;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 655; Indels 8; Gaps 3;

Qy 16 CCGGACCGCGCTGAGAGACACCTCCAGCGCGACCGCAAGAGCTGTGCGCTCTGTC 75
Db 230 CAGAGACCGAGTGAAGACACTCTCTCTCTACCGTACAGCACTATTTCTCTCTC 289
Qy 76 CAAATACGTGAACAAAGGGAGGAGGATCTGTGAGCGCACCAATCTCGAGCGCTGCA 135
Db 290 CAGGTATGTGTGTGAGGGAGAGGAGATTTTGCAACCCCAATTAATTTGATGATGA 349
Qy 136 CGAGGTCCAGGGC-----TCGGGGGGCGCGCGCTAGCCGAGGAGACCTTCTGTACGT 189
Db 350 CAAATCTCCCTGGCATGATCAAGCAATAGTGTATTTAAATGTCTTGTGTGTAAT 409
Qy 190 CTTCCGCTCCGCGAGAGGCGATCGTGTGCGCGCTTGTGTGCGCATCGCGTGGCC 249
Db 410 CGTCAAGTGTGCAAGAGAGACCAATGTTTGTCTCTTGTGTGTGTGTGTGTGTGTGTGT 469
Qy 250 GCGCCCGGAGTTTGGAGTACGTCCGCGTCAACGTTACAGAGCTCAGCGTGTGAGCT 309
Db 470 AAGACCTGTGTGTGGGAATATGTCCGTATATGTCTGTGAGCTCAGCGTGTGAGCAAT 529
Qy 310 CACAGTCTGAGTACCTCCGCTTCAAGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 368
Db 530 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
Qy 369 CTTACGTTCTGAGCTGTGCTTGTGAGCGCTGTCAATGTCTCACTCCACCGCAATCGT 428
Db 590 ATTTGTATGTGAGCTGTGTTTGTGAGCATTTAATGCCAATTTCTCTGTCAACCTGCT 649
Qy 429 CATCATCTATTGGAACCGT-GTGCATCTCTGAAACCGACACTGTCTCTCATCATGTTTC 467
Db 650 CAGCATTCATTTGGCAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
Qy 488 CGCAACAGGATTTGTGTGAGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547
Db 710 CGCAAGAGATTTCTGTGAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
Qy 548 CATGTATGATGCTTAAATGATGAATACAAAGCTTGGAGGCTTGTGTGTGTGTGTGTGT 607
Db 770 CATGCTGTATGTAAATGATGAATACAAACATTTCCAAATTTCAAGTCTGATGTGGC 829
Qy 608 AAGCTGAGGACCTTGTCAAAAGCTCCCTGTGTGACACCAATCTCAATTTGTCTTAT 657
Db 830 AAGGCTGAGGATTTCTCTTAAGCTGTGACATGATACCTCTATTCAGAGTTGAATAT 889
Qy 668 AATTTCAAGATGTGGGCTGTGAGAAAGTGTGGGAGATACAGAGACATGTTTGA 727
Db 890 GTATTGCAAGAAATGGCTTTTGAAGAGGTGTGGGAGTACGTGTGAACGGGATTTGA 949
Qy 728 ATGATCATCTCTCTTGAACATCATTCAGGCGCAAGCCATCTACCTTGAAGAAATTC 787
Db 950 ATGATCATCTCTCTTGTGATTTCTTTCAGGCTCCGATCTCTTCACTAGAGATTTT 1009
Qy 788 TTGGGAGAGATCCCATATTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
Db 1010 CTTGGAGAGTACCAATGTATTCATATGTTATATTTATCTCTCTATGTGCTTCTTGA 1069
Qy 848 CAGCTAATGATTTAGCTTGTGCAAGACAGAGAGACAGATGCTATATCTGACCA 907
Db 1070 CAGCAATGTCTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1125
Qy 908 GTCCGTGACATGAAGAAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
Db 1130 GTCCGTGACCTTGAAGAAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189

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QY 968 CCAAGATCTCTATTGTTACTCGGCTGATACCAAGATGCAAAAGGAACATCATGCATCAG 1027
DB 1190 CCAAGATCTCTATTGTTACTCGGCTGATACCAAGATGCAAAAGGAACATCATGCATCAG 1249
QY 1028 CGGCTTGAGAGAAATTAGTGAACACAGCATCTTACATTAATTAACAGATTCCCTTCAGAAAT 1087
DB 1250 CGGCTTGAGAGAAATTAGTGAACACAGCATCTTACATTAATTAACAGATTCCCTTCAGAAAT 1309
QY 1088 GAAAATGGGATCTTAAAGAAATGATATCAAGATTTGATGTGGGCCATATCTGSAACA 1147
DB 1310 GAGTCAGGAATCTCCGSAATTAAGATTTGATGTGGGCCATATCTGSAACA 1369
QY 1148 TTGCTGAGAGATGCTGCTGGAATTTGCTGCTGATTAACAGGATCTCCAGATCTTATA 1207
DB 1370 TATGAGAGATGCTGCTGGAATTTGCTGCTGATTAACAGGATCTCCAGATCTTATA 1429
QY 1208 ATTGGAATCTACAGTATGGAATTTGCTGCTGATTAACAGGATCTCCAGATCTTATA 1267
DB 1430 ATTGGAATCTACAGTATGGAATTTGCTGCTGATTAACAGGATCTCCAGATCTTATA 1489
QY 1268 ACCAGATGCAATCTGCTGATGCTGGAAGAAAGCTAAGTATCAAGATCTCAAGATTT 1327
DB 1490 ACCAGATGCAATCTGCTGATGCTGGAAGAAAGCTAAGTATCAAGATCTCAAGATTT 1549
QY 1328 TGAAGATCTGATGAGAGATACCATTTCTCTGCAAGTCTCACTGCTGATTAATTTGCT 1387
DB 1550 TGAAGATCTGATGAGAGATACCATTTCTCTGCAAGTCTCACTGCTGATTAATTTGCT 1609
QY 1388 ATGAAATCTGATGAGAGATACCATTTCTCTGCAAGTCTCACTGCTGATTAATTTGCT 1447
DB 1610 ATGAAATCTGATGAGAGATACCATTTCTCTGCAAGTCTCACTGCTGATTAATTTGCT 1669
QY 1448 ACTGCTGAGAGATGAGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507
DB 1670 ACTGCTGAGAGATGAGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1729
QY 1508 CATGGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1567
DB 1730 CATGGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1789
QY 1568 ATATATCTTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
DB 1790 ATATATCTTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1849
QY 1628 AATTGATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687
DB 1850 AATTGATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1909
QY 1688 AAGCCATCTCTCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747
DB 1910 AAGCCATCTCTCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1969
QY 1748 GAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1807
DB 1970 GAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2029
QY 1808 TACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1867
DB 2030 TACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2089
QY 1868 GAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1927
DB 2090 GAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2149
QY 1928 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1987
DB 2150 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2209
QY 1988 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2047
DB 2210 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2269

QY 2048 ACTTTCGCAAGCTTCATGAGAGCTGCAAGTATCATAGATGAGCTGCTCGGCTTC 2107
DB 2270 ACTTTCGCAAGCTTCATGAGAGCTGCAAGTATCATAGATGAGCTGCTCGGCTTC 2329
QY 2108 CACTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2167
DB 2330 CACTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2389
QY 2168 TGCAGCAAGACCCAGATCACTGAGGATATATCTGAGAGAGGCTGCTGAGATATAC 2227
DB 2390 TGCAGCAAGACCCAGATCACTGAGGATATATCTGAGAGAGGCTGCTGAGATATAC 2449
QY 2228 GAGAGTACATGAGAGATATATCTGAGAGAGGCTGCTGAGATATAC 2287
DB 2450 GAGAGTACATGAGAGATATATCTGAGAGAGGCTGCTGAGATATAC 2509
QY 2288 TTCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2347
DB 2510 TTCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2569
QY 2348 TACATCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2407
DB 2570 TACATCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2629
QY 2408 TAGCTTC 2415
DB 2630 TAGCTTC 2637

RESULT 7
US-10-425-114-5285
; Sequence 5285, Application US/10425114
; Publication No. US2004003488B1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalev, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5285
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454567_F11
US-10-425-114-5285

Query Match 47.9%; Score 1309.8; DB 13; Length 1340;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 128; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 1357 CTCCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416
DB 1 CTCCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 1417 CACATACCAAGAAATTTGCTGAGCAAAATCTGTTGAGCAAGTATGAGAGCTATCTG 1476
DB 61 CACATACCAAGAAATTTGCTGAGCAAAATCTGTTGAGCAAGTATGAGAGCTATCTG 120
QY 1477 CTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1536
DB 121 CTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 1537 CAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596
DB 181 CAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 1597 GCGACTCACTCTCTCATGATCAATCGAAATTTGATTATGATGACCCGAGCAAAACGA 1656
 DB 241 GCGACTCACTCTCTCATGATCAATCGAAATTTGATTATGATGACCCGAGCAAAACGA 300
 QY 1657 TGAACACATTGGGCACTTGAGATGACCGGTCAAAAGCCATCTTCTTCATGAGCAAGACT 1716
 DB 301 TGAACACATTGGGCACTTGAGATGACCGGTCAAAAGCCATCTTCTTCATGAGCAAGACT 360
 QY 1717 CGACAGGATGAAACATTAACAGGGCTGTGCGAAGCTTTGCTAAGTGGCGCTAAGCTGAG 1776
 DB 361 CGACAGGATGAAACATTAACAGGGCTGTGCGAAGCTTTGCTAAGTGGCGCTAAGCTGAG 420
 QY 1777 GAGAGCTGTAAACCTTGTGCTGCTGCGGGGTACAAATGATGTCAACAAAGTCCAAAGACAG 1836
 DB 421 GAGAGCTGTAAACCTTGTGCTGCTGCGGGGTACAAATGATGTCAACAAAGTCCAAAGACAG 480
 QY 1837 GGAAGAGATGCGGAGATGAGAAGATGATGATGATCAAGAACCCCAACTTGTTCG 1896
 DB 481 GGAAGAGATGCGGAGATGAGAAGATGATGATGATCAAGAACCCCAACTTGTTCG 540
 QY 1897 GCAATTCGCTGATATCTTGCCCGACAAACAGGGCCGTTAAAGGGAGCTTAATGCTTA 1956
 DB 541 GCAATTCGCTGATATCTTGCCCGACAAACAGGGCCGTTAAAGGGAGCTTAATGCTTA 600
 QY 1957 CATGCTGATACCATGATGCTTTCGTAACAGCCGCTTGTATGAAGCGTTCCGCTCAC 2016
 DB 601 CATGCTGATACCATGATGCTTTCGTAACAGCCGCTTGTATGAAGCGTTCCGCTCAC 660
 QY 2017 CGTGTGTAAGGCGCATGACCTGTGGGCTTCTTACTTTGCGAGCGCTCCATGAGGCTCCAGC 2076
 DB 661 CGTGTGTAAGGCGCATGACCTGTGGGCTTCTTACTTTGCGAGCGCTCCATGAGGCTCCAGC 720
 QY 2077 TGAATCATATGACATGAGCGCTGCTGCGCTTCCATGATGACCCGTAACCCCGAACAAGC 2136
 DB 721 TGAATCATATGACATGAGCGCTGCTGCGCTTCCATGATGACCCGTAACCCCGAACAAGC 780
 QY 2137 TGTATATCTGATGAGCGCACTTCTTCCACCGGTGCAAGCAAGACCCAGATCACTGGTGA 2196
 DB 781 TGTATATCTGATGAGCGCACTTCTTCCACCGGTGCAAGCAAGACCCAGATCACTGGTGA 840
 QY 2197 TATATCTGAGCAAGGGCTGCGAGCGCATATACAGAAATGATCAATGAAATATATCTGAG 2256
 DB 841 TATATCTGAGCAAGGGCTGCGAGCGCATATACAGAAATGATCAATGAAATATATCTGAG 900
 QY 2257 GATGTTGATGACACTGGCGCGGGGCTTAAGGTTCTGGAATGATGCTGCAAGCTCCAGAG 2316
 DB 901 GATGTTGATGACACTGGCGCGGGGCTTAAGGTTCTGGAATGATGCTGCAAGCTCCAGAG 960
 QY 2317 GCTGAGACGAGGCGCTACTTGTGATGATCTTAATATCTGAAGTTCGCGAGCTGGAG 2376
 DB 961 GCTGAGACGAGGCGCTACTTGTGATGATCTTAATATCTGAAGTTCGCGAGCTGGAG 1020
 QY 2377 GACCGTGGCGCTTGGCAATTGACCAACGCGATGACTTGGCAACTGGGACTGGGTAGAC 2436
 DB 1021 GACCGTGGCGCTTGGCAATTGACCAACGCGATGACTTGGCAACTGGGACTGGGTAGAC 1080
 QY 2437 TTGATCAACAACTGAAACCTGAAAGACTTCAATATTTAGGCGCGGACAGCGGTAGCCA 2496
 DB 1081 TTGATCAACAACTGAAACCTGAAAGACTTCAATATTTAGGCGCGGACAGCGGTAGCCA 1140
 QY 2497 ATAAATATGTCGCGAGCTGAAGCTTTTATTTATTTATGATCAATATGCAATATTAACAA 2556
 DB 1141 ATAAATATGTCGCGAGCTGAAGCTTTTATTTATTTATGATCAATATGCAATATTAACAA 1199
 QY 2557 TTAATGAGGCAAGTGGGTTGCAATTTGCTGCTTACTGTTTACTGTTATATGTTAGTAA 2616
 DB 1200 TTAATGAGGCAAGTGGGTTGCAATTTGCTGCTTACTGTTTACTGTTATATGTTAGTAA 1259
 QY 2617 CTGCGGCTCAATTTCTTGTGCTGCGAAGCGGAGGCACTGATGAAAGTGTGATTAATAC 2676
 DB 1260 CTGCGGCTCAATTTCTTGTGCTGCGAAGCGGAGGCACTGATGAAAGTGTGATTAATAC 1319

QY 2677 ATCATATCTGTTGACCTGTG 2697
 DB 1320 ATCATATCTGTTGACCTGTG 1340

RESULT 8
 US-09-938-842A-2415
 ; Sequence 2415, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krebs, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OR INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OR INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCDP1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2415
 ; LENGTH: 2430
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-2415

Query Match 45.2%; Score 1238.4; DB 9; Length 2430;
 Best Local Similarity 70.4%; Pred. No. 0;
 Matches 1672; Conservative 0; Mismatches 696; Indels 6; Gaps 1;

QY 18 GCGACGCGCTGAGGACACCTTCCAGCGGACCGCAACGAGCTGTGCGCTCTCTGTCGA 77
 DB 38 GCGATGCGCTGAGGACACCGCTTCCGCTCACCGCAACGAACTGCTTCTTCTTCA 97
 QY 78 AGTAACGTGAACAGGGGGAAGGAGCATCTGAGCGGACCAATCTGAGCGGCTGACG 137
 DB 98 GGTATGTGATGCAAGGGGGAAGGATTTTCAACCTCAATTAATGAGCAATCTGAAT 157
 QY 138 AGGTCCAGGCGCTCCGAGGCGCGCGC-----CTAGCCAGGAGACCTTCTCTGAGCTCC 191
 DB 158 CTGTTATCGGAGAGATGAAACAAAGAGAGTCTCTGATGATCTTTGAGAGATCC 217
 QY 192 TCCGCTCCGCGAGAGGCGCATGTGCTGCCCGCGTTCGTGCGCATGCGGTGGCCGCGC 251
 DB 218 TTAATATGCAATGGAAGCTATATGTTGTACCACTTGTGTGCGTTAGCCGTTAGACCAA 277
 QY 252 GCCCGGAGTTGGGAGTACGTCCGCGGTCAACGTTCAAGACTCAAGGCTGAGGAGCTCA 311
 DB 278 GACCTGCTGTTGGGAATATGTTGTTAATGTTCTTCAAGCTTAAGTTGAACATTTAA 337
 QY 312 CAGCTTCGAGTACCTTCCGCTTCAAGGAGAGCTTGTGACGCGGACCAATGATCCCT 371
 DB 338 CAGCTTCGAGTACCTTCCGCTTCAAGGAGAGCTTGTGACGCGGACCAATGATCCCT 397
 QY 372 ACGTTTCGAGCTTGAATTTGAGCGCTTCAATGCTCAATGCTCCAGCGGCAATGCTCAT 431
 DB 398 TTTGTTCTGAGCTTGAATTTGAGCGCTTCAATGCTCAATGCTCCAGCGGCAATGCTCAT 457
 QY 432 CATCATTTGGAACAGGTTGCAATTTCTTCAACGACACTTGTCTCTCAATCAATGTTCCGA 491
 DB 458 CTTCGATTTGGAATGAGGTTCAAGTTCTGAATGCTCACTTGTCTCTCAATCAATGTTCCGA 517
 QY 492 ACAAGGATTCCTTGAAGCCCTGTTGATTTCTTCCGTCACCGGACCGGACAGGCGCATG 551
 DB 518 ACAAGGATTCCTTGAAGCCCTGTTGATTTCTTCAAGTTCAATGATCAATGAGGTCATC 577
 QY 552 TTAATGCTTATGATGAAATCAAAAGCTTGGGGAAGCTTCACTGTGTGACCAAG 611

LENGTH: 2430
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2415

Query Match 45.2%; Score 1238.4; DB 11; Length 2430;
Best Local Similarity 70.4%; Pred. No. 0;
Matches 1672; Conservative 0; Mismatches 696; Indels 5; Gaps 1;

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QY 18 GCGACCGGTGAGAGACCCCTCCACCGGCAACCGAGAGTGGCCCTCCCTGTCGA 77
DB 38 GGGATCGGTGCAACACACGCTTCCGCTCACCGCAAGAACTGGTGGCTCTCTCCCA 97
QY 78 AGTACGTAAACAGGGGAGGAGGATCTCTGACGCGCACCACTCTGACGCGCTCGACG 137
DB 98 GGTATGTGATCAGGGGAAAGGATTTCTTCAACACATTAATTTAGACCACTCGCAT 157
QY 138 AGGTCCAGAGGCTCCGGGGCCCGCGC-----CTAGCCAGAGGCCCTTCTCGAGTCC 191
DB 158 CTGTATCGGAGACGATGAAACAAAGAAAGTCTCTGATGATGCTCTTTGGAGAGATCC 217
QY 132 TCCGCTCCGCGCAGAGGCGATCGTCCGCGCGCTTGGCCATCGCGTGGCGCGCC 251
DB 218 TTAAATCAGCAATGGAACCTATAGTTGTAACACCTTTGTGCGTTAGCGCTTACACA 277
QY 252 GCCCGGAGTTTGGAGTACGTCGCGCTCAACGTTCAAGCTCAGCGCTCGAGCAGCTCA 311
DB 278 GACCTGCTGTTGGGAAATATGTTGGTTATGTTGAGAGCTAGTGTGAAACAATTA 337
QY 312 CAGTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGACGCGCAACAATGATCCCT 371
DB 338 CAGTCTCGAGTACCTCGTTCAAGAGAACTCGTGTGATGAGAACTATAGTACCCCT 397
QY 372 AGCTTCTGAGCTTACCTTCGAGCGCTTCAATGCTCAGTCCGACGCGCAATGGTCA 431
DB 398 TTTGCTTGAAGCTTATTTGAGCCCTTAAACGCAACGTCGACGCTCTCTCTGCT 457
QY 432 CATCATTTGMAACGATGTCAGTCTCTCAACGACATCTGCTCAATCATGTTCCGA 491
DB 458 CTTCATTTGATATGATGAGATCGCTTCTGATCTGATCTGCTCTGTTATGTTCCGA 517
QY 492 ACAGGAGTTGCTTGAAGCCCTGTTGATTTCTCCGCGGACCAACGCGCAAGGGGATG 551
DB 518 ACAAGATTTGCTGAGCTCTGCTGATTTCTTGAAGTCTATAGTCAAAAGGTCATC 577
QY 552 TTATATGCTTATATGATGAAATCAAAAGCTTGGGAGGCTTCAAGTGTGTCGACCAAG 611
DB 578 CGTTGATGTTGATATGATGATCAAGCATATCTAGGCTTCAATCCAGCTTAGTAAG 637
QY 612 CTGAGGAGACTTGTCAAGCTCCCTGCTGACACACCATACTCACAAATTTGCTTAAAT 671
DB 638 CAGAGATCATATCTCTAAGCTTTCACAGAAATCTCCGTTCTGGAAATTCGAAACGG 697
QY 672 TTCAAGAGTGGGGCTGAGAAAGTTGGGGTGATACAGAGACATGTTTGGAAATGA 731
DB 698 TCGAAGGATGGGTTTGGAAAGAGATGGGGAGATACCCAGGGAGAGTCTTGAATATA 757
QY 732 TCCATCTCTCTTACACATTCATGAGGGGCGCAGAACCATCTAACCTTAGAATTTGG 791
DB 758 TGCATCTTCTCTGATATCTTCAAGCTCTGATCTTGTGCTTGGAGAGTTTCTTG 817
QY 792 GAGAGATCCCATGATTTTAAAGTTGTGTGTATCCCTCATGAGATACTTGTGTAAG 851
DB 818 GGAATGATCAATATGTTTCAAGGTTGTATCTTATCTCAATGATATTTGGGCAAG 877
QY 852 CTAAATGATTAAGCTTTCAGACACAGAGACATGCTCTTATATCTGACCAAGTCC 911
DB 878 CCAATGTTTAAAGCTTACCTGACACTGGGACAACTGTGCTATATCTTGGACCAAGTCC 937
QY 932 GTGCACTAAGAAATGATGATGCTCTCGTTTAAAGAAACAAGGGCTGATGTTCCCA 971
DB 938 GTGCTTGAAGACTGAATGCTCTGAGAAATTAAGAGACAGGGGTTGATATACCTTA 997
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DB 1058 TAGAAGATGACCGGAAACAGGACATCTCAATTTCTCGGGTCTCTTTAGGCTGAGA 1117
QY 1092 ATGGATCTTAAAGAAATGATATCAAGATTTGATGTGTGGCCATATCTGAAACAATTTG 1151
DB 1118 AAGGATCTCTCGTATGATGATTTCAAGATTTGAGATATGAGCTTATCAGAGAACTATG 1177
QY 1152 CTGAGATCTCTGATGAAATTTGCTGCTGAATTAACAAGTATCTCAAGCTTATATTTG 1211
DB 1178 CTACAGATGACGCAAGCAGATTTGCGGTGATGCAAGGCGCTACCGGCTTATATCATG 1237
QY 1212 GAATCTACAGATGAAATCTGTGGGCTCATGCTTCAAGATGAGGAAATTAACCC 1271
DB 1238 GTTACTATATGATGACGAAACCTTGTGATCTTAAATGAGCACTAAGATGGGTGTAAC 1297
QY 1272 AGTCAACATTTGCTCATGCTCTGAAAAAGACTAAGTATCCAGATTCAACATATTTGGA 1331
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QY 1332 AGAATTTGATGAGAAATCAATTTCTCTGCTGCACTTCACTGCTGATATATTTGCTTGA 1391
DB 1358 AAGCTTTCAGCAACAGATATCAATTTCTCTGCAATTCACAGCTGATCTTATTCGATGA 1417
QY 1392 ACAATGCTGATTTTATCAATCAACAGACATACCAAGAAATTTCTGGAACCAAAATATCTG 1451
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DB 1538 GATGATGCTTTCATGATCCAAAGTTCAATATATGCTCTCTGAGCTGACATGATCAT 1597
QY 1572 ACTTTCACATACCGGAAAGGCAAGCGACTACCTCTCTTCAATGATGATGAAATTT 1631
DB 1598 ATTTCCCGATTTCCAGAAAGAACTTAGAGACTTACAGCTTATCATGATTTCAATAGAGG 1657
QY 1632 TGATTTATGACCCGAGCAAAACGATGAAACATATGAGGATCTGATGACCTGCTCAAGC 1691
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QY 1692 CCATCTCTTCTCATGAGACATCTGACAGGCTGAAAGAACTAACAGGCTGTGGAAG 1751
DB 1718 CAATCTCTTCTTATGAGGAGGCTGACAAAGTGAAGAACTCTCGGTTTATGTTGAGA 1777
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DB 1778 TGTATATGTAAGAACAAAGTTGAGGAGCTGTTATCTGTGTATATAGCTGTATACA 1837
QY 1812 ATGATGTCAACAGTCCAAAGACAGGAAAGATGCGGAGATAGAAAGATCATGAAAC 1871
DB 1838 TTGATGTGAACAAGTCCAAAGATAGAGAAATCTAAGATTTGAAAGATGCAATACCC 1897
QY 1872 TCAATCAAGCCCAAACTTGTGCGCACTTCCGCTGATCTCTGCGCAGACAAAGAGG 1931
DB 1898 TTATAGAAATTAACAAGCTTGAATGACAGTTTGTGTGAAATATGCTCAAGCTAACCG 1957
QY 1932 CCGGTAAACGAGAGCTCTATGCTATGCTATGCTGATACCAATGATGCTTCTGTAACGCG 1991
DB 1958 CTGAAATGATAGCTTACCGCTATGCTGATGCTGATGCTGATGCTGCTGCTGCTG 2017
QY 1992 CCTTGTATGAAGGCTTGTGCTGACCTGTGTGAGGCTGATGCTGCTGCTGCTGCTG 2051
DB 2018 CGTCTTACAGAGGCTTTTGAATTTACCGTATGAGAAACGATGATTTGCGGCTCCGACT 2077
QY 2052 TCGCAGGCTCATGAGAGTCCAGCTGAGATCATAGAGATGAGCTCTCGGGCTTCCACA 2111
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Db 2078 TTGCGACCTTGTACAGGTGTGTCAGACAGATTCAGACAGGGCTCTCGGGTTTCCACA 2137
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Db 2138 TCGATTCATACCTCCGAGACCGGTAACATTAATGAGCTGATTTCTTGGAAAGTTGTA 2197
Qy 2172 AGCAAGCCAGATCATCTGGGTGAATATCTGAGACAGGGCTGACAGCATATACAGA 2231
Db 2198 AGGAGATCCAAACATTGGAGAAAGTTCAGACGCTGCTTCGAAAGATATACAAA 2257
Qy 2232 AGTACATGAAAGATATCTACAGAGAGTTGATGACATGCGCGGGTCTACGGTTCT 2291
Db 2258 GTATACATGAAAGATATATCTCGAGAGATTGATGACATGAGTGTGTATGTTCT 2317
Qy 2292 GGAAGTACGTGTGAAAGCTTGAGAGGCTGAGACAGAGCGCTACTTGAATGTTTACA 2351
Db 2318 GGAATAACGTATGAAATTGAGAGGTGTGAGACTCGGCATATCTGAAATGTTTACA 2377
Qy 2352 TACTGAAGTCCGCGAGCTGCGAGACCGTGC 2385
Db 2378 TTCTCAATTCGCGACTTGTTGAAAATCTGTCC 2411

RESULT 10
US-10-217-939-29
; Sequence 29, Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENDORF, VOLKER
; APPLICANT: HAERTEL, HEIKO A.
; APPLICANT: CIPRUS, PETRA
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ. ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 29
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-217-939-29

Query Match 43.2%; Score 1181.2; DB 15; Length 2394;
Best Local Similarity 70.5%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 164 CTGACCGAGGAGCCCTTCTCGACGTCTCCGCTCGGCGACAGAGGGGATCGTCCGG 223
Db 151 CTTAACAAAGTCATTCATGAAAGTCTGAGCTCTGAGAGAGACATATGTTGCTT 210
Qy 224 CCGTTCGTGGCCATCGCGGTGCGCCGCGCCGAGATTGGAGTACGTCCGCTACAC 283
Db 211 CCATTGTGTGCTTGGCTATACGTCCAGACCTGTGTAGGGAATATGTCGCTGAT 270
Qy 284 GTTACAGAGCTCAGCGTGCAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAGAG 343
Db 271 GTGATAGCTGAGCGTAGATCATTTAATGTTCTGATAATCTTCGTTTAAAGAAAG 330
Qy 344 CTGTGAGGCGAGCAGCAATGATCCGTAGTCTCGAGGCTGACTCGAGCGTTCAAT 403
Db 331 CTGTATATGCCATGCGCAATGAGATATCTCTTGAATTTGAATTTGAATTTCAAT 390
Qy 404 GTCTAGTCCCAAGCCCAATTCGTATCATCTATTGAAAAGGTGTGCAAGTCTCAAC 463
Db 391 GCAACATGTGCTGCGCCCAATCGTTTATCATTCATTGGGAATGAGGTTCCTCAAT 450
Qy 464 CGACACTTGTCTATCATGTTCCGCAAGAGGATGCTTGAAGCCCTGTGGATTTTC 523
Db 451 CGTCACTCTCTTCAATATATGTTCTGTAACAAAGAAAGCATGAGACCTTGTGAGTTT 510

Qy 524 CTCGTTGGCAACCGGCAAGAGGCGATTTATGATGCTTATGATAGATACAAAGCTTGG 583
Db 511 CTCGCACTCAAAACATGATGCGCTCTATGATGCTGAATGATCGAATACGAATATC 570
Qy 584 GAGAGCTTCAAGTGTGTGACCAAGCTGAGAGCACTGTCAAGCTCCCTCTGAC 643
Db 571 CCCATCTTCAAGGAGCTTTGCAAGACAGAGAGTTCCTTTCTAACTTCTCTGCA 630
Qy 644 ACACATCTCAAAATTTGCTTATTAATTTCAAGTGGGCTGAGAAAGTTGGGT 703
Db 631 ACACATCTCTGAATTCGAATTTGAATCAAGAGGATGGGATTTGAAGGGGAGTGGGT 690
Qy 704 GATACAGAGACATGTTTGGAAATGATCAATCTCTTACAGATCAATTCAGGCGCA 763
Db 691 GACAGACACAAAGGTTTCAAAATGATGATCTTCTTGACATATCTCAGGCACTT 750
Qy 764 GACCATCTACCTTAGAGAAATCTTGGAGAGATCCCATGATTTTAAAGTGTGTG 823
Db 751 GATCTTCTGTGTGAGAGCTTCTAGAGAGATTCCTATGATGTTCAATGTTGTGAT 810
Qy 824 GTATCCCTCATGATCTTGTGTAAGCTATGATTTAGGCTTCCAGACAGAGAGA 883
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Db 991 GCAAGGAAACAAAGTCAACCAAGGTTAAAGATGATGTGTACCAACACACAC 1050
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Qy 1184 TTCAAGTACTCCAGCTTCATTAATTTGAAATCACTAGTGAATCTTGTGCGTCA 1243
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Db 1291 AAGTACCCGAGTGTGACATTTACGAGAAACATGAAAGTAAATGATCACCTTCAAGT 1350
Qy 1364 CAGTTCAGTGTATATATTTGCTATGAGAAAGTGTATTTATATCATCAGACATATC 1423
Db 1351 CAGTTCAGTGTATATTTGCTATGAGAAATGCTGATTCATATCATCAGACATATC 1410
Qy 1424 CAAGAAATGCTGAGAGCAAAATATCTGTGACAGATGAGATCATATGCTCTTATCT 1483
Db 1411 CAAGAAATGCTGAGAGCAAAATATCTGTGAGAGATGAGATCATATGCTCTTATCT 1470
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Db 1471 ATGCTGTGTCTTTCAGAGTGTGATGAGATGATGCTTGTGATCCAAAGTTTAAATG 1530
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 QY 1282 TACTATGCTGTGAAGAACTAAGTATCCAGATTCAACATATTTGGAAAGATTGCA 1341
 DB 1293 TCTCATGCTTTAGAGAAACCAAGTACCAGCTGACATTTACTTGGAGAAACCATGA 1352
 QY 1342 TGAAGATACCTTTCTCTGCGAGTTCACTGCTGATTAATTTGCTATGAACATGCTGA 1401
 DB 1353 AATATAGATCACTTTCAAGTCACTGCTGCAATCTTAATTTGCTATGAATATGCTGA 1412
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 DB 1413 TTTTATCATCAGCAGACATACCAAGAAATGTGAGAGCAAAAATGTTGGGCAAT 1472
 QY 1462 TGAAGTCACTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
 DB 1473 CGAGAGCCACAGCTTCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1532
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 DB 1533 CTTCGATCCAACTTCAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1592
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 DB 1593 TTTCTGCAAGAGAAAGAAAGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1652
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 DB 1773 GATTAACAGGCTTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1832
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 DB 1833 TCAAGTCAAGGAGATAGAGAGAGATGCTGATACAAAGATGCAAGCTGATGAGCA 1892
 QY 1882 CCACAACTGCTTGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1941
 DB 1893 GTATGATTTACAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1952
 QY 1942 CGAGCTCTATCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2001
 DB 1953 TGAAGCTTACCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2012
 QY 2002 AGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2061
 DB 2013 AGCATTTGGGCTTACGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2072
 QY 2062 CCATGAGTCCGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2121
 DB 2073 TATGATGAGCCGCGAGATTAAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2132
 QY 2122 CCACCCCGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2181
 DB 2133 TATGAGAGAGAGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2192
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 DB 2193 AATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2252

QY 2242 GAAGATATACAGAGAGGTTGATGACACTGACCGGGGTTACAGGTTCTGGAATACGT 2301
 DB 2253 GAGAGAGTACTAGAGAGAGTCTTACCTGGTGGAGTGTATGATCTGGAACATGT 2312
 QY 2302 GTGGAAGCTGAGAGGCTGAGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2361
 DB 2313 GTCTAAGCTGGAAG 2372
 QY 2362 CGCAGAGCTGCGAAG 2397
 DB 2373 TCGTATTTGGCCCAATTCATCCGCTGCGACAGA 2408
 RESULT 12
 US-10-080-114a-6
 ; Sequence 6, Application US/10080114a
 ; Publication No. US20030005482A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dhurga, Kanwarpal S.
 ; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
 ; TITLE OF INVENTION: to Improve Stalk and Grain Quality
 ; FILE REFERENCE: 1301P
 ; CURRENT APPLICATION NUMBER: US/10/080,114A
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/270,777
 ; PRIOR FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 2908
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (28) ... (2478)
 ; US-10-080-114a-6
 Query Match 42.5%; Score 1162; DB 15; Length 2908;
 Best Local Similarity 68.3%; Pred. No. 0;
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 DB 66 CCAGAGGCTCGAG 125
 QY 67 CTTCTGCTCCAGTACTGAAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
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 QY 127 CGCGCTGAGC--GAGGTCCAGGAGCTCGGGGAGCGGCTGAGCCGAGAGAGAGAGAGAGAG 183
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 QY 184 CGAGTCTTCGCTCGCGAG 243
 DB 246 GAGATGCTTGAAGGAG 305
 QY 244 GCGCGCGCGCGCGAG 303
 DB 306 CCGCGCTGAG 365
 QY 304 GCAAGTCAAGTCTCGAG 363
 DB 366 GAGAGTGAAGTCTCTGAG 425
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 DB 426 CAACAACTTGTGTTTGAAGCTGAG 485
 QY 424 TGGGATCAATCAATGGAAG 483
 DB 486 TCTGTCAAGTTCATTTGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545

484 GTTCGCAACAGGATGCTTGGAGCCCTGCTGATTTCTCCGTGACCACCGACAA 543
546 CTTCATGACAGAGAGAGATGATACCTTGTCTCAACTCTTCCGGCCCAACAATACAA 605
544 GGGGCACTTATGATCTCTTAATGATGAAATACAAAGCTTGGAGGCTTCACTGTGCT 603
606 GGGGATGACCAATGATGATGACAGACAAATCCGCACTCTCAGTGTCTTCAAGTGTGCT 665
604 GACCAAGCTGAGAGACCTTGTCAAGCTCCTGCTGACACCACTATCCAAATTTTC 663
666 GAGGAGGCTGAGAGACCTTGTCAAGCTCCTGACAGCTGATCCCACTACTCTGAATTTCA 725
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726 CCACAGGTTCCAGAACTGTGCTGAGAGAGGTTGGGTGATGTGGCTTAAGTGTGACA 785
724 GGAATATGATCTCTCTTCTGACATCTTACGCGCCAGACCACTTACCTTAGAA 783
786 GAGGACTATCCACCTCTCTGTGAGCTCTGAGGCCCCAGATCCGTCACCTGAGAA 845
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844 TGCTCAAGCTAATGATTAAGCTTGGCAGACACAGAGAGACAGATGCTATATACCTGA 903
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904 CCAAGTCCGTGACATGAGAAATGAGATGCTTCCCTTTAAAGAAACAAGGCTTATGT 963
966 TCAAGTCCGTGACATGAGAAATGAGATGCTTCCCTTTAAAGAAACAAGGCTTATGT 1025
964 TTTCCCAAGATTTCTATGTTTACTGCTGATACAGATGCAAAAGAAACATCATGCA 1023
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1564 GTTCATATATCTTCCATACAGAGAGGCAAGGCACTCACTCTTCTTCAATGCTTCAAT 1623

1626 GTTCATCTACTTCCGCTTACACGAGTGCACAAAGGCTGAGCTTCTTCAACCGAGAT 1685
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1686 TGAAGAGCTCTGTATAGCCAAACGAGAAACAGAGGCAAGTGTGTTGAGACAG 1745
1684 GTCAAGCCCATCTCTTCTGATGAGCAAGTCTGACAGGCTGAGAAACATTAACAGGCT 1743
1746 GAAACAGCCATATCTTCTTCACTGAGCTGTCTGACCGGTGAGAAACATTTGAGCT 1805
1744 GGTGAGGCTTTTGTATAGTGTGCTGAGAGGCTGAGAGGCTTAACTTGTGCTTGC 1803
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1866 CGGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 1922
1864 GCATGATCAATCAAGACCAACTTGTGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 1923
1923 GTTGAATCTCATGAGACATGACATGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 1982
1924 AAGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 1983
1983 GAAAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2042
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2103 GCTCAAGTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2162
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2163 CTACACATTAAGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2222
2164 CGGATCAAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2223
2223 CAGTCCAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2282
2224 ATACAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2283
2283 CAGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2342
2284 CGGATCAAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2343
2343 CGGATCAAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2402
2344 GTTCTCATATCAAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2403
2403 GCTGTACGAGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCT 2462
2404 GC 2405
2463 GC 2464

RESULT 13
US-10-425-114-2283
; Sequence 2283, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yilun
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

Db 2105 GAACCGCGTCCGCAACGGGCGAGGTGATACCTGATCTGCGACCAAGGCGCCCTTCGT 2164
Qy 1984 ACAGCGCGGCTTGTATGAGAGGCTTGGCTGACCGCTGTTGAGGCGATGACCTGTGGCT 2043
Db 2165 GAGAGCTGCTTTCTACAGAGGCTTTGCGGCTGACGCTGTTGAGGCGATGACCTGTGGCT 2224
Qy 2044 TCTACTTTCGCGACGCTGACATGAGGCTGACCTGATGATCATAGAGCATGCGCTTCGAG 2103
Db 2225 GCCACGCTTGTCCACAGGCTTACGCGGCTCCGCGCAGATCATGCGACAGCGCTGTGCG 2284
Qy 2104 CTTCACATTTACCGCTTACGACCCCGAACAAGCTGTTAATCTGATGCGGCACTTCTTGA 2163
Db 2285 CTACCAATTCGACCTTTACCGAGGCGACAGCGCTGCGCCCTGCTGCGATCTTCTGGA 2344
Qy 2164 CCGGTGCAAGCAAGACCCAGATCACTGCGGTATATATCTGAGACAGGCGCTGACGCGAT 2223
Db 2345 CAAGTCCAGCGCGAGCCCGAGGCTGAGAGGAGGATCTCCAGAGGCGGCGCTGACGCT 2404
Qy 2224 AACGAGAGATGACATGAGAGATATATCTGAGAGGCTGATGACCTGCGCGGCTCTA 2283
Db 2405 CGAGAGAGATGACCTGAGAGCTTACTCTGAGAGGCTGATGACCTGACCGGCTGTA 2464
Qy 2284 CGGTTTCTGAGAGTACGCTGTTGAGAGCTGAGAGGCTGAGAGGAGGCGCTTCTGAGAT 2343
Db 2465 CGGCTTCTGAGAGTACGCTGTTGAGAGGAGGCGGAGAGCGGCGGCTGAGAGAT 2524
Qy 2244 GTTCTACTACTGAGAGTCCCGGAGCTGCGGAGAGCGGCTGCGCTTGCATTTGACCAAC 2403
Db 2525 GCTGTACCGCTGACAGTACCGGACCATGCGAGGACCGCTGCGGCTGCGGCTGAGAGAG 2584
Qy 2404 GC 2405
Db 2585 GC 2586

RESULT 14
US-10-425-114-26430
Sequence 26430, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingsheng
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26430
LENGTH: 2986
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: L1B4172-051-C3_F11
US-10-425-114-26430

Query Match 42.5%; Score 1162; DB 13; Length 2986;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 755; Indels 6; Gaps 2;

Qy 7 CGAGCGGCTGCGGACCGGCTGAGAGACCTCCACGCGGACCGGCAAGAGCTGCGC 66
Db 2188 CGAGCGGCTGCGGACCGGCTGAGAGACCTCCACGCGGACCGGCAAGAGCTGCGC 247
Qy 67 CTTCTGCTCAAGTACGTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
Db 248 GCTCTTCAACGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
Qy 127 GCGGCTGAC--GAGGCTCAGGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183

Db 308 CGAGTCAACCAATCGATCCCTGAGGCTGAGCGGAGAGGCTCAAGAGTGGCTTTTGA 367
Qy 184 CGAGTCTCTGCTCGGCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Db 368 GGAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 427
Qy 244 CGGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
Db 428 CGGCGCTTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 487
Qy 304 GAGCTCAACGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
Db 488 GAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
Qy 364 TGATCCCTAAGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
Db 548 CAACACTTGTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 607
Qy 424 TCGGTCAATCTATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 483
Db 608 TCTGTCAAGTCCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 667
Qy 484 GTTCCGCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
Db 668 CTTCATGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
Qy 544 GAGGAGGAGTATGAGTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
Db 728 GGGGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
Qy 604 GACCAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 663
Db 788 GAG 847
Qy 664 TTATTAATTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 723
Db 848 CCAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 907
Qy 724 GGAATGATTCATCTCTCTTCTGAGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
Db 908 GGAAGCTATTCACCTCTCTTCTGAGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 967
Qy 784 ATTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843
Db 968 GTTCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1027
Qy 844 TGGTCAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
Db 1028 GCTCAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1087
Qy 904 CCAGTCCGTGACCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 963
Db 1088 TCAAGTGGCGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1147
Qy 964 TTCCCAAGGATTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
Db 1148 CAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1207
Qy 1024 TCAGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1083
Db 1208 CGAGCGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1267
Qy 1084 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143
Db 1268 AACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1327
Qy 1144 AACATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
Db 1328 GACTTCACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1387
Qy 1204 CATATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1263

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Dh 1388 GATCATCGAACTACAGTACGGAACCTTGTGCTGCTTGTGCTGCCCAAGATGGG 1447
Qy 1264 AATTACCAATGCAACATGCTGCTGCTGGAAGAAAGCAAGATTCAGATTCAGCAT 1323
Db 1448 TGTACTACCTGACACATGCTGCTGCTGGAAGAAAGCAAGATTCAGATTCAGCAT 1507
Qy 1324 AATTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1383
Db 1508 CTACTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1567
Qy 1384 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1443
Db 1568 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1627
Qy 1444 AATTGCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1503
Db 1628 GGAACCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1687
Qy 1504 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1563
Db 1688 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1747
Qy 1564 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1623
Db 1748 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1807
Qy 1624 GGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1683
Db 1808 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1867
Qy 1684 GGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1743
Db 1868 TGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1927
Qy 1744 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1803
Db 1928 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1987
Qy 1804 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1863
Db 1988 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2044
Qy 1864 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1923
Db 2048 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2104
Qy 1924 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1983
Db 2108 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2164
Qy 1984 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2043
Db 2168 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2224
Qy 2044 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2103
Db 2228 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2284
Qy 2104 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2163
Db 2288 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2344
Qy 2164 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2223
Db 2348 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2404
Qy 2224 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2283
Db 2408 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2464
Qy 2284 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2343
Db 2468 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2524
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Qy 2344 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2403
Db 2528 GGTCTGGAAGATTCAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2584
Qy 2404 GC 2405
Db 2585 GC 2586
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RESULT 15
US-10-425-114-5310
; Sequence 5310, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
; APPLICANT: Lnu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5310
LENGTH: 2992
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700451030_FLI
US-10-425-114-5310
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Query Match 42.5%; Score 1162; DB 13; Length 2992;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 755; Indels 6; Gaps 2;
Qy 7 CCAAGGCTCCGAGGACCGGCTGAGAGACCTTCAGAGCGGACCGGACGAGCTGTGGC 66
Db 194 CCAAGGCTCCGAGGACCGGCTGAGAGACCTTCAGAGCGGACCGGACGAGCTGTGGC 253
Qy 67 CCTCTGTCGAAGTACGAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
Db 254 CCTCTGTCGAAGTACGAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
Qy 127 CGCGCTGAC---GAGGTCCAGGAGGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183
Db 314 CGAGTACCAAGATGAGATTCCTGAGGCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 373
Qy 184 CGAGTCTCCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Db 374 CGAGTCTCCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 433
Qy 244 GCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
Db 434 GCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Qy 434 GCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Db 494 GAGGCTGAGAGGTTCTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 553
Qy 304 GCAAGTCAAGTCTGAGAGTACCTCCGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
Db 494 GAGGCTGAGAGGTTCTTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 553
Qy 364 TGATCCCTGAGTCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 423
Db 554 CAAAGGCTGAGTCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 613
Qy 424 TGCGTCTGAGTCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 483
Db 614 TGCGTCTGAGTCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 673
Qy 484 GTTCGGAAGGAGGATGCTTGAAGCCCTGTGGAATTTCTCGTGGCCACCGGACGAA 543
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Db 674 CTTCATGCAAGAGAGATGATACCCCTGCTCAACCTTCCTGCGCCCAACAATAAA 733
QY 544 GGGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
Db 734 GGGGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793
QY 604 GACCAAGCTGAGAGACCTGTCAGAAAGCTCCCTGTCAGACACCACTACTCAATTTTC 663
Db 794 GAGGAAGCTGAGAGACCTGTCAGAAAGCTCCCTGTCAGACACCACTACTCAATTTTC 853
QY 664 TATTAATTTCAAGAGTGGGCTGAGAAAGTTGGGGTGAATACAGACAGACATTTT 723
Db 854 CCACAGGTTCCAGGAACTTGTGTGAGAAAGGTTGGGGTGAATACAGACAGACATTTT 913
QY 724 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
Db 914 GAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 973
QY 784 ATTTTGGGAGAGATCCCATGATTTTAAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
Db 974 GTTCCTGGAACGATCCCATGATTTTAAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1033
QY 844 TGCTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
Db 1034 CGCTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093
QY 904 CCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
Db 1094 TCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153
QY 964 TTCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
Db 1154 CAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1213
QY 1024 TCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db 1214 CAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1273
QY 1084 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
Db 1274 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1333
QY 1144 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
Db 1334 GATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1393
QY 1204 CATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
Db 1394 GATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1453
QY 1264 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
Db 1454 TGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1513
QY 1324 ATTTTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
Db 1514 CTACTGAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
QY 1384 TGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443
Db 1574 TGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1633
QY 1444 AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1503
Db 1634 GATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1693
QY 1504 TGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
Db 1694 TGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1753
QY 1564 GTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
Db 1754 GTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1813

QY 1624 CCAAAATTTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
Db 1814 TGAAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1873
QY 1684 GTCAAGCCATGCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
Db 1874 GAAAGCCATGCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1933
QY 1744 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
Db 1934 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1993
QY 1804 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
Db 1994 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2050
QY 1864 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
Db 2051 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2110
QY 1924 AAGAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
Db 2111 GAAAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2170
QY 2044 TCTTACTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
Db 2231 GCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2290
QY 2104 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
Db 2291 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2250
QY 2164 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
Db 2351 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2410
QY 2224 ATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
Db 2411 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2470
QY 2284 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343
Db 2471 CCGGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2530
QY 2344 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
Db 2531 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2590
QY 2404 GC 2405
Db 2591 GC 2592

Search completed: May 26, 2004, 02:25:54
Job time : 789.142 secs

CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant, or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plant (e.g.
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is corn Sus3 CDNA

XX Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;

Query Match 100.0%; Score 2737; DB 6; Length 2737;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTGACCCACGCGCTCCGCGACCGCTCGAGACACCTTCACGCGCCACCGCAACGCT 60
DB 1 GTGACCCACGCGCTCCGCGACCGCTCGAGACACCTTCACGCGCCACCGCAACGCT 60
QY 61 CGTCCGCTCTCTGTCACAGTACGTGAACAAGGGGAGGGGATCTGACGCGCCACCAT 120
DB 61 CGTCCGCTCTCTGTCACAGTACGTGAACAAGGGGAGGGGATCTGACGCGCCACCAT 120
QY 121 CCTCGACGCGCTCGACGAGGCTCCGCGGCGCTCCGCGCGCTAGCCGAGGACCTTT 180
DB 121 CCTCGACGCGCTCGACGAGGCTCCGCGGCGCTCCGCGCGCTAGCCGAGGACCTTT 180
QY 181 CTTGACGCTCTCTGCTCCGCGCGAGAGGAGATCTGCTGCGCGCTTGTGTCGCTTCCG 240
DB 181 CTTGACGCTCTCTGCTCCGCGCGAGAGGAGATCTGCTGCGCGCTTGTGTCGCTTCCG 240
QY 241 GGTGCGCGCGCGCGCGGAGATTGGAGATACGTCCGCGTCAACGCTTCAAGAGCTCA 300
DB 241 GGTGCGCGCGCGCGCGGAGATTGGAGATACGTCCGCGTCAACGCTTCAAGAGCTCA 300
QY 301 CGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGACGCGCA 360
DB 301 CGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGACGCGCA 360
QY 361 CAATGATCCCTAGCTTCTGAGAGTGAATTCGAGCGGTCGAATGCTCACTCCACGCG 420
DB 361 CAATGATCCCTAGCTTCTGAGAGTGAATTCGAGCGGTCGAATGCTCACTCCACGCG 420
QY 421 AATTCGCTCATCATCTATTGGAACGCTGTGAGTCTCAACGCTTGTCTCAAT 480
DB 421 AATTCGCTCATCATCTATTGGAACGCTGTGAGTCTCAACGCTTGTCTCAAT 480
QY 481 CATGTTCCGACACAGGAGATTGCTTGAAGCCCTGTGGAATTTCTCCGTGCGCAC 540
DB 481 CATGTTCCGACACAGGAGATTGCTTGAAGCCCTGTGGAATTTCTCCGTGCGCAC 540
QY 541 CAAGGGGCGATGTTATGATGCTTAATGATTAATCAAGCTTGGGAGGGCTTCAGTGT 600
DB 541 CAAGGGGCGATGTTATGATGCTTAATGATTAATCAAGCTTGGGAGGGCTTCAGTGT 600
QY 601 GCTGACCAAGCTGAGGAGCACTGTCAAGCTCCCTGTCGACACACCATTACTCAAT 660
DB 601 GCTGACCAAGCTGAGGAGCACTGTCAAGCTCCCTGTCGACACACCATTACTCAAT 660
QY 661 TGCTTATTAATTTCAAGAGTGGGCTCTGAGAGAGTTGGGTGATACAGAGACAT 720
DB 661 TGCTTATTAATTTCAAGAGTGGGCTCTGAGAGAGTTGGGTGATACAGAGACAT 720
QY 721 TTTGGAATATGATCATCTCTCTTCAAGATATTCAGGCGCCAGACCATTAACCTTGA 780
DB 721 TTTGGAATATGATCATCTCTCTTCAAGATATTCAGGCGCCAGACCATTAACCTTGA 780
QY 781 GAAATCTTGGGAGAGATCCCATGATTTTAACTTGTGTGTGTGATCCCTCAATGATA 840
DB 781 GAAATCTTGGGAGAGATCCCATGATTTTAACTTGTGTGTGTGATCCCTCAATGATA 840
QY 841 CTTTGTCAGCTAATGATTAATGCTTCCGACACAGAGAGACAGATGCTTATATCT 900
DB 841 CTTTGTCAGCTAATGATTAATGCTTCCGACACAGAGAGACAGATGCTTATATCT 900
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DB 841 CTTTGTCAGCTAATGATTAATGCTTCCGACACAGAGAGACAGATGCTTATATCT 900
QY 901 GGACCAAGCTCCGTGACATGAAATAGATGCTTCCGTTTAAAGAACAGGCGCTTGA 960
DB 901 GGACCAAGCTCCGTGACATGAAATAGATGCTTCCGTTTAAAGAACAGGCGCTTGA 960
QY 961 TGTTCCTCCCAAGATTCTCATGTTTACTCGGCTGATACAGATGCAAAAGGAACTCAT 1020
DB 961 TGTTCCTCCCAAGATTCTCATGTTTACTCGGCTGATACAGATGCAAAAGGAACTCAT 1020
QY 1021 CATACAGCGCTTGAGAGATTAAGTGAACAAGCATATCTTACATTAAGATCCCT 1080
DB 1021 CATACAGCGCTTGAGAGATTAAGTGAACAAGCATATCTTACATTAAGATCCCT 1080
QY 1081 CAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATTGATGTGGCCATATCT 1140
DB 1081 CAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATTGATGTGGCCATATCT 1140
QY 1141 GGAACATTTGCTGAGAGATCTGCTGTAATTTGCTGTAATTCAGAGTCTCAGA 1200
DB 1141 GGAACATTTGCTGAGAGATCTGCTGTAATTTGCTGTAATTCAGAGTCTCAGA 1200
QY 1201 CTTGATTAATTTGAAATAGAGATGAGAAATCTTGTGGGCTCATGCTATCTTAACA 1260
DB 1201 CTTGATTAATTTGAAATAGAGATGAGAAATCTTGTGGGCTCATGCTATCTTAACA 1260
QY 1261 GGGATTAATCCAGTGAACATGCTCATGCTCTGAGAAAGATTAAGTATCCAGATT 1320
DB 1261 GGGATTAATCCAGTGAACATGCTCATGCTCTGAGAAAGATTAAGTATCCAGATT 1320
QY 1321 CATATTTTGGAGAAATTTGATGATGAGAAATGCAATTTCTCTGCGCATCTGCTGAT 1380
DB 1321 CATATTTTGGAGAAATTTGATGATGAGAAATGCAATTTCTCTGCGCATCTGCTGAT 1380
QY 1381 AATTCGATGAACATGCTGATTTTATCATCAACAGACATCAAGAAATTTGCTGAAG 1440
DB 1381 AATTCGATGAACATGCTGATTTTATCATCAACAGACATCAAGAAATTTGCTGAAG 1440
QY 1441 CAAAAATTAATCTTGAACAGATGAGAGTCACTGCTTTACTGCTGCTGCTGAT 1500
DB 1441 CAAAAATTAATCTTGAACAGATGAGAGTCACTGCTTTACTGCTGCTGCTGAT 1500
QY 1501 AGTTGTCATGAGATGATGCTTTCGATCCAAAGTTCAATTAATCTCTCTGAGAGCT 1560
DB 1501 AGTTGTCATGAGATGATGCTTTCGATCCAAAGTTCAATTAATCTCTCTGAGAGCT 1560
QY 1561 CATGTCATATTAATCTTCAATACAGAGAGGCGAAGCTCACTCTCTTCAATGCTT 1620
DB 1561 CATGTCATATTAATCTTCAATACAGAGAGGCGAAGCTCACTCTCTTCAATGCTT 1620
QY 1621 AATGAAATTTTATGATTAAGACCGGAGCAAAACGATGAACAATTTGGGATG 1680
DB 1621 AATGAAATTTTATGATTAAGACCGGAGCAAAACGATGAACAATTTGGGATG 1680
QY 1681 CCGGTCAAGCCCATCTCTTCTTCATGCGAGACTGACAGGCTGGAAGAACTAAGAG 1740
DB 1681 CCGGTCAAGCCCATCTCTTCTTCATGCGAGACTGACAGGCTGGAAGAACTAAGAG 1740
QY 1741 GCTGTGGAAGCTTTTCTAAGTGGGCTGAGGAGAGGCTGGAACCTTGTGCTGT 1800
DB 1741 GCTGTGGAAGCTTTTCTAAGTGGGCTGAGGAGAGGCTGGAACCTTGTGCTGT 1800
QY 1801 TGCCGGTACATGATGTCACAAAGTCCAGAGAGAGAGAGATGCGGAGATGAGAA 1860
DB 1801 TGCCGGTACATGATGTCACAAAGTCCAGAGAGAGAGAGATGCGGAGATGAGAA 1860
QY 1861 GATGACATGATCTCAACAGACCACTTGTGGGAGATTTCCCTGATCTGCGCCA 1920
DB 1861 GATGACATGATCTCAACAGACCACTTGTGGGAGATTTCCCTGATCTGCGCCA 1920
QY 1921 GACAAACAGGCGCGTAAACGCGAGCTCTATCGCTACATGCTGATACCATGCTGCT 1980
DB 1921 GACAAACAGGCGCGTAAACGCGAGCTCTATCGCTACATGCTGATACCATGCTGCT 1980
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QY 1981 CGTACAGCCGCGCTCTGATGAAGCGTTCGCTCACCCTCGTGAAGGCATGACCTGGG 2040
Db 1981 CGTACAGCCGCGCTCTGATGAAGCGTTCGCTCACCCTCGTGAAGGCATGACCTGGG 2040
QY 2041 GCTTCTACTCTTCCGCGACGCTCCATGAGAGTCCAGCTGAGATCATAGAGCATGAGCTG 2100
Db 2041 GCTTCTACTCTTCCGCGACGCTCCATGAGAGTCCAGCTGAGATCATAGAGCATGAGCTG 2100
QY 2101 GGGCTTCCACATTGACCCGTTACACACCCCGAAGAGGCTTTATCTGATGAGCCGACTTCT 2160
Db 2101 GGGCTTCCACATTGACCCGTTACACACCCCGAAGAGGCTTTATCTGATGAGCCGACTTCT 2160
QY 2161 CGACCGGTGCAAGAGAGACCCAGATCACTGGGTATATATCTGAGAGAGGCTTGAACACTG 2220
Db 2161 CGACCGGTGCAAGAGAGACCCAGATCACTGGGTATATATCTGAGAGAGGCTTGAACACTG 2220
QY 2221 CATATACGAGAGATGACATGAGAGATATATCTCAGAGAGGTTGATGACACTGCGCGGGGT 2280
Db 2221 CATATACGAGAGATGACATGAGAGATATATCTCAGAGAGGTTGATGACACTGCGCGGGGT 2280
QY 2281 CTACGGTTTCTGGAAGTACGCTGTGAAAGCTGAGAGGCTGAGAGAGGCGCTTACTTGA 2340
Db 2281 CTACGGTTTCTGGAAGTACGCTGTGAAAGCTGAGAGGCTGAGAGAGGCGCTTACTTGA 2340
QY 2341 GATGTTCTACATACTGAAAGTCCGCGAGCTGCGAGAGACGCTGCGCTTGAATTGACCA 2400
Db 2341 GATGTTCTACATACTGAAAGTCCGCGAGCTGCGAGAGACGCTGCGCTTGAATTGACCA 2400
QY 2401 ACCGCACTAGCTTCCGCACTGCGACTGCGTGAACCTTGTGACAACTGAACTGAAAG 2460
Db 2401 ACCGCACTAGCTTCCGCACTGCGACTGCGTGAACCTTGTGACAACTGAACTGAAAG 2460
QY 2461 GACCTTCACTAATTTAGCCGCGGCGAGCGTGAAGCATTAATTTGCGGAGCTGAACTG 2520
Db 2461 GACCTTCACTAATTTAGCCGCGGCGAGCGTGAAGCATTAATTTGCGGAGCTGAACTG 2520
QY 2521 GTTTTATATATGACATTAATGAGAGTAAACAAATTAATTAATTAATTAATTAATTAATTA 2580
Db 2521 GTTTTATATATGACATTAATGAGAGTAAACAAATTAATTAATTAATTAATTAATTAATTA 2580
QY 2581 TTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
Db 2581 TTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
QY 2641 GCAGCCGCGAGCGCTGAGAGTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2700
Db 2641 GCAGCCGCGAGCGCTGAGAGTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2700
QY 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

RESULT 2
AAD45856
ID AAD45856 standard; DNA; 2757 BP.
AC AAD45856;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
KW Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric; gene; ds.
XX
OS Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX

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FH Key Location/Qualifiers
FT CDS 1..2430
FT /tag= a
FT /product= "Corn Sus3-Sorghum EST chimeric protein"
FT misc_feature 1..39
FT /tag= b
FT /note= "Sorghum propinquum EST DNA"
FT misc_feature 40..2757
FT /tag= c
FT /note= "Corn Sus3 DNA"
XX
XX WC200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugya KS, Helentjaris TG, Niu X;
XX
XX WPI; 2002-691625/74.
XX
XX P-PSDB; AAE28502.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Claim 1; Page 116-119; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX CC maize, reducing grain breakage during combining, transport or movement
XX CC into storage, or improving plant or grain strength. The present sequence
XX is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;
XX
XX Query Match 99.2%; Score 2714; DB 6; Length 2757;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 2717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 16 CGGCGACCGCGCTCGAGACACCTTCACGCGCACCGCAACGAGCTGCGCCCTCTGTC 75
Db 16 CGGCGACCGCGCTCGAGACACCTTCACGCGCACCGCAACGAGCTGCGCCCTCTCTGTC 95
QY 76 CAAGTACGTGAACAAGGGAAGGAGGCTCTGAGCGGACCAATCTCTGAGCGGCTGCA 135
Db 76 CAAGTACGTGAACAAGGGAAGGAGGCTCTGAGCGGACCAATCTCTGAGCGGCTGCA 155
QY 96 CAAGTACGTGAACAAGGGAAGGAGGCTCTGAGCGGACCAATCTCTGAGCGGCTGCA 195
Db 96 CAAGTACGTGAACAAGGGAAGGAGGCTCTGAGCGGACCAATCTCTGAGCGGCTGCA 215
QY 136 CGAGTCCAGGAGCTCCGAGGAGGAGGAGGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 195
Db 136 CGAGTCCAGGAGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 215
QY 156 CGAGTCCAGGAGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
Db 156 CGAGTCCAGGAGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275
QY 196 CTCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255
Db 196 CTCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275
QY 216 CTCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275
Db 216 CTCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 295
QY 256 GGAAGTTGGAGAGTACGCTCCGCTGACAGCTTCAAGCTCAGAGCTGAGAGCTGCAAGT 315
Db 256 GGAAGTTGGAGAGTACGCTCCGCTGACAGCTTCAAGCTCAGAGCTGAGAGCTGCAAGT 335
QY 276 GGAAGTTGGAGAGTACGCTCCGCTGACAGCTTCAAGCTCAGAGCTGAGAGCTGCAAGT 335
Db 276 GGAAGTTGGAGAGTACGCTCCGCTGACAGCTTCAAGCTCAGAGCTGAGAGCTGCAAGT 355
QY 316 CTGCGAGTACTCCGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375

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Db 336 CTGGAGTACCTCCGCTTCAAGAGSAGCTTGCAGCGGCGACACAAATGTCCTACGT 395
QY 376 TCTCGAGCTTGACTTCGAGCCGTTCAATGTCTCAGTCCCAAGCCAAATCGTCATC 435
Db 396 TCTCGAGCTTGACTTCGAGCCGTTCAATGTCTCAGTCCCAAGCCAAATCGTCATC 455
QY 436 TATGGAAAGGTGTGAGTCTCTCAACCGACATCTTCTCTAATATATGTCGGAACG 495
Db 456 TATGGAAAGGTGTGAGTCTCTCAACCGACATCTTCTCTAATATATGTCGGAACG 515
QY 496 GATGCTTGAAGCCCTGTTGATTTCTCCGCTGACCGGCAAGGGGACATGTTAT 555
Db 516 GATGCTTGAAGCCCTGTTGATTTCTCCGCTGACCGGCAAGGGGACATGTTAT 575
QY 556 GATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 615
Db 576 GATGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 635
QY 616 GAGGACTTGTCAAGCTTCTCTCTCAACCATCTCAATTTGCTTATTAATTTCA 675
Db 636 GAGGACTTGTCAAGCTTCTCTCTCAACCATCTCAATTTGCTTATTAATTTCA 695
QY 676 AGAGTGGGCTGAGAGAGTGGGGTGAATACAGAGACATGTTTGGAAATGATCCA 735
Db 696 AGAGTGGGCTGAGAGAGTGGGGTGAATACAGAGACATGTTTGGAAATGATCCA 755
QY 736 TCTCTTTCAAGATCAATTAAGGCGCAAGCCATCTACCTTGAAGAAATTTCTGGGAG 795
Db 756 TCTCTTTCAAGATCAATTAAGGCGCAAGCCATCTACCTTGAAGAAATTTCTGGGAG 815
QY 796 GATCCCATGATTTTAAAGTGTGTGTGTATCCCTCATGATGATTTGGTCAAGCTAA 855
Db 816 GATCCCATGATTTTAAAGTGTGTGTGTATCCCTCATGATGATTTGGTCAAGCTAA 875
QY 856 TGTATTAGGCTTGCAGACACAGAGAGACAGATCGTATATATCTGACCAAGTCGTC 915
Db 876 TGTATTAGGCTTGCAGACACAGAGAGACAGATCGTATATATCTGACCAAGTCGTC 935
QY 916 ACTTGAATAGATGATGTTCTCCGTTTAAAGAAACAAAGGCTTATGTTTCCCAAGAT 975
Db 936 ACTTGAATAGATGATGTTCTCCGTTTAAAGAAACAAAGGCTTATGTTTCCCAAGAT 995
QY 976 TCTCATTTGTTCTCGGCTGATACAGATGCAAAAGGAAATCATGCAATCGAGGCTTGA 1035
Db 996 TCTCATTTGTTCTCGGCTGATACAGATGCAAAAGGAAATCATGCAATCGAGGCTTGA 1055
QY 1036 GAGAAATAGTGAACACAGCATACTTACATATACAGATTCCTTCAGAAATGAAATGG 1095
Db 1056 GAGAAATAGTGAACACAGCATACTTACATATACAGATTCCTTCAGAAATGAAATGG 1115
QY 1096 GATATCTTAAAGATGATATCAAGATTTGATGTGTGCGCATATCTGAAACATTTGCTGA 1155
Db 1116 GATATCTTAAAGATGATATCAAGATTTGATGTGTGCGCATATCTGAAACATTTGCTGA 1175
QY 1156 GGAATGCTGCTGTAATTTGCTGATTAACAAGTCTCAGACTTCAATATGAAAT 1215
Db 1176 GGAATGCTGCTGTAATTTGCTGATTAACAAGTCTCAGACTTCAATATGAAAT 1235
QY 1216 CTAACGATGATGAAATCTTGTGGGTCAATGTCTTACAAAGATGGAATTAACCACTG 1275
Db 1236 CTAACGATGATGAAATCTTGTGGGTCAATGTCTTACAAAGATGGAATTAACCACTG 1295
QY 1276 CAACATGCTCATGCTTGGAAAGAAAGTATTCAGATTCAGACATATTTTGGAAAGAA 1335
Db 1296 CAACATGCTCATGCTTGGAAAGAAAGTATTCAGATTCAGACATATTTTGGAAAGAA 1355
QY 1336 TTTGATGAGAGATGATCAATTTCTCTGCAAGTTCATCTGATATATTTGCTATGAACA 1395
Db 1356 TTTGATGAGAGATGATCAATTTCTCTGCAAGTTCATCTGATATATTTGCTATGAACA 1415
QY 1396 TGTGATTTTATCATCAACAGACATACCAAGAAATTCGTGAGCAAAATATCTGTTGG 1455

Db 1416 TGTGATTTTATCATCAACAGACATATCCAAAGAAATTCGTGAGCAAAATATCTGTTGG 1475
QY 1456 AACGATGAGAGTCAATGCTCTTATCTGCTGCTGCTGATACAGATTTCCATGGAT 1515
Db 1476 AACGATGAGAGTCAATGCTCTTATCTGCTGCTGCTGATACAGATTTCCATGGAT 1535
QY 1516 CGATGCTTCAATCCAAAGTCAATATAGTCTCTCTCTGAGCTGACATGTCATATATCT 1575
Db 1536 CGATGCTTCAATCCAAAGTCAATATAGTCTCTCTCTGAGCTGACATGTCATATATCT 1595
QY 1576 TCCACATCCGAGAGAGGCTCAGGCTCAGCTCTCTCTCATGTTCAATCCAAATTTGAT 1635
Db 1596 TCCACATCCGAGAGAGGCTCAGGCTCAGCTCTCTCTCATGTTCAATCCAAATTTGAT 1655
QY 1636 TTAATGACCCGAGACAAAGATGAACAATTTGGGATCTGATGATGACCGTCAAGCCAT 1695
Db 1656 TTAATGACCCGAGACAAAGATGAACAATTTGGGATCTGATGATGACCGTCAAGCCAT 1715
QY 1696 CCTCTTCTCCATGGCAAGACTCGACAGGATGAAACATTAACAGGCTGCTGAGCTTT 1755
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Db 1776 TGTAAAGTGGCTTAAAGCTGAGGAGCTGTGTAATCTTGTGCTGCTGCTGCTGCTGCT 1835
QY 1816 TGTCAACAGTCCAAAGACAGGAGAGATCGCGAGATGAGAAATGATGAATCAT 1875
Db 1836 TGTCAACAGTCCAAAGACAGGAGAGATCGCGAGATGAGAAATGATGAATCAT 1895
QY 1876 CAAGACCCCAACTTGTTCGGGAGTTCCTGCTGATCTCTCCCAAGACAAACAGGCCCCG 1935
Db 1896 CAAGACCCCAACTTGTTCGGGAGTTCCTGCTGATCTCTCCCAAGACAAACAGGCCCCG 1955
QY 1936 TAAAGGAGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1995
Db 1956 TAAAGGAGAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 2015
QY 1996 GTATGAAGCTTCCGCTCAACCGTCTGTTAGAGGCTCATGCTGCTCTCTCTCTCTCTG 2055
Db 2016 GTATGAAGCTTCCGCTCAACCGTCTGTTAGAGGCTCATGCTGCTCTCTCTCTCTCTG 2075
QY 2056 GAGCTCCATGAGAGTCCAGCTGATGATCATGATGATGATGATGATGATGATGATGAT 2115
Db 2076 GAGCTCCATGAGAGTCCAGCTGATGATCATGATGATGATGATGATGATGATGATGAT 2135
QY 2116 CCGTATCAACCCCGAAACAGGCTTAAATCTGATGATGATGATGATGATGATGATGAT 2175
Db 2136 CCGTATCAACCCCGAAACAGGCTTAAATCTGATGATGATGATGATGATGATGATGAT 2195
QY 2176 AGACCCAGATCACTGCTGATATATCTGAGCAGGCTGACAGGCTATATGAGAGATTA 2235
Db 2196 AGACCCAGATCACTGCTGATATATCTGAGCAGGCTGACAGGCTATATGAGAGATTA 2255
QY 2236 CACATGAGAGATATCTGAGAGAGTATGACACTGCTCGGCTGCTGCTGCTGCTGCTG 2295
Db 2256 CACATGAGAGATATCTGAGAGAGTATGACACTGCTCGGCTGCTGCTGCTGCTGCTG 2315
QY 2296 GTAGCTGCTGAGAGCTCGAGAGGCTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2355
Db 2316 GTAGCTGCTGAGAGCTCGAGAGGCTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 2375
QY 2356 GAACTTCCGAGAGCTGCGAAGACCGTCCGCTTGAATGACAAACCGCAGTACTTGC 2415
Db 2376 GAACTTCCGAGAGCTGCGAAGACCGTCCGCTTGAATGACAAACCGCAGTACTTGC 2435
QY 2416 GCAACTGCTGAGCTGCTGATCACTTGTATCAAGCTTAAACCTGTAAGAGCTTGAATTT 2475
Db 2436 GCAACTGCTGAGCTGCTGATCACTTGTATCAAGCTTAAACCTGTAAGAGCTTGAATTT 2495
QY 2476 AGGCGGCGAGAGCGGTAGCAACAAATGCTGCGAGCTGATCTGTTTATTAATGTA 2535
Db 2496 AGGCGGCGAGAGCGGTAGCAACAAATGCTGCGAGCTGATCTGTTTATTAATGTA 2555

QY 78 AGTACGTGAACAAGGAGGAGCATCTGAGCGGACCAATCTCGACGCGCTCGAGC 137
DB 98 GGTATGTGGATCGAGGGAAAAGGATTTCTTAACACATTAATTAATGAAGAACTCGAAT 157
QY 138 AAGTCCAGGAGCTCCGGGGGCGCGCG-----CTAGCGAGAGGACCTCTCTCGACGCTC 191
DB 158 CTGTCTATCGAGAGCATGAACAAAGAAAGATCTCTGATGATGCTTTTGGAGAGATTC 217
QY 192 TCGGCTCCGGGAGAGGCGATCTGCTCGCGCGCTCGGCGCATGCGCGTGGCGCCCGC 251
DB 218 TTAAATCAGAAATGAAAGCTATAGTTGTACACCTTTTGTGGGTAGCGGTAGACAA 277
QY 252 GCGCGGAGATTTGGAGATCTAGCTCGCGCTCAAGCTTCAAGCTCAAGCTCGAGAGCTCA 311
DB 278 GACCTGGTATTTGGAAATATGCTGTATATGCTTCAAGCTTCAAGCTTGAACATTA 337
QY 312 CAATCTCGAGATCTCCGCTTCAAGAGAGAGCTTGTGACGCGCGAGCAATATGCTCT 371
DB 338 CAGTCTGTAGTATCTCGTTTCAAGAGAACTCGTTGATGAGCTATATAGTACCTT 397
QY 372 AGCTTCGAGCTGATCTGAGCGCTTCAATGCTCAGTCCGAGCGCGCAATGCGTCA 431
DB 398 TTGTCTTGAGCTTGAATTTGAGCGCTTTAAGCAAACTGACAGCTCTCTCTGCTG 457
QY 432 CATCTATGAAACGAGTGTGAGTCTCAACGAGCACTGTCTCAATGATGTTCCGCA 491
DB 458 CTTCGATGATGATGAGGATCAATTTCTGATGATGCTCACTTGTCTGTATATGTTCCGTA 517
QY 492 ACAAGGATCTCTGAGCGCTCTGTTGATTTCTCTCGTGGCCACCGGCAAGAGGAGCTG 551
DB 518 ACAAGATCTCTGAGCGCTCTGCTGATTTCTTAAAGTTCATTAAGTACAAAGGATATC 577
QY 552 TTATGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 611
DB 578 CGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 637
QY 612 CTGAGAGCACTGTCTCAAGCTCTCTGCTGACACACATCTCAAAATTTGCTTAAAT 671
DB 638 CAGAGATCTATCTCTCAAGCTTCAAGAGAACTCTGCTCTGAGATTTGAAATGAGCGT 697
QY 672 TTCAAGAGTGGGCGCTGAGAGAGGATGAGGATGATGATGATGATGATGATGATGATG 731
DB 698 TGCAAGGAAATGAGTGTGAGAAAGATGAGGAGATGATGATGATGATGATGATGATG 757
QY 732 TCCATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 791
DB 758 TGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 817
QY 792 GAGAGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 851
DB 818 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 877
QY 852 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 911
DB 878 CCAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937
QY 912 GTGATCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 971
DB 938 GTGCGCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
QY 972 AGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1031
DB 998 GTATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
QY 1032 TTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1091
DB 1058 TAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1117
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DB 1118 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1177
QY 1152 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1211

DB 1178 CTGAGATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1237
QY 1212 GAAATCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1271
DB 1238 GTATCTATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1297
QY 1272 AGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1331
DB 1298 ATGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1357
QY 1332 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1391
DB 1358 AAGATCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1417
QY 1392 ACATGCTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1451
DB 1418 ACAAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1477
QY 1452 TTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511
DB 1478 TCGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1537
QY 1512 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1571
DB 1538 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1597
QY 1572 ACTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1631
DB 1598 ATTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1657
QY 1632 TGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1691
DB 1658 TGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1717
QY 1692 CCATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1751
DB 1718 CAATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1777
QY 1752 CTTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1811
DB 1778 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1837
QY 1812 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1871
DB 1838 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1897
QY 1872 TCATGAG 1931
DB 1898 TTATGAG 1957
QY 1932 CCGGTAAG 1991
DB 1958 CTGAAAG 2017
QY 1992 CTTGATGAG 2051
DB 2018 CGTTCTAG 2077
QY 2052 TCGAG 2111
DB 2078 TTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2137
QY 2112 TTGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2171
DB 2138 TCGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2197
QY 2172 AGCAAG 2231
DB 2198 AGGAG 2257
QY 2232 AGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2291

Db 2258 GGTACACATGGAGATATATCTCGAGAGATTGATGACACTAGTGGTGTGATGCTTCT 2317
 Qy 2292 GGAAGTACTGTCTGACAGCTCGAGAGGCTGAGACAGAGCGCTACTGTGAGTGTCTACA 2351
 Db 2318 GGAATATGATGATGAGAGCTGCTGAGAGCTCGAGATATCTGAAATGTTCTACA 2377
 Qy 2352 TACTGAGTCCGCGAGCTGCGAGAGACCGTCC 2385
 Db 2378 TTTCAAAATTCGCGACTTGGTGAATACTGTTCC 2411

RESULT 5
 ABZ76372
 ID ABZ76372 standard; cDNA; 2394 BP.
 AC ABZ76372;
 XX 12-JUN-2003 (first entry)
 DE A. thaliana LMP encoding cDNA-clone ID PK118-1.
 XX Lipid metabolism protein; LMP; seed storage; plant; transgenic; gene; ss.
 XX Arabidopsis thaliana.
 XX Key Location/Qualifiers
 XX CDS 1..2394
 XX /tag= a
 XX /product= "LMP"
 XX /note= "Lipid metabolism protein"
 XX MO2003014376-A2.
 XX 20-FEB-2003.
 XX 12-AUG-2002; 2002WO-US025586.
 XX 10-AUG-2001; 2001US-0311414P.
 XX (BAD1) BASF PLANT SCT GMBH.
 XX Miltendorf V, Haertel H, Cirpus P,
 DR MPI; 2003-256595/25.
 XX P-PSDB; ABR39586.
 XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX Claim 1; Fig 12c; 108pp; English.
 XX The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polymucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR7658-373 represent A. thaliana LMP encoding cDNA sequences
 XX
 SQ Sequence 2394 BP; 671 A; 480 C; 564 G; 679 T; 0 U; 0 Other;
 Query Match 43.2%; Score 1181.2; DB 7; Length 2394;
 Best Local Similarity 70.5%; Pred. No. 4e-257;
 Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 164 CTACCCGAGGAGCCCTTCTGAGCTCTCCGCTCCGCGAGAGGAGATGCTGCGG 223
 Db 151 CTTAAACAAAGATCATCATGAAAGTTCTGAGCTCTGAGAGAGAGCATGTTTCT 210

Qy 224 CCGTTCGAGCATCGCGAGGCGCCGCGCGAGTTTGGAGTACGCTCCGCTCAC 283
 Db 221 CCATTGTGCTTGGCTATACGTCCAGACCTGTGTGAGGAATATGCTCGTGTGAT 270
 Qy 284 GTTACAGAGCTCAGGCTGAGAGCTCAGCTCGGAGTACTCCGCTTCAAGAGAG 343
 Db 271 GTGTATGAGCTGAGAGGTGATATTTAACTGTTCTGATATCTTGGTTTAAAGAG 330
 Qy 344 CTGTGAGCGGACAGCAATGATCCCTACGTTCTGAGCTTGAAGCTTCAAGCGTCAAT 403
 Db 331 CTGTTAATGCGCAATGCAATGAGATATTTCTCTTGAACCTTGATTTGACCTTCAAT 390
 Qy 404 GTCTGAGTCCAGCCCAATATGATATCATATCTATGAAACGGTGTGAGTCTCAAC 463
 Db 391 GGAACATGCGCTGCGCCAACTGTTTCAATCATCATGAGATGAGGTTTCACTTCAAT 450
 Qy 464 CGACCTGTGCTCAATCATGTTCCGCAACAGGATGTTGAGGCCCTGTGATTC 523
 Db 451 CGTCACTCTCTTCAATATATGTTCCGTACAAAGAAAGATGAGCCTTGTGAGTTT 510
 Qy 524 CTCCGCGGCAAGGCAAGGAGCAATGATGATCTTAAATGATGATGATGATGATGAT 583
 Db 511 CTCCGCACTGCAAAACATGATGAGCTGCTTATGATCTGATGATGATGATGATGATGAT 570
 Qy 584 GGAAGGCTTCACTGTGCTGACCAAGCTGAGAGCACTTGCAAAAGCTCCCTGCTGAC 643
 Db 571 CCATATCTTCAAGGAGCTTGGCAAGAGAGAGAGTCTTCTTAACTTCTCTGCGCA 630
 Qy 644 ACACATCTCTCAATTTGCTTATTAATTCAAGAGTGGGAGCTTGAAGAGTGGAGT 703
 Db 631 ACACATCTCTCAATTTGCAATTTGAATCAAGAGTGGAGTGGAGTGGAGTGGAGT 690
 Qy 704 GATACAGAGAGATGTTTGAATATGATCATCTCTCTTACATCATTCATGAGGCGCA 763
 Db 691 GACACAGAGAGATGTTTGAATATGATCATCTCTCTTACATCATTCATGAGGCGCA 750
 Qy 764 GACCACTACCTTGAAGAAATCTTGGAGAGATCCCATGATTTTAAAGTTTGTG 823
 Db 751 GACCTTCTGCTTGGAGAGATCTTGAAGAGATCTTGAAGAGATCTTGAAGAGATCTTGAAG 810
 Qy 824 GTATCCCTCAGAGATCTTGTGCAAGTATGATGATGATGATGATGATGATGATGATGAT 883
 Db 811 TTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 870
 Qy 884 CAGATGCTTATATATCTGACCAAGTCCGTGCACTGAGAAATGAGATGATGATGATGAT 943
 Db 871 CAGTGTCTTACATCTTGTATCAAGTACGTGCAATGAGAAATGAGATGATGATGATGAT 930
 Qy 944 AAGAAACAGGCGCTTGAATGTTTCCCAAGATTTCTATGTTACTGCGCTGATACCGAT 1003
 Db 931 CAGAAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 990
 Qy 1004 GCAAAAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1063
 Db 991 GCAAAAGAGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1050
 Qy 1064 ATATTACAGTTCCTTCAAGAAATGAGATGATGATGATGATGATGATGATGATGATGAT 1123
 Db 1051 ATTGTGAGATTCATTTAGAGATGAGAAAGGAAATCTTCCAGATGATCTCAAGGTTT 1110
 Qy 1124 GATGTGCGCATATCTGAGAAACATTTGCTGAGATGATGATGATGATGATGATGATGAT 1183
 Db 1111 GATGTGCGCATATCTGAGAAACATTTGCTGAGATGATGATGATGATGATGATGATGAT 1170
 Qy 1184 TTACAGGTACTCCAGACTTCAATATGAGAAATCACTGATGATGATGATGATGATGATGAT 1243
 Db 1171 TTGAGAGGTGATCAAAATCTCATTTGCGCAATCACTGATGATGATGATGATGATGATGAT 1230
 Qy 1244 TTGCTATCTTCAAGATGAGATTTACCAAGTGAACATTTGCTCATGCTCTGAGAAAGAT 1303
 Db 1231 TTGTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1290

QY	1304	AAGATATCCAGTTCAGACATATTTTGGAGAATTTGCAAGAGTCACTATTCCTGCG	1363
Dp	1291	AAGTATCCCGAGCTTCGACATTTACTCGGAGAAACCATAGAGATATGTAACCTTTTCAAGT	1350
QY	1364	CAGTTCACCTGCTGATATTAATTTGCTATGAAACCATGCTGATTTTATCATCCACAGACATAC	1423
Dp	1351	CAGTTCACTGCAATCTATATTTGCCATGATCTAATGCGATTTTCATCATCACAGACATAC	1410
QY	1424	CAGAAATTCGTGAGCAAAAATACTGTGTGACATGATAGAGTCACTACTGCTTTACT	1483
Dp	1411	CAGAGATTCGGGGAGACCAAGAACATATGTTGGCAATACGAGACCACACAGCTTTCACT	1470
QY	1484	CTGCTCGTCTGTATACCAAGTTTGTCCATGAGGATCGATGCTCTTCGATCCAAAGTTCAATATA	1543
Dp	1471	ATGCTCTGGTCTTTACCGAGTGTTCATGGAATTAATGATGTCTTATGCTTAAGTTAAATAG	1530
QY	1544	GTCCTCTCTGAGCTGACATGTCCATATATCTTTCCACATACCGGAGAGGCCAAGCCGACTC	1603
Dp	1531	GTCCTCTCAGAGCTGATATATACATATACCTTTCCATATTTCCGACAAAGAAAGAACTC	1590
QY	1604	ACCTCTCTTCATAGGTTCAATGAAAATTTGATTTATGACCCGGAGCAAAACGATGAACAC	1663
Dp	1591	ACTGACCTTCATGAGTCAATTTGAAAGAACTCCTCTTTTAGTGCCGAACAGAAATGATGACAT	1650
QY	1664	ATTGGGCATCTGATATACCCGCTCAAAAGCCATCCTCTTCTCCATAGGGAAGACTGACAG	1723
Dp	1651	GTTGGTTTACTAGACGACCAATCGAAGCAATCATCTTCTATAGGCAAGCTTGACAGG	1710
QY	1724	GTGAAGAACATATACAGGGCTGGTGAAGCTTTTGCTAAGTCCGCTAAAGCTAGGGAAGCTG	1783
Dp	1711	GTGAAAACCTTGACTGGGCTAGTGGTAAAGCTATGCTATGCGAAGATATACCAAGCTTAAAGCTT	1770
QY	1784	GTAAACCTTGTGTCGTGTTGCCGGGTACATGATGTCAACAAGTCCAAAGACAGGGAAGAG	1843
Dp	1771	GCAATCTGTATTATAGTCGATGGGCAATCATGATGAAATGATGTCAGGGAATAGAGAGAA	1830
QY	1844	ATCGCGAGATATAGAAAGATGCAATGACTCATCAAGCCCAACCTTGTTCGGGCAATTC	1903
Dp	1831	ATGCTGTGATATACAAAAAGATGACACAGCTGTGATGACAGTATGATTTACAGCGTGAAGTTT	1890
QY	1904	CGCTGGAACCTTGCCCCAGACAAACAGGGCCCGTATACGGCCGAGCTCATACGGTCAATCGCT	1963
Dp	1891	AGGTGATATGCTGCTCAATATGACCGTGTCTGAAATGTGTAGCTTTACCGTTATATGCA	1950
QY	1964	GATACCCATGCTGCTTTGCTACAGCCGGACCTGTATAGAGCGTTCGATCAACCGTCTT	2023
Dp	1951	GACACAAAGGTGTTTTTTGTTCAAGCTGCTTCTATATGAAAGATTTGGCTTACGGTTGTG	2010
QY	2024	GAGGCCATGACCTGTGGGCTTCTATCTTCGCGAGCTCCATGAGAGTTCAGCTGAGATC	2083
Dp	2011	GAATCAATGACTGTGCACTCCCAACGTTTGCTATCTGATGTGAGAACCCGCAAGATTT	2070
QY	2084	ATAGAGCATGGGCGTCTGGGCGCTCCACATGTAACCCGTAACCCCGCAACAGGCTGTAT	2143
Dp	2071	ATCGAAACGGAATTTCTGGGTTCCACATTTGACCCATATCATCCAGACCAAGTTGCAGCT	2130
QY	2144	CTGATGCGCACTTTTCGACCGGTGCAAGCAAGACCCAGTCACTGCGGTGATATATCT	2263
Dp	2131	ACCTTGTGACGTTCTTTTGAGACCTGTAAACCAACCAATCCAAATCAATTTGGGTTAAATCTCT	2190
QY	2204	GGAGCAGGCGCTGACAGCGCATATACAGAAAGTACACATGGAAGATATCTCAGAGAGTTG	2266
Dp	2191	CAAGGAGGCGCTCAACCGAATCTATGAAAGGTCAATATGGAAGAACTACTCAGAGAGACTG	2255
QY	2264	ATGAACATGCGCCGGGCTCAAGGTTTCTTGGAAGTACGTGTGAACTGAGAGCGCTGAG	2322
Dp	2251	CTTACCTCGGCTGAGGTCTATGCAATCTGGAACATGTGTCTAACTCTGAAGAGAGAA	2310
QY	2324	ACGAGGCGCTACCTTGAGATGTTCTAACAATCTGAAGTTCCGCGAGCTGCGCAAGACCGTG	2383
Dp	2311	ACAGCACTGTACTGAAAGATGTTTTTACTCATTGAAATTTTCGTGATTTGGCGAATTCATTC	2370
QY	2384	CCGCTTGCAATTTGA	2397

```
DB      2371 CCGCTGGCAACGA 2384  
RESULT 6  
AA080005  
ID      AA080005 standard; cDNA; 2563 BP.  
XX  
XX  
AC      AA080005;  
XX  
DT      25-MAR-2003 (revised)  
DI      05-AUG-1995 {first entry}  
XX  
DE      Sucrose-synthase.  
XX  
XX      Sucrose-synthase; sugarbeet; sucrose; crop improvement; ss.  
XW  
OS      Beta vulgaris.  
XX  
FH      Key          Location/Qualifiers  
FT      CDS          3..2303  
              /*tag= a
```

PB DE4317596-Al.

PD 01-DEC-1994.

PF 24-MAY-1993; 93DE-04317596.

PR 24-MAY-1993; 93DE-04317596.

PS (SCHD) SCHERING AG.

PI Hesse H., Mueller-Roeber B;

DR WPI: 1995-007485/02.

DR P-PADB; AAB66222.

PT New DNA sequences encoding sucrose regulating enzymes of sugar beet - for

PP regulating sucrose concn. specifically ADP glucose pyrophosphorylase,

PT sucrose phosphate synthase and sucrose synthase.

XX Claim 4; Page 72-78; 78pp; German.

CS cDNA encoding sugarbeet sucrose-synthase was isolated from a cDNA library

CC in phase lambda Zap. Alterations to the coding sequence may be designed

CC to by-pass the plant's regulatory mechanisms, allowing manipulation of

CC the sucrose content of sugarbeet. (Updated on 25-MAR-2003 to correct PN

CC field.)

SQ Sequence 2563 BP; 736 A; 480 C; 602 G; 745 T; 0 U; 0 Other;

KM Lipid metabolism protein; LMP; seed storage; plant; transgenic; gene; ss.
 XX Arabidopsis thaliana.
 OS
 XX Key Location/Qualifiers
 FH 1..2418
 FT CDS /*tag= a
 FT /product= "LMP"
 FT /note= "Lipid metabolism protein"
 XX
 XX W02003014376-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 12-AUG-2002; 2002MO-US025586.
 XX
 XX 10-AUG-2001; 2001US-0311414P.
 XX
 XX (BAD1) BASF PLANT SCI GMBH.
 XX
 XX Miltendorf V, Haertel H, Clirpus P;
 XX
 XX WPI; 2003-256595/25.
 DR P-PSDB; ABR39585.
 XX
 XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX
 PS Claim 1; Fig 12A; 108pp; English.
 XX
 CC The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polynucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR76358-373 represent A. thaliana LMP encoding cDNA sequences
 CC
 XX
 SQ Sequence 2418 BP; 676 A; 491 C; 562 G; 689 T; 0 U; 0 Other;
 Query Match 42.8%; Score 1172; DB 7; Length 2418;
 Best Local Similarity 70.9%; Pred. No. 4.9e-255;
 Matches 1556; Conservative 0; Mismatches 640; Indels 0; Gaps 0;
 QY 232 GCAGAGGCGATCGTGGCCGCGGCTGGTGGCCATGGCGGCGCCGCGGAGT 261
 DB 213 GCAGAGGCGATCGTGGCCGCGGCTGGTGGCCATGGCGGCGCCGCGGAGT 272
 QY 262 TTGGAGAGTACGTCGCGTCAAGTTCACAGAGTCAAGTCAAGTCAAGTCAAGT 321
 DB 273 TAGGAGATATTCGCGTGAATGTGTATGAGCTAGAGCTAGATTAATCGTTTCTGA 332
 QY 322 GTACCTCGCTTCAAGAGAGCTTGTGACGCGCCAGCAATGATCCCTACGTTCTGA 381
 DB 333 ATATCTTCGTTTAAAGAGAGCTGTGATATGCGCATGAGATGATATCTCTTGA 392
 QY 382 GCTGACCTGAGCGCTTCATATGTCAGTCCAGCGCCCAATGGGTATATGATGG 441
 DB 393 ACTGATTTTGAACCTTTCATATGCAACATGCTGCGCAACTGTTATATCTATGG 452
 QY 442 AAACGCTGTGAGTCTTCAACGACACTGTCTCATATCATGTTCCCAACAGGATGG 501
 DB 453 GAATGGGGTTCAGTTCCTCAATCGTCACTCTTTCATATATGTTCCGTAACAAGAG 512
 QY 502 CTTGAGAGCCCTGTTGATTTCTTCGTCGACCAAGCGGCAAGAGGCAATGTTATATCT 561
 DB 513 CATGAGGCTTGTGCTGAGTTTCTCCGCACTCAACAAATGATGGCCGCTCATGATGCT 572

QY 562 TAATGATGAATACAAAGCTTGGGAGGCTTCACTGCTGTGCTGACCAAGCTGAGAGCA 621
 DB 573 GAATGATGAAATACAAATATCCCATATCTTCAAGAGCTTGGCAAGAGAGAGATT 632
 QY 622 CTTGTCAAGCTCCCTGCTGACACACCATATCTCAAAATTTGCTATTAATTTCAAGTGG 681
 DB 633 CTTTTCATTAATCTCTCTGGCAACACCATATCTGAAATTTGAAATTTGAAACAGGAT 692
 QY 682 GGGCTTGAAGAAAGTTGGGCTGATACAGAGAGACATGTTTGGAAATGATCTCTCT 741
 DB 693 GGGATTTGAAAGGAGATGGGGTGAACAGACAGAGAGTTTCAGAAATGGTGCATCTCT 752
 QY 742 TCTAGACATATTTAGCGGCGGACGCCATCTACCTAGCAAAATCTTGGGAGGATCCC 801
 DB 753 TCTGACATCTTCCAGGACCTGATCCTTCTGTCTTGAAGAGCTTCTAGAGAGATTC 812
 QY 802 CATGATTTTAAAGCTTGTGTGTATCCCTCATAGATATCTTGTCAAGCTTAATGTAT 861
 DB 813 TATGATTTGAATGTTGATTTGTCTCCCATGTTACTTGGCCAAAGCCATGTCTT 872
 QY 862 AGGCTTCCACACACAGAGAGACATGTCTATATCTGAGACCAAGTCCGTGACTGA 921
 DB 873 GGGTCTGCTGATATCTGTGACAGAGTGTCTACATTTGATTAAGTACGTGCAATGGA 932
 QY 922 AATGAGATGGTTCGCGCTTAAAGAAACAAGGCTTGTATGTTCCCAAGATCTCAT 981
 DB 933 AATGAGATGCTCTCTTGAATACAGAGACAGAGCTGAGAGATTTCCAAATCTCAT 992
 QY 982 TGTACTGCTGATATCCAGATGCAAGAGAAACATCATCATGACGAGCTTGAAGAT 1041
 DB 993 TGTAAACAAGCTGCTACCCGAAGCAAGAGAAACAAGTGAACAGAGGTTGAAGAGT 1052
 QY 1042 TAGTGAACACAGCATATCTATATACAGTTCCTTCCGAATTTGAATTTGAGATCT 1101
 DB 1053 TAGTGAACACAGCAACAGCAATCTGCAATCATTTAGAGCTGAAAGAGATTTCT 1112
 QY 1102 TAAGAAATGATATCAAGATTTGATGTGTGCGCATATCTGAAACATTTGTGAGAGATC 1161
 DB 1113 TCGAAGTGAATCTCAAGATTTGATGTGTGCGCATATCTGAGAGATTTGTGAGAGATC 1172
 QY 1162 TGTGTGAAATTTGCTGTGAATTAACAAGTATCTCAAGCTTCATATTTGAAACTACAG 1221
 DB 1173 ATCAATGAAATTTTGGGAGTTGCAAGGATGACAGGATTCATCATTTGCAACTACAG 1232
 QY 1222 TGATGAAATTTGTTGGGCTGATTTCTATTTCAAGATTTGAAATTTGCAAGT 1281
 DB 1233 TGATGAAATTTGTTGGGCTGATTTCTATTTCAAGATTTGAAATTTGCAAGT 1292
 QY 1282 TGCTATCTCTGAAAGAAAGATTAAGTATTCAGATTTCAAGATTTTGAAGATTTTGA 1341
 DB 1293 TGCTATCTCTTGAAGAAACCAAGTATCCCGAGCTGACATTTACTGAGAAACCAATGA 1352
 QY 1342 TGAGAAATACATTTCTCTGCAATTAACAAGTATCTCAAGTATTAATTTGTAACAATCTGA 1401
 DB 1353 AGACAAATATATCTTTCAAGTCAATGATCTCAAGTATTAATTTGCAATTAATTTGCA 1412
 QY 1402 TTTATATCAACAGCAATATCCAGAAATTTGTAAGCAAAATTTGTTGGAAGTGA 1461
 DB 1413 TTTATATCAACAGCAATATCCAGAAATTTGTAAGCAAAATTTGTTGGAAGTGA 1472
 QY 1462 TGAGATATATCTGCTTACTCTGCTGTGCTGTATCCAGAGTTCATGGAATGATGT 1521
 DB 1473 CGAGAGCAACAGGTTTCAATATGCTGTCTTTTACCGAGTGTCTATGAAATGATGT 1532
 QY 1522 CTTGATCCAAAGTTCAATATATGCTCTCTGAGAGTGAATGCAATATCTTTTCA 1581
 DB 1533 CTTTATATCTTAAGTTTAAATAGTCTCTCCAGAGCTGATATGCAATATCTTTTCA 1592
 QY 1582 TAACGAGAAAGGCAAGCATCAACCTCTTATGATGTTCAATGCAAAATTTGATTTATGA 1641
 DB 1593 TTTGCAAGAGAAAGCACTACCTGCTTATGATGTTTATGAGAACTCTCTTTAG 1652
 QY 1642 CCCGAGCAAAACGATGAACATGAGGATCTGATGACCGGATCAAGCCCATCTCTT 1701

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DB      1653  TGGCGAAGAGATGATGAGCATGTTGTTTACTGAGCGAGCAATGAAAGCCATCATCTT 1712
QY      1702  CTCATGCGAAGACTTCGACAGGGTAAAGAACTAAACAGGGCTGCTGAAAGCTTTGCTAA 1761
DB      1713  CTCTATGCGAAGACTTGAACAGGGTAAAGAACTTGAACAGGGCTGCTGAAAGCTTTGCTAA 1772
QY      1762  GTGGGCTAGCTGAGAGGGAGCTGTAAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1821
DB      1773  GAAATGCAAGCTTGAAGAGCTTGAAGATTTGTTAGTGGTGGTACATGATGAGAA 1832
QY      1822  CAAATGCAAGAGCAAGAGAGAGATGCGAGATAGAGAAATGATGATGATGATGATGATGATGAT 1881
DB      1833  TCAATGCGAAGAGTAAAGAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1892
QY      1882  CCAATGCTTTGCTGCGAGCTTCCGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1941
DB      1893  GTATGATTTAAGACCGGTGAGTTAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1952
QY      1942  CGAGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2001
DB      1953  TGAATGCTTACCGCTTATGCGAGACACAAAGAGTGTGTTTGTGCTGCTGCTGCTGCTGCTGCT 2012
QY      2002  AGCGTTCCGCTCTCAACCGTCTGAGAGCGCAATGACCTGTGCGCTTCTTACTTTGCGAGCGCT 2061
DB      2013  AGCATTTGGGCTTACCGGTGAGAGCGCAATGACCTGTGCGCTTCTTACTTTGCGAGCGCT 2072
QY      2062  CCAATGAGGCTCGAGCTGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2121
DB      2073  TCAATGATGAGAGCGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2132
QY      2122  CCAACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2181
DB      2133  TCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2192
QY      2182  AGATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2241
DB      2193  AATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2252
QY      2242  GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2301
DB      2253  GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2312
QY      2302  GTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2361
DB      2313  GTCTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372
QY      2362  CCGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2397
DB      2373  TCGATGATTTGCGCAATTCATCCCGCTGCGCAAGAG 2408

RESULT 8
AAD45852
ID      AAD45852 standard; cDNA; 2908 BP.
AC
XX      AAD45852;
XX
DT      27-DEC-2002 (first entry)
XX
DE      Corn sucrose synthase (Sus1) cDNA.
XX
XX      Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX      transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX      cellulose; corn; chromosome 9; gene; 85.
OS
XX      Zea mays.
XX
XX      Key      Location/Qualifiers
XX      FT      28..2478
XX      FT      CDS      /tag= a
XX      FT      /product= "Corn Sus1 protein"
XX

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PN      WO200267662-A1.
XX
XX      06-SEP-2002.
PD
XX      21-FEB-2002; 2002WO-US005137.
XX
XX      22-FEB-2001; 2001US-0270777P.
XX
XX      (PION-) PIONEER HI-BRED INT INC.
XX
XX      Dhusga KS, Helentjaris TG, Niu X;
XX
XX      MPI; 2002-691625/74.
XX
XX      P-PsDB; AAE28501.
XX
XX      New polynucleotide and its encoded sucrose synthase, useful for
XX      modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX      or soybean) to improve stalk length, reduce grain breakage, or improving
XX      plant or grain strength.
XX
XX      Example 10; Page 110-114; 125pp; English.
XX
XX      The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX      constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX      acids. The polynucleotide, or its encoded protein, is useful for
XX      modulating the level of sucrose synthase in a transgenic plant,
XX      increasing cellulose production in the stalk tissue of a transgenic
XX      plant, or increasing the concentration of cellulose in the tissues of a
XX      seed of a transgenic plant. This is particularly useful in plant (e.g.
XX      maize or soybean) breeding, especially for e.g. improving stalk length in
XX      maize, reducing grain breakage during combining, transport or movement
XX      into storage, or improving plant or grain strength. The present sequence
XX      is corn Sus1 cDNA. Corn Sus1 gene is located at chromosome 9
XX
XX      Sequence 2908 BP; 623 A; 815 C; 808 G; 662 T; 0 U; 0 Other;
XX
XX      Query Match      42.5%; Score 1162; DB 6; Length 2908;
XX      Best Local Similarity 68.3%; Pred. No. 9, 5e-253;
XX      Matches 1641; Conservative 0; Mismatches 755; Indels 6; Gaps 2;
XX
QY      7  CCAAGGCTCGGCGAAGCGGCTGAGAGACCCCTCCAGCGAGCAAGAGAGCTGCTGCG 66
DB      66  CCAAGGCTCGGCGAAGCGGCTGAGAGACCCCTCCAGCGAGCAAGAGAGCTGCTGCG 125
QY      67  CCTCTGCTCAAGTATGTAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
DB      126  CGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
QY      127  CGGCTGAGC---GAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
DB      186  CGAGTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
QY      184  CGAGTCTCTCGGCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
DB      246  GATGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
QY      244  GCGCCCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
DB      306  CCGCCCTAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
QY      304  GCAATGCAAGATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
DB      366  GAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
QY      364  TGAATCCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
DB      426  CAAACATTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
QY      424  TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
DB      486  TCGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
QY      484  GTTCCGCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543

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546 CTTCCATGACAGAGAGCATGTACCCCTTGCTCACTTCCTTGAGGCCACAACTACAA 605
544 GGGGCGATGTTATGATCTTATATGATAGAAATCAAGCTTGGGAGGCTTCACTTGCT 603
606 GGGGATGACCATATGTTGAAACGACAAATCCGAGTCTCAAGTCTGCAAGGTGCGCT 665
604 GACCAAGCTGAGAGCATTTGTCAAAGCTCCCGTGCACACATCTACCAAAATTGCG 663
666 GAGAGAGGCTAGAGAGCATCTGTCCACCTCAAAAGTATACCCCATATCTTGAAATTC 725
664 TTATTAATTTCAAGAGTGGGCGCTTGAGAAAGTTGGGAGTATACAGACAGACATGTTT 723
726 CCAAGGTTCCAGGAACTGTGTGGAGAAAGGTTGGGAGTATGGGCTAAGGCTGACA 785
724 GGAATGATCAATCTCTTCTTACATCATTCAGGCGCCAGACCCATCTACCTTAGAA 783
786 GGAAGATACCACTCTCTCTGTGACCTCCGAGGCGCCAGATCCGTCACCTCGAGAA 845
784 ATTCTTGGGAGAGATCCCAATGATTTTAAAGTTGTGTGATACCCCTGATGATCTT 843
846 GTTCTTGAACATCCCAAGGTGTTCAATGTGTATATCTCTCCCTCAATGATATCTT 905
844 TGGTCAAGCTAATGATTTAGGCTTGCACAGACAGAGGACAGATCGTATATATCTGA 903
906 CGCTCAAGCTAATGTGTGGGTTACCTGACACGAGAGCCAGGTTGTCTACATCTTGA 965
904 CGAGTCCGCTGCTAGAAATAGATGTCTCTCTTTAAAGAAACAAGGCTTGATGT 963
966 TCAAGTCCGCTGCTAGAAATAGATGTCTCTCTTTAAAGAAACAAGGCTTGATGT 1025
964 TTCCCAAGATCT 1023
1026 GAGCTGAGATCT 1085
1024 TACGCGCTTGAAGATTTAGGAAACAGACATCTTACATATTTAGAGTTCCTTCA 1083
1086 CCAAGCTCTTGAAGATTTAGGAAACAGACATCTTACATATTTAGAGTTCCTTCA 1145
1084 AATGAAATGAGATCTTGAAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1143
1146 AATGAAATGAGATCTTGAAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1205
1144 AATGAAATGAGATCTTGAAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1203
1206 GATCTGATCTGATGAGTGTGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1265
1204 CATATTTGAAATCTAGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1263
1266 GATCTGATCTGATGAGTGTGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1325
1264 AATTTACCATGCACTTGTCTATCTCTGAGAAAGATTTAGATTCAGATTTAGAT 1323
1326 TGTACTGATCTGATGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1385
1324 AATTTGAAATCTAGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1383
1386 CTACTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1445
1384 TGTCTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1443
1446 TGTCTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1505
1444 AATTTACTGTTGACATGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1503
1506 GGAACACCTGCGGACATGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1565
1504 TGTCTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1563
1566 TGTCTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1625
1564 GTTCTGAAATCTGATGAGATTTAGGAAACAGACATCTTACATATTTAGAGTTC 1623

1626 GTTCATCTACTTCCCTGACACCGAGTGCACAAAGGCTGACCTCCCTTCAACCCGAGAT 1685
1624 GGAATTTGATTTATATGACCCGAGGCAAAAGATGAACATTTGGGACATCTGATGACG 1683
1686 TGAAGACTCTCTGACAGCCAAACCGAGAAACAGAGACAAAGTGTGTTGAAAGACAG 1745
1684 GTCAAAAGCCATCTCTCTCTCAATGAGCAAGCTGACAGAGGTTGAAGAACATTAAGGCT 1743
1746 GAACAGCCCATATCTCTTCTTCAATGCTCTGCTGACCTGTTGAAAGCTTGAAGCT 1805
1744 GGTGAAAGCTTGTGCTAAGTGTGCTAAGCTGAGGAGCTGTAAACCTTGTCTGTGTC 1803
1806 GTGTGACTGTAGAGGCGGAAACAGCGGCTGACAGAGCTGTGAACCTGTGTGTCTG 1865
1804 CGGTTCAATGATTTCAACATGCTCAAGACAGGAAAGATTCGCGGATATGAAAGAT 1863
1866 CGGAGACCTTGTGCAACCTTCAAGACAGAGGAGGAGGCGGATTCAGAAAT 1922
1864 GCATGACATGATCAAGACCCCAACCTTGTGAGGACATTCGCTGATCTGACCCAGAC 1923
1923 GTTGTACCTCTGACAGATGACATCTGAAAGGACATTCGCTGATCTGACCCAGAT 1982
1924 AAACAGGAGCCGTAAACCGGAGCTCTATCTGCTACATGCTGATACCAATGATCTTGT 1983
1983 GAACCGCTGTGCAAGCGGAGGAGTGTACCTGCTACATCTGACACAAAGGAGCTTGT 2042
1984 ACAGCGGCTGTGATGAAAGCTTGTGCTTCAAGCTGTTAGAGGATGATCTGAGGCT 2043
2043 GCAAGCTGTCTTCTGACAGAGCTTGTGAGGCTGACAGGAGGAGGAGGAGGAGGAGG 2102
2044 TCTTACTTGTGCGAGCGCTCCATGAGGCTGAGGCTGAGATCTAGAGCATGAGCTGCGG 2103
2103 GCGGACCTTGTGACAGCGCTGACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2162
2104 CTTCATCTGACCGCTGACAGCGCTGACAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2163
2163 CTACCATGATGACCTTACAGAGGCGGACAAAGGCTGAGGCTGAGGCTGAGGCTGAGG 2222
2164 CCGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2223
2223 CAGGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2282
2224 ATACGAGAGGATGACATGAGGAGGATGATCTGAGAGGATGATGACATGAGGAGGAGG 2283
2283 CGAGGAGAGGATGACATGAGGAGGATGATCTGAGAGGATGATGACATGAGGAGGAGG 2342
2284 CCGTTTCTGAGAGGATGATGAGGAGGATGATCTGAGAGGATGATGACATGAGGAGG 2343
2343 CCGGTTTCTGAGAGGATGATGAGGAGGATGATCTGAGAGGATGATGACATGAGGAGG 2402
2344 GTTCTGATCTGAGAGGATGATGAGGAGGATGATCTGAGAGGATGATGACATGAGGAGG 2403
2403 GCTGTAGGCTCTCAAGATGACGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2462
2404 GC 2405
2463 GC 2464

RESULT 9
ADA71337
ID ADA71337 standard; DNA; 2450 BP.
XX
AC ADA71337;
XX
XX 20-NOV-2003 (first entry)
XX
DB Rice gene, SEQ ID 4660.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
OS Oryza sativa.

Db 1599 GTCCATCTACTCCCTTACTCTGAGTCTGTAAGAGGCTTCACTCCCTCCACCCAGAGAT 1658
 Oy 1624 CGAAATCTGATTATGACCCGAGGAGCAAAACATGAAACATTTGGCATCTGANTGACCG 1683
 Db 1659 TGAAGAGTGTCTCTAGAGGAGTTGACAAACAGAGCAAACTTATATGTAAGAGACAG 1718
 Oy 1684 GTCAAGCCCATCTCTTCTTCCATGCGAAGACTTCGACAGGGTGAAGAACATAACAGGGCT 1743
 Db 1719 GAAACAGCCATCATCTCTCCATGCTGCTCTTGAACCGGTTCMAAACCTTGACTGGTCT 1778
 Oy 1744 GGTCCGAGCTTTTGTCTAAGTGGCTAAGCTGAGGAGGCTGTGTAACCTTGTGCTGTTGC 1803
 Db 1779 GGTGAGCTGTATAGTCCGAAACCTTCCCTTCAAGAGCTGAGTTTAACTTGTGTTGCTC 1838
 Oy 1804 CGGATCATGATGTCACAAAGTCCAAAGACAGAGGAGAGAGATGCGAGATAGAGAGAT 1863
 Db 1839 TGTGATCCATGCG---CAACCCATCTAAGAGCAAGAGAGAGAGAGCTGAGTTCAAGAGAT 1895
 Oy 1864 GCTATGACTCATCAAGACCAACACTTGTTCGGCAGCTTCCGCTGATCTCTGCCAGAC 1923
 Db 1896 GTTGAACCTTATGACCAATACAACTGAAATGAGCCACATCCGCTGATCTCCGCGAGAT 1955
 Oy 1924 AAACAGAGCCCGGTAACGCGAGAGCTTATGCTATGCTATCATGCTGATACCCATGCTTGT 1983
 Db 1956 GAACCGTGTCCGAAAGTGAAGCTTACGCTTAAGATTCGCAACAGAGTCTTTGT 2015
 Oy 1984 ACAGCCGCTTGTATGAAGCGTTGCTTACCGCTTCAAGGCTTGAAGCCATGACTGTGCT 2043
 Db 2016 GAGGCCGCTTCTTATGAGAGCACTTCCGCTTCACTGTTGAGTCCATGACCTTGTGCT 2075
 Oy 2044 TCCCTTTTGGCAGCCTTCCATGAGGTCCAGCTGAGATCATAGAGATGCGCTTGGG 2103
 Db 2076 CCGACATTCGCAACCGCTTATGCTGCTCAGCTGAGATATGCTGAACGAGAGTCTGG 2135
 Oy 2104 CTTCGACATGACCCGTAACACCCGCAACAGGCTTATCTGATGCTGCACTTCTTGA 2163
 Db 2136 CTTCGACATGACCCGTAACACCCGTAACAGGCTTATCTGATGCTGCACTTCTTGA 2195
 Oy 2164 CCGGTCGACAGAGCCGTAACACCCGTAACAGGCTTATCTGATGCTGCACTTCTTGA 2223
 Db 2196 GAGTGTCAAGAGAGCCGTAACACCCGTAACAGGCTTATCTGATGCTGCACTTCTTGA 2255
 Oy 2224 ATACGAGATGACACATGAGAGATATCTGAGAGGTTATGACATGCTGCGCGCTGCTA 2283
 Db 2256 CGAGGAGAAATACACCTGAGAGCTTATCTGAGAGGCTGATGCTGCGCGCTGCTA 2315
 Oy 2284 CGGTTCTGAGAGAGTGTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTTATGAGAT 2343
 Db 2316 CGGATCTGAGAGAGTGTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTTATGAGAT 2375
 Oy 2344 GTTCTACATCTGAGAGTGTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCTTATGAGAT 2403
 Db 2376 GGTCTAGAGCTTCAAGAGTGTGAGAGGCTGAGAGGCTGAGAGGCTTATGAGAT 2435
 Oy 2404 GCACTAG 2410
 Db 2436 GCGCTCG 2442

RESULT 10
 ADC08208
 ID ADC08208 standard; DNA: 2451 BP.

AC ADC08208;

DT 18-DEC-2003 (first entry)

XX Rice DNA sequence Seq ID513 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KM tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarcane;
 KM wheat; rice; oil; starch; fibre; moisture content; cereal grain;

KM gene; ds; plant.
 OS *Oryza sativa*.
 PN MO2003000905-A2.
 XX
 XX
 PD 03-JAN-2003.
 XX
 XX
 PF 21-JUN-2002; 2002MO-IB002450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 26-DEC-2001; 2001US-0342327P.
 XX
 XX (SYN) SYNGENTA PARTICIPATIONS AG.
 PA Zhu T, Cheng W, Briggs S, Cooper B, Goffe SA, Moughamer T;
 PI Glazebrook J, Kaegele F, Krepis J, Provart N, Riecke D;
 XX
 DR NPI; 2003-229341/22.
 DR P-PSDB; ADC08208.
 XX
 XX
 PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 XX Claim 35; SEQ ID NO 513; 130pp; English.
 PS
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarcane, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence encoding a rice protein of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/publichedpct_sequences.
 CC
 SQ Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;

Query Match 42.1%; Score 1152.6; DB 9; Length 2451;
 Best Local Similarity 68.0%; Pred. No. 1.2e-254;
 Matches 1637; Conservative 0; Mismatches 764; Indels 6; Gaps 2;

Oy 7 CCAGCGCTCCGCGACCCGCTGAGAGACACCTTCCAGGCGCACCGCAACGAGCTGCTGC 66
 Db 39 CCACAGCGCTCAGGAGCGCATGCGACTCTCTCCGCGCACCCCAATGAGAGCTGCTGC 98
 Oy 67 CCTCTGTCAAGTACGTGAACAGGAGGAGGATCTCTGACGCGCACCAATCTCTGA 126
 Db 99 GGTCTTACAGGCTGTGTAACCTCGAAGAGGAGATGCTTACGCGCACCAATCTCTGA 158
 Oy 127 CGGCTGACGAGG---TCCAGGCTCTCGGAGGCGCGCGCTGAGAGAGGAGGAGGCTCTCT 183
 Db 159 TGAGTACAAACAGCAATCTCTGAGGCTGATCTGAGAGCTGAGAGAGGAGGAGGCTTGA 218
 Oy 184 CGAGTCTCTGCTCCGCTCCGCGAGAGGAGGAGGAGGCTGAGGCTGAGGAGGCTTGA 243
 Db 219 GATGTCTCTGAGAGTGAACAGAGGAGGAGGATGTATCTCTCCAGAGGAGGCTTGA 278
 Oy 244 GCGCCGCGCGCGAGGAGTGTGAGAGTGAAGTCCGCTCAAGCTTCAAGAGCTGAGCTGA 303
 Db 279 CCGCCGAGAGGCGCGGTCTGAGAGTGAAGGAGTCAATGAGAGGAGGAGGCTTGA 338
 Oy 304 GAGTCTCAAGTCTGAGAGTCTCGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
 Db 339 GTTCTGACAGTCCCGAGGATCTTCAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 398

364 TATCCCTACGTTCTCGAGCTTGACTCGAGCCGTTCAATGTCATGCCACGCCCAA 423
399 CAACAACTTGTGCTGAGCTGGATTTCGAGCCATTCAATGCTCTTCCCTGCTTC 458
424 TCGCTATCATCTATTGAAACGCTGCTGCTGCTCAACCGACACTTCTCTCAATCAT 483
459 TGTGTCGAAGTCCATTGGCAATGCTGAGTCTCCCAACAGGCAATGCTCATCAAGCT 518
484 GTTCGCAACAGGGATGCTTGGAGCCCTGTTGATTTCCCTCCGTTGCGACCGCAACA 543
519 CTTCATGACAAAGAGAGATGATCCACTGCTCAACTCTCTTGTGTCACAACTGACA 578
544 GGGCATGTTATGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 603
579 GGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
604 GACCAAGCTGAGAGCACTTGTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
639 GAGGAAGCTGAGAGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 698
664 TTTTAAATTTCAAGAGTGGGCTGAGAAAGTTGGGTTGATGACGACGACATGTTT 723
699 CCAAGGTTCCAGAACTTGTGCTGAGAAAGTTGGGTTGATGACGACGACATGTTT 758
724 GGAATGATCCATCTCTCTGACATCATTCAGGCGCCAGACCCATCTACCTAGAGAA 783
759 GGAAGCATCTACCTCTCTTGTGACCTTCTTGAAGCCCTGATCCGCTCACTGAGAA 818
784 ATTCTGGGAGAGATCCCATGATTTTAACTGTTGTTGTTGTTGTTGTTGTTGTTGTT 843
819 GTTCTTGGAAATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
844 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
879 CCGGAGAGCAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
904 CCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
939 CCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998
964 TTTCCCAAGATTTCTCATTTGTTACTGCTGATCCAGATGCAAAAGAAATCATGATCA 1023
999 TACACACGATCTCTTATGTCACAGTGTGCTCTCTGATGCACTGAGACCACTGCG 1058
1024 TGAAGGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
1059 TGAAGGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
1084 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
1119 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
1144 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
1179 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
1204 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
1239 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
1264 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
1299 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
1324 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
1359 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
1384 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443
1419 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1478

1444 AATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1503
1479 GGAACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1538
1504 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
1539 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
1564 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
1599 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1658
1624 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
1659 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
1684 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
1719 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
1744 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
1779 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
1804 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
1839 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1895
1864 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
1896 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1955
1924 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
1956 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2015
1984 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
2016 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2075
2044 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
2076 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2135
2104 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
2136 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2195
2164 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
2196 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2255
2224 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
2256 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2315
2284 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343
2316 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2375
2344 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
2376 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2435
2404 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2463
2436 TGTGTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2495

RESULT 11
AD007855
ID AD007855 standard; DNA; 2451 BP.
XX


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Db      1299 TGTACCATGTGACCATGGCCATGGGCTGAGAAACCAATACCCCACTTGACCT 1358
QY      1324 ATTGTGAAGAAATTTGATGAGAGATGACATTTCTCTCCGACGTTGACTGTGATTAAT 1383
Db      1359 CTACTGGAAGAGTTTGAGAGTCACTACCACTCTCATGCGAGTTCAACAATGACTTGAT 1418
QY      1384 TGTATGAACAATGCTGATTTATATCATCCACGACATACCAAGAAATGCTGGAAGCAA 1443
Db      1419 TGGATGAACACAGCTGACTTCAATCAACAGTACTTCCAGAGATTTGCCGGAACAA 1478
QY      1444 AATATCTGTGACAGTATGAGAGTATCTGCTTACTCTGCTGCTGTGACCGAGT 1503
Db      1479 GGAACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1538
QY      1504 TGTCCATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
Db      1539 TGTCCACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
QY      1564 GTCCATATATCTTCCACATACGAGAGGCAAGGCACTCACTCTCTCATGATTCAT 1623
Db      1599 GTCCATATATCTTCCACATACGAGAGGCAAGGCACTCACTCTCTCATGATTCAT 1658
QY      1624 CGAAATTTGATTTATGACCCGAGCAAAAGATGACACATTTGGGATCTGGATGACCG 1683
Db      1659 TGAAGAGTTGCTCTACAGGAGATTTGACAAACAGGACACAGTTTATGCTGAAGACAG 1718
QY      1684 GTCAAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1743
Db      1719 GAACAGGCAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1778
QY      1744 GGTGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1803
Db      1779 GGTGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1838
QY      1804 CGGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
Db      1839 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1895
QY      1864 GCATGATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
Db      1896 GTTTGACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1955
QY      1924 AAAACGGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
Db      1956 GAAACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2015
QY      1984 AACACCGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
Db      2016 GCAGCCCGCTTCTAGAGGCAATGGCTCTCACTGTTGTTGATGATGATGATGATGAT 2075
QY      2044 TCTTACTTTGCGAGGCTCTCAATGAGAGTCCAGTGTGATGATGATGATGATGATGAT 2103
Db      2076 CCCGACATTCGCAACCGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 2135
QY      2104 CTTCACATTTGACCCGATACACCCGCAACAGGCTGTTATGATGATGATGATGATGAT 2163
Db      2136 CTTCACATTTGACCCGATACACCCGCAACAGGCTGTTATGATGATGATGATGATGAT 2195
QY      2164 CGGTCGACAGCAAGCCAGATCACTGGTGAATATATCTGAGACAGGCTGACGAGCAT 2223
Db      2196 GAAATGCCAGAAAGCCAGCACTGACCAAGATCTGACAGGGGGGCTTCAAGGCTAT 2255
QY      2224 ATACGAGAACTACATGAGAAATATATCTGAGAGAGTGTGATGATGATGATGATGAT 2283
Db      2256 CGAGAGAAATACACTGAGAACTTACCTGAGAGGCTGATGATGATGATGATGATGAT 2315
QY      2284 CGGTTCTGGAAGTACGTGCAAGCTGCAAGAGCTGAGAGAGGAGGCTTACCTTGAAT 2343
Db      2316 CGGATTTGGAAGTACGTGCAAGCTGCAAGAGCTGAGAGAGGAGGCTTACCTTGAAT 2375
QY      2344 GTTTCATATCTGAAGTTCCGAGCTGCGAAGACGCTGCGCTTGAATTTGACCAAC 2403
Db      2376 GCTATATGCTTCAAGTACCGACCACTGCTAGACCTGTCGTTGGCCGTGAGAGGCGCA 2435

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QY      2404 GCAGTAG 2410
Db      2436 GCGGTG 2442

RESULT 12
AAD45851
ID AAD45851 standard; DNA; 2746 BP.
AC AAD45851,
XX
DT 27-DEC-2002 (first entry)
XX
DE Corn sucrose synthase shrunken-1 (Sh1) DNA.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; chromosome 9; gene; ds.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 72..2480
FT FT /*tag= a
FT PT /product= "Corn Sh1 protein"
XX
PD WO200267662-A1.
XX
XX 06-SEP-2002.
XX
PP 21-FEB-2002; 2002WO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helentjaris TG, Niu X;
XX
XX WPI; 2002-691625/74.
XX
XX P-PSDB; AAB28500.
XX
PT New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.
XX
XX Example 10; Page 105-108; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is corn Sh1 DNA. Corn Sh1 gene is located at chromosome 9
XX
SQ Sequence 2746 BP; 635 A; 727 C; 710 G; 674 T; 0 U; 0 Other;
XX
Query Match 41.2%; Score 1127.6; DB 6; Length 2746;
Best Local Similarity 67.7%; Pred. No. 5,7e-245;
Matches 1612; Conservative 0; Mismatches 759; Indels 9; Gaps 2;
QY      18 GGAACCGGCTGAGACACCTTCCAGCGACGCAAGAGCTGTCGCTCTGTCGA 77
Db      106 GGAACCGCTTGTGTCACCTTCTCTCCATTCATGATGATGATGATGATGATGAT 165
QY      78 AGTACGTGAACAAGGAGGAGCATCTGACGCGACCAATCTCTGAGCGCTGAGC 137

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Db 166 GGTATGTTCCAGAGGCAAGGAATGCTTCAAGCCCATCAGCTGCTTGGAGTTTGATG 225
Qy 138 AGGTCCAGGGGCTCCGGGGGCGCGGCGCTAGCCGAGGAGCCCTTCTGCGCTCCGCT 197
Db 226 CCT-----GTTGATATGACAGAGAAAGATACACCATTTGAAGCACTTCTG 279
Qy 198 CCGCGAGAGGAGATCGTCTGCGCGCTCGTGGCCATCGCGAGTCCGCCGCCG 257
Db 230 CTGCTCAGAGAGCAATGTGTCTCCGCCATGGTTTCACTGTGTATCAAGCCAGGCTG 339
Qy 258 GAGTTTGGAGATGCTCGCGCTCAACCTTCAAGCTCAGCGTGGAGCTCAAGCTCT 317
Db 340 GTGTCTGGAGATTAATTCGGGTGAATGTAGTGAAGCTGCTGAGAGAGAGTGT 399
Qy 318 GGAAGTCTCGCTTCAAGAGAGAGCTTGGAGCGGCGAGCAACATATCCCTAGCT 377
Db 400 CTGAGATCTTGGCATTCAGAGAACAGCTGTGTGATGATCAATCAACAGCACTTGTG 459
Qy 378 TCGAGCTTACTCGAGCCGTTCAATGTCTCACTCCAGCCCAATCGCTCATCTTA 437
Db 460 TTGAGTTGATTTTGAAGCCCTTCAATGCTCTTCTGCTCTTCCATGTGAGATCCA 519
Qy 438 TTGGAACGCTGCTGCTCTCAACGACACTTGTCTCATCATGTTCCGCAAGG 497
Db 520 TCGGAATGAGTGCATTCCTTACCGACACCTGTCTCAAGTTGTTCCAGAGCAAG 579
Qy 498 ATTGCTGGAGCCCTGTGGATTTCTCTCGTGGCCAGCCGAGCAAGGGGCAATGTATG 557
Db 580 AAGATTGATCCCTTCTGACACTTCTCAAGCTCATTAACAGAGGACAGACATGA 639
Qy 558 TGCCTAATGATAGATATCAAGAGCTTGGAGAGCTTCACTGTCTGCTGACCAAGCTGAG 617
Db 640 TTGTGATGACAGATTCAGAGCTTGTGTGTCTCAATCATCCCTGAGAAAGCGAGAG 699
Qy 618 AGCATTTGCAAGCTTCTGCTGACACACATCTCAATTTGCTTAAATTTCAAG 677
Db 700 AGATCTACTGATGTCTTCTCAAGACATCTCTACTCGAGTTCAACCAATAGTTCCAAG 759
Qy 678 AGTGGGCGCTGAGAAAGTTGGGTGATACAGACAGACATGTTTGGAAATGATCATC 737
Db 760 AGCTTGGCTTGGAGAGGTTGGGTGACCTGAGAGCGTGTCTGACACACTCACT 819
Qy 738 TCCCTTCAAGCATCATTCAGGCGCCAGACCCATCTACCTTAGAATAATCTTGGAGAG 797
Db 820 TGTCTTCAAGCTTCTTGAAGCCCTGATCTGCAACTTGGAGAGTTCTTGGAACTA 879
Qy 798 TCCCAATGATTTTAAAGTTGTGTGTATCCCTCATGATATCTTGTGCAAGCTATG 857
Db 880 TACCAATGATGTTCAACGTTGTATCTGTCTCTCATGTACTTCCGACGTCCATG 939
Qy 858 TATTAGGCTTGCAGACAGAGAGAGACAGATCGCTATATAGGAGCAAGTCGTCAC 917
Db 940 TGTGTGATACCTGACACTGCGCGGTGAGTTGTATCATTTGATCAAGTCCGT 999
Qy 918 TAGAAATGATGATGTTCTTCTTAAAGAAAGAGGCTTGAATGTTTCCCAAGATTC 977
Db 1000 TGAAGATGATGATGCTTCTGAGATTAAGACAGAGCTTGAATCATCCGAAAGATCC 1059
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1661 GGAGCTTCTCTACATGAGATGCAAGATGAAACACAACTTTGATTTGAAGACAGAA 1720
1687 AAGGCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1746
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1747 CGAAGCTTTTGTCTAAGTCCGCTAAGCTGAGGAGAGCTGTAACCTTGTCTGTGCGCG 1806
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1958 CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2017
1987 GCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2046
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RESULT 14
ID ADC68521
XX ADC68521 standard; cDNA; 2754 BP.
AC ADC68521;
XX
DT 18-DEC-2003 (first entry)
XX
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:13.
XX
XX Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
XX biosynthetic pathway; plant; gene; ss.
XX
XX Schedonorus arundinaceus.
XX
XX W02003040306-A2.
XX
XX 15-MAY-2003.
XX
XX 07-NOV-2002; 2002WC-N2000239.
XX
XX 07-NOV-2001; 2001US-0337703P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIGHT) WRIGHTSON SEEDS LTD.
XX
XX Demmer J, Forster RL, Gibson JB, Shenk MA, Norris MG, Glenn M;
XX Saulsbury KW, Hall C;
XX
XX WPI: 2003-441544/41.
XX P-PSDB; ADC68365.
XX
XX New polynucleotide encoding polypeptides from Lolium perenne or Festuca
XX arundinacea, useful for modulating the biosynthesis of lignin, fructan or
XX tannin in a plant.
XX
XX Claim 1; SEQ ID NO 13; 240BP; English.
XX
XX The present invention describes isolated polynucleotides (i) encoding
XX proteins (ii) from Lolium perenne and Festuca arundinacea which are
XX active in lignin, fructan and tannin biosynthetic pathways. Also
XX described: (1) an isolated oligonucleotide probe or primer comprising at
XX least 10 contiguous residues complementary to 10 contiguous residues of
XX (i); (2) a kit comprising the oligonucleotide probe or primer; (3) a
XX genetic construct comprising (i); (4) a transgenic plant cell comprising
XX the genetic construct of (3); (5) a plant or its seed, fruit or progeny
XX comprising the transgenic plant cell of (4); (6) modulating one or more
XX of the lignin, fructan or tannin compositions of a plant; (7) producing a
XX plant having one or more of the lignin, fructan or tannin compositions;
XX and (8) modifying the activity of (ii) involved in a lignin, fructan or
XX tannin biosynthetic pathway in a plant. (i) can be used for modulating
XX the biosynthesis of lignin, fructan or tannin in a plant. The present
XX sequence is used in the exemplification of the present invention.
XX
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XX
XX Query March 41.1%; Score 1125.2; DB 9; Length 2754;
XX Best local similarity 67.5%; Pred. No. 2e-244;
XX Matches 1615; Conservative 0; Mismatches 766; Indels 9; Gaps 2;
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XX 7 CCACGCGTCCGCGACACGCGTGGAGACACCTTCACGCGACCGCAAGAGCTGTGCG 66
XX 136 CCAAGATCTCCGAGAGCGCTTGGTGCACCTTCTCCATCCCAAGAGCTCATTCG 195
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XX 67 CCTCTCTGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 126
XX 196 CCTCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255
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XX 127 GCGGCTGACAGAGTCCAGAGGCTCCGCGGCGGCTAGCGCGAGGAGACCTTCTCTGCA 186
XX 256 TGAATTTGAAGCATTTGTTGATGCTG-----ACAAGAGAGGATGATGACCTTTTCAAGA 309

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Db	370	GCCCAAGGCTGTGATCTGTGGACCTACATAAGGTGAAATGTTAGGAACTGTGGCGATTGAGGA	429
QY	307	GCTCACAGTCTCGGAGTACCTCGGCTTCAAGAGAGAGCTTGTGACGCGCCGACAAATGA	366
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Db	490	CAAGTTGTGTGTGAGCTGATATTTGAGCCCTTCAGTCAAGCTCTCTCCAGTCTTCAT	549
QY	427	GCTATCACTATTGGAAACGGTGTGACAGTCTTCACACCGACATTGCTCATCATGTT	486
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QY	547	GCATGTATGATGCTTAAATGATAGAAATCAAAAGCTTGGGAGGCTTCACTGTGTGAC	606
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QY	607	CAAGCTGAGAGACATTGTCAAAAGCTCCCTGTGACACACCACTACTCAATTTGCTTA	666
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QY	667	TAAATTTCAAGAGTGGGCGCTGAGAAAGTTTGGGCTGATACAGACGACATGTTTGG	726
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QY	847	TCAAGCTATGTATTAGGCTTGCACGACACAGAGACAGATGCTTAATACTGACCA	906
Db	970	TCAATCCAAATGTGTGGATACCTGATACCGGTGGCCAGGTTGTATACATTTGATCA	1029
QY	907	AGTCCGTGCACTAGAAATAGATGATGTTCTCCGTTAAAGAAACAAAGGCTGATGTTTC	966
Db	1030	AGTCCGTGCTTTGAGAAATGAAATGCTTCTAGAAATTAAGACGAAAGGCTTGAATATAC	1089
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D	b	1570	CAGGTGGSCAGTATGAGTCTCACTTGTCTTCACTCTCCCTGATCTCAACCGTGTGT	1622
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D	b	2407	TTTCTGGAAGTACGTCTCAGAGCTCGAGGCTGAGACGAGCGCTATCTTGAATGTT	2466
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JOURNAL
Plant Mol. Biol. (2001) In press
2 (bases 1 to 2710)

AUTHORS
Helentjars, T.
Direct Submission
Submitted (10-OCT-2001) Agronomic Traits/Tend, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA

FEATURES
Location/Qualifiers

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CDS

ORIGIN

Query Match 99.0%; Score 2710; DB 8; Length 2710;
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QY 78 AGTAGCTGAACAAGGGAGGAGGATCTCTGACGCCGACCAATCTCTGACGGCTGAAG 137
DB 61 AGTAGCTGAACAAGGGAGGAGGATCTCTGACGCCGACCAATCTCTGACGGCTGAAG 120
QY 138 AGTCCAGAGGCTCCCGGGGGCGCGGCTAGCGGAGGACCTTCTCTGACGCTCGAGT 197
DB 121 AGGTCGAGGCTCCCGGGGGCGCGGCTAGCGGAGGACCTTCTCTGACGCTCGAGT 180
QY 198 CCGCGCAGAGGCGATCTGCTGCGCGCGCTCTGCTGCGCAATGCGGTCGCCGCGCG 257
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QY 258 GAGTTTGGAGTACGTCGCGCTCAAGTTTCAAGACTCAGGCTCGAGGAGCTCAAGTCT 317
DB 241 GAGTTTGGAGTACGTCGCGCTCAAGTTTCAAGACTCAGGCTCGAGGAGCTCAAGTCT 300
QY 318 CCGAGTACCTCGCTTCAAGAGAGAGCTTGTGAGCGGCGACCAATGATCTCTAGCTTC 377
DB 301 CCGAGTACCTCGCTTCAAGAGAGAGCTTGTGAGCGGCGACCAATGATCTCTAGCTTC 360
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DB 361 TCGAGCTTACCTTGAAGCGCTTCAATGCTCACTGCTCCACGCCCAATCGGTCAATCTTA 420
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RESULT 2
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DEFINITION Zea mays sucrose synthase 3 mRNA, complete cds.
ACCESSION  AY124703
VERSION     AY124703.1  GI:22121989
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REFERENCE   1 (bases 1 to 2837)
            Holstgraewe,D.L., Scholz,A., Altmann,B. and Winter,H.
            Complete coding sequence of a third sucrose synthase isoform in
            maize
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 2837)
            Holstgraewe,D.L., Scholz,A., Altmann,B. and Winter,H.
            Direct Submission
JOURNAL     Submitted (20-JUN-2002) Biology, University of Osnabrueck, Barbara
            Straube 11, Osnabrueck 49076, Germany
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ORIGIN
polya_site
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Qy      76  CAAGTACGTGAACAAGCGGAGAGGCGATCTGACGCGGACCAACCATCTCGAGCGGCTGCA 135
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QY	196	CTCCCGCAGAGAGGCGATCGTCTCCGCGCTTCGTGGCCATCGCGAGTCCGCCCGCC	255
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Db	396	GAGATTGGGAGTACGTCGCCGCTCAAGCTTACGAGCTCAAGCTGAGAGAGCTCAAGT	455
QY	316	CTGGAGTACCTCCGCTCAAGAGAGAGTTGTGACGCGGACGACATGATCCCTAGT	375
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QY	736	TCTCCTCTTACGACATCTTGAAGGGCCGACGACCATCTACCTGAGGAATCTTGGGGAG	795
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QY	856	TGATTTAGCTTGGCCAGACACAGAGGACAGATCTCTATATATCTGACCAAGTCCGTGC	915
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QY	976	TCTCATTTTACTCGGCTGATACAGATGCAAAAGAAACATATGCAATCAGCGGCTTGA	1035
Db	1116	TCTCATTTTACTCGGCTGATACAGATGCAAAAGAAACATATGCAATCAGCGGCTTGA	1175
QY	1036	GAGATTGTGGACACAGGCACTTACATATTAGAGTCCCTCAGAAATGAAAATGG	1095
Db	1176	GAGATTGTGGACACAGGCACTTACATATTAGAGTCCCTCAGAAATGAAAATGG	1235
QY	1096	GATACTTAAGAAATGATATCAAGATTTGATGTGTGGCATATCTGAAAACATTTGCTGA	1155
Db	1236	GATACTTAAGAAATGATATCAAGATTTGATGTGTGGCATATCTGAAAACATTTGCTGA	1295
QY	1156	GGAATGCTGCTGAAATTTGCTGCTGAAATTAAGATCTCGAGCTCATTAATTGGAA	1215
Db	1296	GGAATGCTGCTGAAATTTGCTGCTGAAATTAAGATCTCGAGCTCATTAATTGGAA	1355
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Qy	1456	AACGATGAGAGTCAACTGCTTTTACTCTGCTGATCTGACGAGTTTCATGGAT	1515
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Qy	1816	TGTCACCAAGTCCAAAGGACAGGGAAGAGATGCGCGAGATAGAGAAAGATGCAATCACTAT	1875
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Db	2016	CAAGACCCCAACTTGTTCGGGCAAGTTCGGGTGAGATCTCTGCCACAGCAAAACAGGGCCCG	2075
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Db	2551	-----	2550C
QY	2556	CATATGCGCAGTATTAACAAATTAATCTGAAGCGAGGTGGTGTGCACTTGTGTGCTTAC	2539B
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ACCESSION	AK099406
VERSION	AK099406.1
KEYWORDS	GI:32384615
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ORGANISM	Oryza sativa (japonica cultivar-group)
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REFERENCE

1. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1
The Rice Full-Length cDNA Consortium, National Institute of
Agricultural Sciences Rice Full-Length cDNA Project Team,
Kikuchi, S., Sato, K., Nagata, T., Kawagahira, N., Doi, K.,
Kishimoto, N., Yazaki, U., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yanagi, M., Suzuki, K., Ue, C.,
Onusaki, K., Shishiki, T., Foundation of Advancement of International
Genome Sequencing & Analysis Group, Otono, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, T.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishida, U.,
Keda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumagi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Funada, S.,
Hara, A., Hashidume, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Komoto, H., Miyazaki, A., Oatono, N., Oca, Y.,
Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashiraki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
Japornica rice
Science 301 (5631), 376-379 (2003)
27152273
JOURNAL
MEDLINE
PubMed
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REFERENCE
AUTHORS
2 (bases 1 to 2716)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,

TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression: 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:etikuchi@nias.affrc.go.jp
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/NIRS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohmeda_E_Yahagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_and_Yamamoto_M
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurotaki,T., Kusunegi,T., Iu,M., Masuda,H., Mitra,J., Mizuno,K., Narikawa,R., Nishikura,T., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsumoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arikawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hori,F., Iida,J., Itamura,K., Imotoani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawal,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishii,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibara,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers

FEATURES
source

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/mol_type="mRNA"
/cultiVar="Nippohbare"
/db_xref="taxon:39947"
/clone="J013001M19"

Query Match
Best Local Similarity 86.1%; Pred. No. 0; Mismatches 334; Indels 0; Gaps 0;
Matches 2063; Conservative 0;

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LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AKI02158 2763 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:U033086F24, full
insert sequence.
AKI02158
AKI02158.1 GI:32987367
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.

1
The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Naitoh, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohnuki, K., Shishiki, T., Foundation of Advanced Science of International
Science Genome Sequencing & Analysis Group: Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Naitaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, R., RIKEN,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, U., Carninci, P., Adachi, J., Aizawa, K., Aizawa, T., Fukuda, S.,
Hara, A., Hashidume, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,
Sato, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

2 (bases 1 to 2763)
Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kishimoto, N., Kato, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koyu, S., Kuribara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
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Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
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Yamada, H., Yamamoto, M., Yasumishi, A., Yazaki, J., Yokomizo, S., and
Yoshimura, A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
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Laboratory of Gene Expression, 2-1-2 Kamondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
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This clone is one of the 28k full-length cDNA clones from japonica
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URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Naitoh, T.,
Ishikawa, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.

FEATURES

FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Naitaka, R., Naitaka, Y., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Aizawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasumishi, A., and Hayashizaki, Y.
Location/Qualifiers
1..2763
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="U033086F24"

ORIGIN

Query Match 68.1%; Score 1862.6; DB 8; Length 2763;
Best local similarity 86.1%; Pred. No. 0;
Matches 2063; Conservative 0; Mismatches 334; Indels 0; Gaps 0;

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 AX653034
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 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Euphorbiaceae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M.,
 Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
 Plant genes involved in defense against pathogens
 Patent: WO 03000898-A 2904 03-JAN-2003;
 JOURNAL
 Syngenta Participations AG (CH)
 FEATURES
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ORIGIN

Query Match 65.2%; Score 1784.2; DB 6; Length 2412;
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 KEYWORDS sucrose synthase.
 SCRCR Pisum sativum (pea)
 ORGANISM Pisum sativum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
 Pisum.
 REFERENCE 1 Buchner, P., Poret, M. and Rochat, C.
 Cloning and Characterization of a cDNA (Accession No. AJ001071)
 Encoding a Second Sucrose Synthase Gene in Pea (Pisum sativum L.)
 Plant Physiol. 117, 719-719 (1998)
 JOURNAL 2
 AUTHORS Buchner, P.
 TITLE Direct Submission
 REFERENCE Submitted (11-AUG-1997) Buchner P., Metabolisme, INRA-Versailles,
 Route de St. Cyr, Versailles-cesdex, 78026, FRANCE
 JOURNAL Revised by [3]
 REMARK 3 (bases 1 to 2848)
 REFERENCE Buchner, P.
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5'UTR
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 VERSION AB022091.1 GI:6682840
 KEYWORDS
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 ORGANISM Citrus unshiu

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE
 1 Komatsu A., Moriguchi, T., Koyama, K., Omura, M. and Akiyama, T.
 Analysis of sucrose synthase genes in citrus suggests different
 roles and phylogenetic relationships
 J. Exp. Bot. 53 (366), 61-71 (2002)

JOURNAL
 PUBLISHED 21606208
 11741042
 2 (bases 1 to 2765)
 AUTHORS Komatsu, A.
 TITLE Direct Submission
 JOURNAL Submitted (22-DEC-1998) Akira Komatsu, National Institute of Crop
 Science, 2-1-18, Tsukuba Science City, Ibaraki 305-8518, Japan
 (E-mail: akomatsu@affrc.go.jp, Tel: 81-298-38-8949,
 Fax: 81-298-38-8949)

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QY 1690 GCGCATCTCTTCTCATGAG 1749
DB GCGCATCTCTTCTCATGAG 1749
1776 GCGCATCTCTTCTCATGAG 1835
QY 1750 AGCTTTGCTAAGGCTTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809
DB AGCTTTGCTAAGGCTTAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809
1836 GTGCTTATGATGAG 1895
QY 1810 CAATGATGATCAAG 1869
DB CAATGATGATCAAG 1869
1896 CATAGATGATTAAG 1955
QY 1870 ACTATGATGATCAAG 1929

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Db      1956 GCTTATGAAGACGTAACAGTTGATAGTTCGTTGGATAGACGCTCAACAAATAG 2015
Qy      1930 GGGCCGTACCGCGAGCTCTATCGCTACGCTGATACCCATGCTGCTTGGTAAAGC 1989
Db      2016 GGCACGTATGATGAGCTCTATCGCTATATAGCCGACCAAGGCTCTTTGTGAGCC 2075
Qy      1990 GGCCTGTATGAGGCTTCGCTCTGACCGCTGTTGAGGCGCATGACCTGTGAGCTTCTAC 2049
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Db      2136 ATTCGCACTTCGCAATGATGAGGCTTCAGAGATATCGAGCATGATGATGAGGCTTCCA 2195
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Db      2196 TATTATTCATATTCACCCGATCAGCTGATCTGATCTGATCTGATCTTCTTGGAAGTG 2255
Qy      2170 CAAGAGAGCCAGATCATCGGGGTAATATCTGAGAGCAGGCTGACGAGCATATAGCA 2229
Db      2256 CAAGGAAATTCAGAGCATTTGAAAAAATCTTTCAGAGGAGCTTAAAGATTTATGA 2315
Qy      2230 GAAGTACACATGAGATATCTACAGAGAGTTCATGATGACATGCGCGGCTTACGGTTT 2289
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Qy      2412 GCTTGC 2415
Db      2496 AGCTGC 2501

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RESULT 8
AB045710 2787 bp mRNA linear PLN 03-MAY-2003
LOCUS Pyrus pyrifolia PypSU1 mRNA for sucrose synthase 1, complete cds.
DEFINITION AB045710
ACCESSION AB045710.1 GI:12082280
VERSION
KEYWORDS
SOURCE
ORGANISM
Pyrus pyrifolia (sand pear)
Pyrus pyrifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eustoids I; Rosales; Rosaceae; Maloideae; Pyrus.

REFERENCE
AUTHORS
TANASE, K., SHIRATAKE, K., MORI, H. and YAMAKI, S.
TITLE
Changes in the phosphorylation state of sucrose synthase during
development of Japanese pear fruit
JOURNAL
Physiol. Plantarum 114 (1), 21-26 (2002)
PUBLISHED
11982930
2 (bases 1 to 2787)
AUTHORS
Tanase, K., Yamaki, S. and Mori, H.
TITLE
Direct Submission
Submitted (06-JUL-2000) Koji Tanase, Nagoya University, Graduate
School of Bioagricultural Sciences, Chikusa, Nagoya, Aichi
464-8601, Japan (E-mail:1000043@ombox.media.nagoya-u.ac.jp,
Tel:81-52-789-4028, Fax:81-52-789-4025)
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DLAKSPRALIDAH"

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ORIGIN

Query Match 47.7%; Score 1305; DB 8; Length 2787;
Best Local Similarity 71.6%; Pred. No. 1,7e-220;
Matches 1729; Conservative 0; Mismatches 680; Indels 6; Gaps 1;

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Qy      76 CAAGTACGTGAACAAGAGGAGGCACTCTGAGCGCACCAACACCTTCGAGCGCTGCA 135
Db      192 CAGGTACTGATCAAGGGAAGAAAGATATCTGACCGCAGACCTGATCATGACTGCA 251
Qy      136 CGAGTCCAGAGGCTCCGGG-----GCGGCGCTAGCCGAGAACCTTCTCGAGCT 189
Db      252 CATGTTCATGGGAGAGATGAAGCAAAAGAGCTCAAAAATGAGACTTTCAGCAAGT 311
Qy      190 CTTCCGCTCCGCGAGAGGCGATCTGCTGCGCGCGCTGTGSCCATCGCGTGGCGCC 249
Db      312 CTTCAATCCGACAGAGAACCAATGTTCTGCTCCATGATGAGCTTGAAGAGTCTGCC 371
Qy      250 GCGCGCGGAGTTTGGAGTACGTCGCGCTCAAGCTCACAGCTCAGCGCTGAGAGACT 309
Db      372 AAGACCTGGTCTGGATTAATGCTGTTAATGATTAAGCTTAAGTATGAGAGATT 431
Qy      310 CACAGTCCGAGTACCTCCGCTTCAAGAGAGCTTGTGACGCGCAGCAATGATCC 369
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Qy      370 CTAGCTTCGAGCTTGAATTCGAGCGCTTCAATGCTCACTCCAGGCCCAATCGCTC 429
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Qy      430 ATCATCATTTGAAAGGAGTGGAGTCTTCAACGACCACTTGTCTCAATCATGTTCCG 489
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Qy      490 CAACAGGATTTGCTTGAGCCCGCTTGTGATTTCTCCGTGGGCAACCGGCAACAAGGCA 549
Db      612 TAACAGGAATCGTTGATGATCATTAATGATTTCTTGAAGCAACAATTAAGGCGCA 671
Qy      550 TGTATGATGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609
Db      672 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731
Qy      610 AGCTGAGAGAGCACTGCAAGCTCCCTGCTGACACACCAATCTCAATTTGCTTATTA 669
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QY 670 ATTCAAGAGTGGGCTGAGAGAAAGTTGGGATGATACAGACAGACATGTTTGGAAAT 729
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 QY 730 GATCCATCTCTTCTAGACATCATTCAGGCGCAGACCCATCTACCTTGAAGAAATTTCT 785
 DB 852 GATCATCTCTCTTAGATATCTCTCAGGCTCTGATCTCTTATATGAGAGCAATTCCT 911
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 DB 972 AGCAATTTTATAGGCTTACCGACACTGAGGCGAGATTTGCTATATGAGACCAAGT 1031
 QY 910 CCGTCACTAGAAATGAGATGCTTCTCCGTTTAAAGAAACAGAGGCTTATGATTTCC 969
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DB 1872 GTGCTATGCTTAAATGTTCCAACTGAGGAGATCTGCGAAACCTTGTATATGTTCTGGTTA 1931
 QY 1810 CAATGATGTCAGAAAGTCCAGAGACAGAGAGAGATCCGAGATGAGAGATGATGATGAT 1869
 DB 1932 CATGATGTCAGAAAGATATGAGATGAGAGAGATGAGAGAGATGAGAGATGAGATGAT 1991
 QY 1870 ACTCATCAAGACCAACATTTGTTGAGGAGTTCGCTGATCTCTGAGGAGGAGGAGGAG 1929
 DB 1992 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
 QY 1930 GAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1989
 DB 2052 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
 QY 1990 GGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2049
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 QY 2050 TTTGCGAGCGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2109
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 QY 2110 CATGAGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2169
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RESULT 9
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 LOCUS
 DEFINITION Solanum tuberosum sucrose synthase mRNA, complete cds.
 ACCESSION AY205302
 VERSION AY205302.1 GI:29289942
 KEYWORDS
 SOURCE
 ORGANISM
 Solanum tuberosum (potato)
 Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 (bases 1 to 2679)
 Loureiro, M., Kopke, J., Mueller-Roeber, B. and Trehewey, R.
 Characterization of effects of specific reduction in gene
 expression of two sucrose synthase genes in transgenic potato
 plants
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 2679)
 Kopke, J., Loureiro, M., Mueller-Roeber, B. and Trehewey, R.
 Authors
 Direct Submission
 Submitted (20-DEC-2002) Plant Biology, Federal University of
 Vicososa, Av PH Rolfs S/N, Vicososa, MG 36570-000, Brazil
 JOURNAL
 Location/Qualifiers
 FEATURES
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CDS

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ORIGIN

Query Match 46.0%; Score 1258.2; DB 8; Length 2679;
 Best Local Similarity 70.6%; Pred. No. 3,2e-212;
 Matches 1693; Conservative 0; Mismatches 698; Indels 6; Gaps 1;

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Db 119 GATATGTGGCGCAGGGGAGGAGGATTTTGCACTCTCATTAATTGAGAGTTCAATA 178
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Db 599 TCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
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Db 1679 TGTATTTGATCTTGAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1738
QY 1692 CCATCTCTCTTCCATGAGCAAGACTCGACAGGATGAGAAACATTAACAGGCTGTGGAAG 1751
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QY 1752 CTTTGTGCTAATGCGCTAAGCTGAGGAGCGTGTAAACCTTGTGCTGCTGCGGATCA 1811
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QY 1812 ATGATGCAACAAGTCCAAAGACAGAGAGAGATCGCGAGATAGAGAGATGATGAAC 1871
DB 1859 ACGATGTAATAAATGACACACTCAAGGAAATGGCAACCTTGTCTAGTAGCTGATACA 1918
QY 1872 TCATCAAGACCCCAACTTGTGCGGAGCTTCCGCTGATCTCTCCGACAGACAAACAGG 1931
DB 1919 TTATGAGAGAAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1978
QY 1932 CCGGTAAGGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1991
DB 1979 CACGTAAGGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2038
QY 1992 CTTTGTGCTAATGCGCTAAGCTGAGGAGCGTGTAAACCTTGTGCTGCTGCGGATCA 2051
DB 2039 CATTTATGAGAGCTTGTGAGACTCAAGGAGTGTGAGAGCTGATGATGATGATGATGATG 2098
QY 2052 TCGGAGCGCTCCATGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 2111
DB 2099 TTGCAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2158
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DB 2339 GGAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2398
QY 2352 TACTGAGTTCGCGAGAGCTGAGAGAGCGGAGAGAGCGGCTGATGATGATGATGATG 2408
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RESULT 10
LOCUS CPl132000 2648 bp mRNA linear PLN 25-AUG-1999
DEFINITION Craterostigma plantagineum mRNA sucrose synthase 2.
ACCESSION AJ132000
VERSION AJ132000.1 GI:4468152
KEYWORDS Ss2 gene; sucrose synthase.
SOURCE Craterostigma plantagineum
ORGANISM Craterostigma plantagineum
Bukayocra; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Lamiales; Lamiales; incertae sedis; Lindeberaceae;
Craterostigma.
1
REFERENCE
AUTHORS Kleines M., Elester, R.C., Rodrigo, M.J., Blevacq, A.S., Salamini, F.
and Bartels, D.
TITLE Isolation and expression analysis of two stress-responsive
sucrose-synthase genes from the resurrection plant Craterostigma
plantagineum (Hochst.)
JOURNAL Planta 209 (1), 13-24 (1999)
MEDLINE 99396657
PUBMED 10467027
REFERENCE 2. (bases 1 to 2648)
AUTHORS Kleines M.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1999) Kleines M., Abteilung fuer
Pflanzenzuechtung und Ertragsphysiologie, Max-Planck Institut fuer

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        Best local Similarity 70.0%; Pred. No. 2,7e-211;
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        DB 79 GAGAAAGGCTGAGAGCTCTTCTGCTGCTCAAGAGAGCTGCTGCTTCA 138
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QY	852	CTAATGTTTATAGCTTCCAGACACAGAGAGACAGATCCGCTATATATGAGACCAATGCC	911
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AUTHORS Harper, J. F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 021655-A 2415 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

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Query Match 45.2%; Score 1238.4; DB 6; Length 2430;
Best Local Similarity 70.4%; Pred. No. 1e-208;
Matches 1672; Conservative 0; Mismatches 696; Indels 6; Gaps 1;

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Direct Submission
Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: "RIKEN
Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
Saito, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salix, Stanford, PGEC (SSP) Consortium members carried out the

sequencing and annotation of the RAF1 cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Bann, J., Banno, F., Dale, U.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Tosi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, J., Chen, R., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koese, R., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Tracy, S.E., Davis, R.W., Eckert, J.R. and Theologis, A. Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

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Db 2238 GTTCGGCTGCAACAGATGAGAGC 2262

Search completed: May 25, 2004, 19:58:48
Job time : 7028.39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:28:09 ; Search time 41.6803 Seconds
(without alignments)
5413.769 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247
Sequence: -MSAPKLNRMASIRDRVEDTL.....YILKREIAKTVPLAIDPQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/PC7_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/PC7US_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4247	100.0	809	14	US-10-080-114A-12
2	4177	98.4	802	14	US-10-080-114A-2
3	3427	80.7	824	12	US-10-425-114-45934
4	3420	80.5	651	12	US-10-425-114-49911
5	3407	80.2	812	12	US-10-424-599-241731
6	3129	73.7	797	14	US-10-217-939-30
7	3108.5	73.2	805	14	US-10-217-939-28
8	3011.5	70.9	802	14	US-10-080-114A-5
9	3011.5	70.9	807	12	US-10-425-114-57840
10	3011.5	70.9	811	12	US-10-425-114-53965
11	3001	70.7	823	12	US-10-425-114-53296
12	3001	70.7	823	12	US-10-425-114-56696
13	3001	70.7	823	12	US-10-425-114-57139
14	3001	70.7	823	12	US-10-425-114-72813
15	2999.5	70.6	805	12	US-10-424-599-258404

16	2997	70.6	816	14	US-10-080-114A-7	Sequence 7, Appli
17	2987.5	70.3	806	12	US-10-425-114-54297	Sequence 54297, A
18	2986.5	70.3	805	12	US-10-424-599-154986	Sequence 154986,
19	2976.5	70.1	815	14	US-10-289-757-170	Sequence 170, App
20	2972	70.0	806	13	US-10-003-405-2	Sequence 2, Appli
21	2972	70.0	814	14	US-10-289-757-76	Sequence 76, Appl
22	2949.5	69.4	806	12	US-10-424-599-154300	Sequence 154300,
23	2949.5	69.4	806	12	US-10-424-599-154301	Sequence 154301,
24	2948.5	69.4	811	12	US-10-425-114-55184	Sequence 55184, A
25	2948.5	69.4	811	12	US-10-425-114-50176	Sequence 50176, A
26	2947	69.4	816	14	US-10-289-757-169	Sequence 77, Appl
27	2942.5	69.3	808	14	US-10-289-757-169	Sequence 169, App
28	2938.5	69.2	808	14	US-10-289-757-74	Sequence 74, Appl
29	2924.5	68.9	808	14	US-10-289-757-75	Sequence 75, Appl
30	2892.5	68.1	805	14	US-10-137-036-77	Sequence 77, Appl
31	2892.5	68.1	805	15	US-10-393-840-144	Sequence 44, Appl
32	2892.5	68.1	805	15	US-10-393-840-144	Sequence 44, App
33	2882.5	67.9	749	12	US-10-425-114-56196	Sequence 56196, A
34	2763	65.1	528	12	US-10-425-114-48418	Sequence 48418, A
35	2595.5	61.1	670	12	US-10-425-114-49869	Sequence 49869, A
36	2534	59.7	567	12	US-10-424-599-241719	Sequence 241719,
37	2485.5	58.5	639	12	US-10-425-114-58450	Sequence 58450, A
38	2474.5	58.3	652	12	US-10-425-114-46682	Sequence 46682, A
39	2439.5	57.4	628	12	US-10-424-599-244151	Sequence 244151,
40	2423.5	57.1	619	12	US-10-425-114-68121	Sequence 68121, A
41	2362.5	55.6	596	12	US-10-425-114-62525	Sequence 62525, A
42	2361.5	55.6	593	12	US-10-425-114-50109	Sequence 50109, A
43	2193	51.6	541	12	US-10-425-114-50160	Sequence 50160, A
44	2119.5	49.9	570	12	US-10-425-114-54291	Sequence 54291, A
45	2097.5	49.4	527	12	US-10-425-114-62397	Sequence 62397, A

ALIGNMENTS

RESULT 1
US-10-080-114A-12
Sequence 12, Application US/10080114A
Publication No. US20030005482A1
GENERAL INFORMATION:
APPLICANT: Dhugga, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
TITLE OR INVENTION: to Improve Stalk and Grain Quality
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080, 114A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/270, 777
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 809
TYPE: PRT
ORGANISM: Zea mays
US-10-080-114A-12

Query Match	100.0%	Score 4247	DB 14	Length 809
Best Local Similarity	100.0%	Pred. No. 0		
Matches 809	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSAPKLNRMASIRDRVEDTLHAHRELVALLSKYVNGKGILOPHHIDALDEVGSGVR	60	
DB	1	MSAPKLNRMASIRDRVEDTLHAHRELVALLSKYVNGKGILOPHHIDALDEVGSGVR	60	
QY	61	ALARGPFLDVRSGOEIVLPPEFALIVRPRGWEYRVNVVHLSVEQLTVSRLRKE	120	
DB	61	ALARGPFLDVRSGOEIVLPPEFALIVRPRGWEYRVNVVHLSVEQLTVSRLRKE	120	
QY	121	ELVDGQNDPVYVLEDEPNVSVPRNRSSISNGVOFLRRHSIMFRRDCEPLD	180	
DB	121	ELVDGQNDPVYVLEDEPNVSVPRNRSSISNGVOFLRRHSIMFRRDCEPLD	180	
QY	181	FLRGHRKHGVMLNDRISGLISGLVLTAAEHLXKLPAIDTVSQAAYKQEWGELKGM	240	

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Db      181 FARGHGHKGVMMNDRIOSLGRLOSVLTKAEHLSKLPAOTPYSOFAFKQEMGLEKGM 240
Qy      241 GPCAGGVLEMLHLLDITIQAPDPSTLEKLGRIPMIFNVVVSPPHYFQGANVLGLPDS 300
Db      241 GPTAGGVLEMLHLLDITIQAPDPSTLEKLGRIPMIFNVVVSPPHYFQGANVLGLPDS 300
Qy      301 GOIYVILDOVALLENEMVRLKKQGLDVPKILIVTRLIPDAKGTSCNRLERISGTQHT 360
Db      301 GOIYVILDOVALLENEMVRLKKQGLDVPKILIVTRLIPDAKGTSCNRLERISGTQHT 360
Qy      361 YILRVPPRENGILKKMISRPDWPYLETFADDAAGEIAELQGTPTDFTIGNYSQGNLVA 420
Db      361 YILRVPPRENGILKKMISRPDWPYLETFADDAAGEIAELQGTPTDFTIGNYSQGNLVA 420
Qy      421 SLTSLYKMGITQCNIAHALKTKYPPSDIFPMKNFDEKHYFSCQFTADIAMNNADFLITST 480
Db      421 SLTSLYKMGITQCNIAHALKTKYPPSDIFPMKNFDEKHYFSCQFTADIAMNNADFLITST 480
Qy      481 YOEIAGSKXTVQGVESHRTAFPLPGHYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKAR 540
Db      481 YOEIAGSKXTVQGVESHRTAFPLPGHYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKAR 540
Qy      541 LTSHGSIENLIYDEPQNDERTGHLDDRSKPLIFSMARLDRYKNITGLVEAPAKCAKRE 600
Db      541 LTSHGSIENLIYDEPQNDERTGHLDDRSKPLIFSMARLDRYKNITGLVEAPAKCAKRE 600
Qy      601 LVNLVAVAGYDYNVSKOREETIAETEKHEMLIKTNLFGQFRMISQTNRANGELXYRI 660
Db      601 LVNLVAVAGYDYNVSKOREETIAETEKHEMLIKTNLFGQFRMISQTNRANGELXYRI 660
Qy      661 ADTHGAFVQPALYAEFGITVVEAMTCGLPTFATLHGPAEIIEHGVSGFHIDPYHPEQAV 720
Db      661 ADTHGAFVQPALYAEFGITVVEAMTCGLPTFATLHGPAEIIEHGVSGFHIDPYHPEQAV 720
Qy      721 NIMADFPDRCODPDHVNISGAGIQRIYKTYKTIYSERLMTLAGVYGFMYVSTLERL 780
Db      721 NIMADFPDRCODPDHVNISGAGIQRIYKTYKTIYSERLMTLAGVYGFMYVSTLERL 780
Qy      781 ETRRYLEMFIYIKFRELAKTVPLAIDQPO 809
Db      781 ETRRYLEMFIYIKFRELAKTVPLAIDQPO 809

RESULT 2
US-10-080-114a-2
; Sequence 2, Application US/10080114A
; Publication No. US20030005482A1
; GENERAL INFORMATION:
; APPLICANT: Zhuoga, Karwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080,114A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Zea mays
US-10-080-114a-2

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Query Match      98.4%; Score 4177; DB 14; Length 802;
Best local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      14 DREVTTLAHRNELVALTSKYVKKGIGIOPHHIIDLADDEVQSGVGRALAEGLPDLARS 73
Db      7 DREVTTLAHRNELVALTSKYVKKGIGIOPHHIIDLADDEVQSGVGRALAEGLPDLARS 66

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Qy      74 AOEALVLPPEFVALAARPRGWEYVRVNVHLSVEQLTSEYLRFGELVLDGQHNPPYVL 133
Db      67 AOEALVLPPEFVALAARPRGWEYVRVNVHLSVEQLTSEYLRFGELVLDGQHNPPYVL 126
Qy      134 ELDPPEFVSVPRPNRSSIANGVQPLNRHLSIMFRNDCLEPLLDPLGRHGHKGVMM 193
Db      127 ELDPPEFVSVPRPNRSSIANGVQPLNRHLSIMFRNDCLEPLLDPLGRHGHKGVMM 186
Qy      194 LMDRIOSLGRLOSVLTKAEHLSKLPAOTPYSOFAFKQEMGLEKGMGDAGHVLMIHL 253
Db      187 LMDRIOSLGRLOSVLTKAEHLSKLPAOTPYSOFAFKQEMGLEKGMGDAGHVLMIHL 246
Qy      254 LLDITIQAPDPSTLEKLGRIPMIFNVVVSPPHYFQGANVLGLPDSGOIYVILDOVAL 313
Db      247 LLDITIQAPDPSTLEKLGRIPMIFNVVVSPPHYFQGANVLGLPDSGOIYVILDOVAL 306
Qy      314 ENEWVRLKKQGLDVPKILIVTRLIPDAKGTSCNRLERISGTQHTYILRVPPRENGI 373
Db      307 ENEWVRLKKQGLDVPKILIVTRLIPDAKGTSCNRLERISGTQHTYILRVPPRENGI 366
Qy      374 LKKWISRPDWPYLETFADDAAGEIAELQGTPTDFTIGNYSQGNLVAASLSTYKMGITQCN 433
Db      367 LKKWISRPDWPYLETFADDAAGEIAELQGTPTDFTIGNYSQGNLVAASLSTYKMGITQCN 426
Qy      434 IAHAEKTKYPPSDIFPMKNFDEKHYFSCQFTADIAMNNADFLITSTYOEIAGSKXTVQ 493
Db      427 IAHAEKTKYPPSDIFPMKNFDEKHYFSCQFTADIAMNNADFLITSTYOEIAGSKXTVQ 486
Qy      494 YESHTAFTLPGHYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKARLTSHGSIENLIT 553
Db      487 YESHTAFTLPGHYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKARLTSHGSIENLIT 546
Qy      554 DEPQNDERTGHLDDRSKPLIFSMARLDRYKNITGLVEAPAKCAKRELVNLVAVAGYD 613
Db      547 DEPQNDERTGHLDDRSKPLIFSMARLDRYKNITGLVEAPAKCAKRELVNLVAVAGYD 606
Qy      614 NKSXOREETIAETEKHEMLIKTNLFGQFRMISQTNRANGELXYRIADTHGAFVQPALY 673
Db      607 NKSXOREETIAETEKHEMLIKTNLFGQFRMISQTNRANGELXYRIADTHGAFVQPALY 666
Qy      674 EAFGLTVVEAMTCGLPTFATLHGPAEIIEHGVSGFHIDPYHPEQAVNIMADFPDRCOD 733
Db      667 EAFGLTVVEAMTCGLPTFATLHGPAEIIEHGVSGFHIDPYHPEQAVNIMADFPDRCOD 726
Qy      734 PDHVNISGAGIQRIYKTYKTIYSERLMTLAGVYGFMYVSTLERLERYLEMFIYIK 793
Db      727 PDHVNISGAGIQRIYKTYKTIYSERLMTLAGVYGFMYVSTLERLERYLEMFIYIK 786
Qy      794 PRELAKTVPLAIDQPO 809
Db      787 PRELAKTVPLAIDQPO 802

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RESULT 3
US-10-425-114-45934
; Sequence 45934, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Iju, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45934
; LENGTH: 824
; TYPE: PRT

```

ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3051-038-E10_FLI.pep
US-10-425-114-45934

Query Match 80.7%; Score 3427; DB 12; Length 824;
Best Local Similarity 79.3%; Pred. No. 3.7e-307;
Matches 639; Conservative 81; Mismatches 84; Indels 2; Gaps 1;

QY 4 PKLRNANSDRVDLTHARNEVLTSKYNKKGKILQPHHLLDADYQ--SGVRA 61
DB 17 PKLRPSIRDRVDLTHARNEVLTSKYNKKGKILQPHHLLDADYQ--SGVRA 76
QY 62 LAEGFPLVRSAGAEVLPPEVAIAVRPPGVEYRVVWVHLSVQLTVSEYLRKRE 121
DB 77 LKNGPFEIYKSAKEAIVLPPEVAIAVRPPGVEYRVVWVHLSVQLTVSEYLRKRE 136
QY 122 LVDGQNDPYLELDEEPFNVSVPKRSISGNGVQELNRHLSIMFRNDCLEPLDF 181
DB 137 LVDGKINDNFEVLDEEPFNVSVPKRSISGNGVQELNRHLSIMFRNDCLEPLDF 196
QY 182 LRGRHKGHMMNDRIQSLQSLQSVLTKAEHLSKLPATPYSQPAKYQEWLEKMG 241
DB 197 LRGRHKGHMMNDRIQSLQSLQSVLTKAEHLSKLPATPYSQPAKYQEWLEKMG 256
QY 242 DTAGHVLDEYTHLLDILQADPSTLEKELGRIPIFVWVWVPHGYEQANVGLPTGG 301
DB 257 DTERVLEWVHLLDILQADPSTLEKELGRIPIFVWVWVPHGYEQANVGLPTGG 316
QY 302 QIVYIIDQVRLNENYVRLKKGQLDVSPKILVTRLLIPDAKTSNQRLEISGTHTY 361
DB 317 QIVYIIDQVRLNENYVRLKKGQLDVSPKILVTRLLIPDAKTSNQRLEISGTHTY 376
QY 362 ILRPPRNNGILKKMISRPDVPYLETFAEDAAAGTAAELQSPDIIIGNSDGNV 421
DB 377 ILRPPRNNGILKKMISRPDVPYLETFAEDAAAGTAAELQSPDIIIGNSDGNV 436
QY 422 LLSYKMGITOCNIAHALEKTYPSDSIFMKNDEKHYFSCQFTADIAMNNADEIT 481
DB 437 ILAVKNGVQCTIAHALEKTYPSDSIFMKNDEKHYFSCQFTADIAMNNADEIT 496
QY 432 QETAGSKNTYQYQESHAFLLPGLYRVVHGIDVDFEKNIVSPGADMSIYFPT 541
DB 497 QETAGSKNTYQYQESHAFLLPGLYRVVHGIDVDFEKNIVSPGADMSIYFPT 556
QY 542 TSHGSIENLIYBPQNDHEHGHLDKSKPILFSMARLDVKNITGIVYAPAKAKREL 601
DB 557 TSHGSIENLIYBPQNDHEHGHLDKSKPILFSMARLDVKNITGIVYAPAKAKREL 616
QY 602 VNLVAVAGYCVKSKDREIATIEKMGHELIKTANLFGQFRMISAQTNRRANGEL 661
DB 617 VNLVAVAGYCVKSKDREIATIEKMGHELIKTANLFGQFRMISAQTNRRANGEL 676
QY 662 DTGAFVQPALYEAFGLTVEAMTQGLPTFALHGGPAEIIIEHGVSGFHIDPYH 721
DB 677 DTGAFVQPALYEAFGLTVEAMTQGLPTFALHGGPAEIIIEHGVSGFHIDPYH 736
QY 722 LMADEPDRCKQDDBHWNISGAGLQRIYKKTWKIYSERLMTAGYGVFKYISK 781
DB 737 LMADEPDRCKQDDBHWNISGAGLQRIYKKTWKIYSERLMTAGYGVFKYISK 796
QY 782 TRRYLEMFYILKREPLAKTVPLAID 806
DB 797 TRRYLEMFYILKREPLAKTVPLAID 821

RESULT 4
US-10-425-114-49911
Sequence 49911, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Tongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425.114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49911
LENGTH: 651
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700551647_FLI.pep
US-10-425-114-49911

Query Match 80.5%; Score 3420; DB 12; Length 651;
Best Local Similarity 99.4%; Pred. No. 1.1e-306;
Matches 647; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 159 FLNRHLSIMFRNDCLEPLDFLRGRHKGHMMNDRIQSLQSLQSVLTKAEHLSK 218
DB 1 FLNRHLSIMFRNDCLEPLDFLRGRHKGHMMNDRIQSLQSLQSVLTKAEHLSK 60
QY 219 PACTPYSQPAKYQEWLEKMGDTAGHVLMTILLDITQADPSTLEKELGRIPI 278
DB 61 PACTPYSQPAKYQEWLEKMGDTAGHVLMTILLDITQADPSTLEKELGRIPI 120
QY 279 VVWVSPHGYEQANVGLPTGGQIVYIIDQVRLNENYVRLKKGQLDVSPKILV 338
DB 121 VVWVSPHGYEQANVGLPTGGQIVYIIDQVRLNENYVRLKKGQLDVSPKILV 180
QY 339 IPDAKTSNQRLEISGTHTYILRVPPRNNGILKKMISRPDVPYLETFAEDAG 398
DB 181 IPDAKTSNQRLEISGTHTYILRVPPRNNGILKKMISRPDVPYLETFAEDAG 240
QY 399 AAELOQTPDFLIGNSDGNVVASILSYKMGITOCNIAHALEKTYPSDSIFM 458
DB 241 AAELOQTPDFLIGNSDGNVVASILSYKMGITOCNIAHALEKTYPSDSIFM 300
QY 459 FSCQFTADIAMNNADEITSTYQELIAGSKNTYQYQESHAFLLPGLYRVV 518
DB 301 FSCQFTADIAMNNADEITSTYQELIAGSKNTYQYQESHAFLLPGLYRVV 360
QY 519 FNIVSPGADMSIYFPTBEKAKRLTSHGSIENLIYDEQNDHEHGHLDKSK 578
DB 361 FNIVSPGADMSIYFPTBEKAKRLTSHGSIENLIYDEQNDHEHGHLDKSK 420
QY 579 LDRVKNITGLVEAPAKAKRELNVLVVAGYNDVNSKDEEAELEKMGHELI 638
DB 421 LDRVKNITGLVEAPAKAKRELNVLVVAGYNDVNSKDEEAELEKMGHELI 480
QY 639 GQFRMISAQTNRRANGELIYIADTHGAFVQPALYEAFGLTVEAMTQGLPT 698
DB 481 GQFRMISAQTNRRANGELIYIADTHGAFVQPALYEAFGLTVEAMTQGLPT 540
QY 699 ABIIIEHGVSGFHIDPYHFEQANVLMADFPDRCKQDDBHWNISGAGLQ 758
DB 541 ABIIIEHGVSGFHIDPYHFEQANVLMADFPDRCKQDDBHWNISGAGLQ 700
QY 759 BRMLTLAGYGVFKYISKRELTRRYLEMFYILKREPLAKTVPLAID 809
DB 601 BRMLTLAGYGVFKYISKRELTRRYLEMFYILKREPLAKTVPLAID 651

RESULT 5
US-10-424-599-241731
Sequence 241731, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

```

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241731
; LENGTH: 812
; TYPE: PRF
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(812)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1.pep
US-10-424-599-241731

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Query Match      80.2%; Score 3407; DB 12; Length 812;
Best Local Similarity 78.9%; Pred. No. 2,6e-305;
Matches 635; Conservative 81; Mismatches 87; Indels 2; Gaps 1;

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QY 4 PLNNRNASIRDRVEDTLHAHRLNELVALLSKYVKKKGKGIQPHHILALDEVQ--SGVRA 61
DB 5 PKLGRLESTEDKVEDTLSHAHRLNELSLSKRYAQGGIQLPHHILDELDTPEDDQAIYD 64
QY 62 LAEGPELDYLSAQAELVLPFVAIAVRPRPGWERYVNVHLSYEOLTVSEYLFKEE 121
DB 65 LKNGPGEIYVSKAKELIVLPFVAIAVRPRPGWERYVNVHLSYEOLTVSEYLFKEE 124
QY 122 LVDGQNDYVLELDEPPENVSVPRPNRSSIGNQVQFLNRHLSIMFENRDCLEPDLR 181
DB 125 LVDGKXNDYVLELDEPPENVSVPRPNRSSIGNQVQFLNRHLSIMFENRDCLEPDLR 184
QY 182 LSHRRKHGVMNDRLISQISGRLOSULTKAEHLSLADPTYSOAPYKFGWGLKRGK 241
DB 185 LSHRRKHGVMNDRLISQISGRLOSULTKAEHLSLADPTYSOAPYKFGWGLKRGK 244
QY 242 DTAGVLEMIHLDDIIOADPSTLEKFGZRIPIEMFNVVSPHGYFGQANVGLPDTG 301
DB 245 DTRERLEMMHLLDILQAPDPTLEFGZRIPIEMFNVVSPHGYFGQANVGLPDTG 304
QY 302 QIVYILDQYALENEMVLRLKQGLDVSQKILLVTRILIPAKTSCNQLRISGQHTY 361
DB 305 QIVYILDQYALENEMVLRLKQGLDVSQKILLVTRILIPAKTSCNQLRISGQHTY 364
QY 362 ILRVPFRNGLIKKVISREDVWPLYETFAEDAAAGETAAELQGPPIIGNYSDGNLVAS 421
DB 365 ILRVPFRNGLIKKVISREDVWPLYETFAEDAAAGETAAELQGPPIIGNYSDGNLVAS 424
QY 422 LLSYKNGITQCNIAHALLEKTKYPSDILFWNPFDEKHYFSCPTADILAMNADPITSTY 481
DB 425 LLSYKNGITQCNIAHALLEKTKYPSDILFWNPFDEKHYFSCPTADILAMNADPITSTY 484
QY 482 QELASKNVYQYESTAFGLPGLYRVYVAGIDVDFPKFNIVSPGALMSIYFPTETAKRL 541
DB 485 QELASKNVYQYESTAFGLPGLYRVYVAGIDVDFPKFNIVSPGALMSIYFPTETAKRL 544
QY 542 TSHGSIENLIYDPECNDEHIGLDRSKDILFSMARLDVKNITGLVSEFGAKSLREL 601
DB 545 TSHGSIENLIYDPECNDEHIGLDRSKDILFSMARLDVKNITGLVSEFGAKSLREL 604
QY 602 VNLVYVAGYDVVSKDREIAEIERKHELIKTHNTFGQPRMISAQTNRAANGELYEYA 661
DB 605 VNLVYVAGYDVVSKDREIAEIERKHELIKTHNTFGQPRMISAQTNRAANGELYEYA 664
QY 662 DTGGAIVQRLYALAFGLTYVEANTCGPRTATLHGGAAETIEHGVSGFHTDPYHBRAYN 721
DB 665 DTGGAIVQRLYALAFGLTYVEANTCGPRTATLHGGAAETIEHGVSGFHTDPYHBRAYN 724

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QY 722 LMAFEDRCODPDHWNVNSGAGLRIYKTYKRIYSERLMTLAGYVGFKKYVSKLERLE 781
DB 725 LMAFEDRCODPDHWNVNSGAGLRIYKTYKRIYSERLMTLAGYVGFKKYVSKLERLE 784
QY 782 TRRYLEMPYILKRELAKTVPLAID 806
DB 785 TRRYLEMPYILKRELAKTVPLAID 809

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RESULT 6

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US-10-217-939-30
; Sequence 30; Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENDORF, VOLKER
; APPLICANT: HAERTEL, HEIKO A.
; APPLICANT: CIRPUS, PETRA
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS 111
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 797
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-217-939-30

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Query Match      73.7%; Score 3129; DB 14; Length 797;
Best Local Similarity 74.1%; Pred. No. 1.2e-279;
Matches 580; Conservative 102; Mismatches 99; Indels 2; Gaps 2;

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QY 27 LVALLSKYVKKKGKGIQPHHILDA-LDEVQSG-VRLAEGPELDYLSAQAELVLPFV 84
DB 14 LVVIFIRYVAAQGGIISQHOLIDEFLKTYKNDLTEDLNSPRTMKVLQSAERAIVLPFV 73
QY 85 AIAVRPPGWERYVNVHLSYEOLTVSEYLPFKEELVDGQNDYVLELDEPPENVSV 144
DB 74 AIAVRPPGWERYVNVHLSYEOLTVSEYLPFKEELVNGHANGDYVLELDEPPENVSV 133
QY 145 PRPNRSSIGNQVQFLNRHLSIMFENRDCLEPDLRSHRRKHGVMNDRLISQISGR 204
DB 134 PRPNRSSIGNQVQFLNRHLSIMFENRDCLEPDLRSHRRKHGVMNDRLISQISGR 193
QY 205 QSVLYTAEHLSKLPADPTYSQPAKYKFGWGLKRGMDTAGVLEMIHLDDIIOADPS 264
DB 194 QGALAAAEELSLPLATPSEFEFLQGMFGFRGMDTAKVSEWHLLDILQADPS 253
QY 265 TLEKPIGRIMINNVVSPHGYFGQANVGLPDTGGQIYVILDDQYALENEMVLRLKQ 324
DB 254 TLEKPIGRIMINNVVSPHGYFGQANVGLPDTGGQIYVILDDQYALENEMVLRLKQ 313
QY 325 GLDVSQKILLVTRILIPAKTSCNQLRISGQHTYILRVPFRNGLIKKVISREDVW 384
DB 314 GLDVSQKILLVTRILIPAKTSCNQLRISGQHTYILRVPFRNGLIKKVISREDVW 373
QY 385 PYLETFAEDAAAGETAAELQGPPIIGNYSDGNLVASLSYKNGITQCNIAHALLEKTKY 444
DB 374 PYLETFAEDAAAGETAAELQGPPIIGNYSDGNLVASLSYKNGITQCNIAHALLEKTKY 433
QY 445 DSDIFPKNPDKHYFSCPTADILAMNADPITSTYQELASKNVYQYESTAFGLPGL 504
DB 434 DSDIFPKNPDKHYFSCPTADILAMNADPITSTYQELASKNVYQYESTAFGLPGL 493
QY 505 LRVYVAGIDVDFPKFNIVSPGALMSIYFPTETAKRLTSHGSIENLIYDPECNDEHIG 564
DB 494 LRVYVAGIDVDFPKFNIVSPGALMSIYFPTETAKRLTSHGSIENLIYDPECNDEHIG 553
QY 565 LDRSKDILFSMARLDVKNITGLVSEFGAKSLRELVNLVYVAGYDVVSKDREIAEIER 624
DB 553 LDRSKDILFSMARLDVKNITGLVSEFGAKSLRELVNLVYVAGYDVVSKDREIAEIER 624

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Db 554 LSDOSKPIIFESVABLDRVKNLTGLVECVAKNSKLRRLANLVIYGGYIDENOSRDEBMAE 613
 Qy 625 IERKHEIKTNLFGCFRWISAOCTRRANNGELRYIADTHGAFVOPALYEAFGLTVYAM 684
 Db 614 IQKHSLIEQYDLGFERMIAQONRANNGELRYIADTKGVFQPAFYEAFLTVESM 673
 Qy 685 TCGLPFATLHGPAEIIHGVSGFHHIDPYAPBQAVNLMAFDRCKODPHWVNSGAG 744
 Db 574 TCAI2P2ATCGHGPABIIENGVSGFHIDPYAPDQVAATLVSFFETCNTNPNHWKISBG 733
 Qy 745 LORLYEKTYKLYEERLMTLAGVGFMYKYSKLELTETRYLMEFYILKEFLAKTVPLA 804
 Db 734 LKRIYERYTKKYSERLTLTAGVAFWKMVSKLERRETRYLMEFYSLKFERLANSIPLA 793
 Qy 805 IDQ 807
 Db 794 TDE 796

RESULT 7
 US-10-217-939-28
 ; Sequence 28; Application US/10217939
 ; Publication No. US20030154512A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MITTENDORF, VOLKER
 ; APPLICANT: HAERTEL, HEIKO A.
 ; APPLICANT: CIRPUS, PETRA
 ; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
 ; FILE REFERENCE: 16313-0157
 ; CURRENT APPLICATION NUMBER: US/10/217,939
 ; CURRENT FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: 60/311,414
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ. ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ. ID NO 28
 ; LENGTH: 805
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-217-939-28

Query Match 73.2%; Score 3108.5; DB 14; Length 805;
 Best Local Similarity 74.3%; Pred. No. 1e-277;
 Matches 579; Conservative 98; Mismatches 97; Indels 5; Gaps 3;
 Qy 31 LSKYKNGKGIOPHILDA-IDEVQSG-VRALABGPFEDVLRSGOEAIVLPPVALAY 88
 Db 29 LRVYVAGKCLQSHQIIDEFLTKVKGDTLEDLNSPKPKVL--QEAIVLPPVALAI 95
 Qy 89 RRPQVWYVYVNVVHE:SYEQLTVSEYLRFEKEILVDGQNDPVYLELDFEPNVSVPRPN 148
 Db 86 RRPQVYEVYVNVVYELSDVHLTVSEYLRFEKEILVNGHANGDYILBLDFEPNAKTLFRPT 145
 Qy 149 RSSISNGVQFLNRHSSIFNRNDCLEPLIDPLRGHRKHGMVMTNDRIQSLGRLQSVL 208
 Db 146 RSSISNGVQFLNRHSSIFNRNCSMEPLLEFLRKEHEDGRPMNDRIQNPILQGLAL 205
 Qy 209 TKAEHLSKLPATPVSSCFAYKFOEWGELXGNGDTAGVLEMTLHLLDITQADPSTLEK 268
 Db 206 ARKEEELSKLPATPVSEFFELQGMGFERGMDTKQKSEMYHLLDITQADPSTLET 265
 Qy 269 FLGRIMENVVNVVSPHYFGQANVGLPTGGQIVYLIDQVRLAENEMVRLKKQGLADV 328
 Db 266 FLGRIMENVVNVVLSHGFGQANVGLPTGGQIVYLIDQVRLAENEMVRLKQGLLEV 325
 Qy 329 SPKLLIVTRLLIPAKGTSNORLERISGTQHTYILRVPPNENGILKKMISRPDVPYLE 388
 Db 326 IPKLLIVTRLLIPAKGTTQORLERVSGTEHAHLIPIFETKGIIRKMWISRPDVPYLE 385
 Qy 389 TPAEDAGRIALAELOGTPTGFIIGNVSDGNVYASLSYKMGITQCNALHALEKTKYPSDI 448
 Db 386 TPAEDASNELISALQGVNLLIGNVSDGNLVASLSKGLVIOQNTAHLAEKTKYPSDI 445

Qy 449 FMKNDEKHPSCOPTADIIAMNNADFIITSTYOBIASSKONTVGOYESHTAFTLPGLXY 508
 Db 446 YMRHEBDKTHSSQPTADIIAMNNADFIITSTYOBIASSKONTVGOYESHTAFTLPGLXY 505
 Qy 509 VHGIDVDPKXNIVSPGADMSIYPPHTEKARLTSLHSGIENTLYDPEDONDEHIGHLDR 568
 Db 506 VHGIDVDPKXNIVSPGADMTIYPPYSDKERRLTALHSIELLFSADONDEHVGILSQ 565
 Qy 569 SKPLIFSGARLDRKYNITGLVEAFKAKLRLVNLVYVAGYNDVYKSKDREKRIAEYK 628
 Db 566 SKPLIFSGARLDRKYNLTGLVECVAKNSKLRRLANLVIYGGYIDENOSRDEBMAEIQK 625
 Qy 629 HELIKTNLFGCFRWISAOCTRRANNGELRYIADTHGAFVOPALYEAGLTVYEMTGL 688
 Db 626 HSLIEQYDLGFERMIAQONRANNGELRYIADTKGVFQPAFYEAFLTVESMTCAL 685
 Qy 689 PTFATLHGPAEIIHGVSGFHHIDPYAPBQAVNLMAFDRCKODPHWVNSGAGLORI 748
 Db 686 PTFATCGHGPABIIENGVSGFHIDPYAPDQVAATLVSFFETCNTNPNHWKISBGKRI 745
 Qy 749 YERYTKKYSERLTLTAGVAFWKMVSKLERRETRYLMEFYSLKFERLANSIPLATDE 804
 Db 746 YERYTKKYSERLTLTAGVAFWKMVSKLERRETRYLMEFYSLKFERLANSIPLATDE 804

RESULT 8
 US-10-080-114A-5
 ; Sequence 5; Application US/10080114A
 ; Publication No. US20030005482A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dhugaa, Kanwarpal S.
 ; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
 ; TITLE OF INVENTION: to Improve Stalk and Grain Quality
 ; FILE REFERENCE: 1301P
 ; CURRENT APPLICATION NUMBER: US/10/080,114A
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/270,777
 ; NUMBER OF SEQ. ID NOS: 13
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ. ID NO 5
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 US-10-080-114A-5

Query Match 70.9%; Score 3011.5; DB 14; Length 802;
 Best Local Similarity 70.0%; Pred. No. 9.2e-269;
 Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;
 Qy 3 AFLTLNRASIRDVVEDTLAHRNRLVALLSKYVNGKGGIIOPHHILDAIDDEVQSGVRAL 62
 Db 2 AAKLTRLSRERIGATFSSHPNELIALFRYVAGKGM-QRQDLAEFALFSDDEKRY 61
 Qy 63 AEGPFLVLSAEOAIVLPPVALAVRPPGVWYVNVVHLSVEQTVSEYLRFEEL 122
 Db 62 A--PFEDILRAAOEALVLPVVALAIRPBGWMDYIRVNSSELAVEELSEYLAFLQEL 119
 Qy 123 VDGQNDPVYLELDFEPNVSVPRPNSSISNGVQFLNRHLSIFNRNDCLEPLIDFL 182
 Db 120 VDGQNSNPFYLELDFEPFNASFPSPMSKISNGVQFLNRHLSKPLQDKESLPLNPL 179
 Qy 183 RGRHGRHMMNDRIQSLRLOSULTKAEHLSKLPADPIYSGFAKFOEWGELKMGD 242
 Db 180 KAHNVKGTMMNDRIQSLRLOSULTKAEHLSKLPADPIYSGFENRFDGLSKMGD 239
 Qy 243 TAGVLEMTLHLLDITQADPSTLEKFLGRIPMIENVVNVVSPHYFGQANVGLPTGGQ 302
 Db 240 TAKRVLDTLHLLDITQADPSTLEKFLGRIPMIENVVNVVSPHYFGQANVGLPTGGQ 299
 Qy 303 IVTILDOVRLAENEMVRLKKQGLDVSFKLLITVRLIPDAKGSNORLERISGTQHTYI 362
 Db 300 VVYLIDQVRLAENEMELIRIKQGLDITPKLIVTRLLBDAAGTTCGRLEKIVIGTEHTDI 359

QY 363 LRVFENNGLKMWISRDVWPLYETFAEDAGELAELOGTPTTIGNYSDGNVAST 422
 DB 360 IRVFPENNGILAKWISRDVWPLYETFYEDVSSLEKEMQAPDLIGNSGNVAST 419
 QY 423 LSKVGIITQCNIAHALEKTYKPSDIFWKAFDEKHPSCQFTADIIAMNADFIITSTYQ 482
 DB 420 LAHKGVTOCTIAHALEKTYKPSDIFWKAFDEKHPSCQFTADIIAMNADFIITSTYQ 479
 QY 483 ELAGSKNTVGOVESHAFITLPGLYRVHGDVDPKFNIVSPGADMSIYPPHTEKARLT 542
 DB 480 ELAGSKNTVGOVESHAFITLPGLYRVHGDVDPKFNIVSPGADMSIYPPHTEKARLT 539
 QY 543 SLHGSIENTIYDEPCNDDEHIGLDDRSKPTLFSMARLDRKNTGTGVEAFKACAKRELY 602
 DB 540 AFHPELBELIYSVENSEHFVKDKKKPTLFSMARLDRKNTGTGVEAFKACAKRELY 599
 QY 603 NLVAVAGVYVNSKURBEIAIEKHEMLIKTNLFGQPFMISAQTNRAENGELYYRIAD 662
 DB 600 NLVAVAGVYVNSKURBEIAIEKHEMLIKTNLFGQPFMISAQTNRAENGELYYRIAD 658
 QY 663 THGAFVQPALYEFGLITVEAMTCGLPTATLHGSGAEIIEHGVSGHIDPHYEQAVNL 722
 DB 659 THGAFVQPALYEFGLITVEAMTCGLPTATLHGSGAEIIEHGVSGHIDPHYEQAVNL 718
 QY 723 MADFDRCKODPDHWNISGAGLQRIYKTYKWTXLYSERLMTLAGVYGFMYVSKLEPLET 782
 DB 719 LVNFPKCKADPEYWBISGGGLQRIYKTYKWTXLYSERLMTLAGVYGFMYVSKLEPLET 778
 QY 783 RRYLEMFYILKREELAKTVPLAID 806
 DB 779 RRYLEMFYILKREELAKTVPLAID 802

RESULT 9
 US-10-425-114-57840
 ; Sequence 57840, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 57840
 ; LENGTH: 807
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73215F06_FLI.pep
 US-10-425-114-57840

Query Match 70.9%; Score 3011.5; DB 12; Length 807;
 Best Local Similarity 70.0%; Pted. No. 9,3e-269;
 Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;
 QY 3 APGLNNASIRPDEVETTLHNRNELVALSKYVKNKGKGIOPHILIDALDEVGSGVRL 62
 DB 7 AKUTLHSHREKLTSPSHREKLTALSKRYHOGKMLQKQILAFPALDSDOKEX 66
 QY 63 AEGPFLDLVRSAGEALVDPFVAIAVRPQVMEYVAVVHLSVQLTVSEYLAKEEL 122
 DB 67 A--PFEDILRAAGEALVLPFVAIAVRPQVMDYIRVAVVSELAVELSVSEYLAKEEL 124
 QY 123 VVGQNDPVYVLEDFEPNVSVPRRSSSIGNGVFLNRHSSIMFRNDCLEPLLDPL 182
 DB 122 VVGQNDPVYVLEDFEPNVSVPRRSSSIGNGVFLNRHSSIMFRNDCLEPLLDPL 182

DB 125 VVGQNSNFVLBIDFEFNASFPSPMSKISGNGVFLNRHSSKLFQDKESLYPLNPL 184
 QY 183 RGRHRKWMANDRQSILQSVLTAKBEHLSKLPADTPYQPAFKPQWGLKXGMD 242
 DB 185 KAHNYGTTMNDRLQSLRGLQSLRKAEBYLSPODTPYSEFNRPAIAGLEKMGD 244
 QY 243 TGHVLEMIHLDDIIOADDPSTLEKFLGRIPIFNVVAVSPHGYFQGANVAGLPTDQGO 302
 DB 245 TARKVLDLHLLDLEADDPANLEKFLGRIPIFNVVAVSPHGYFQGANVAGLPTDQGO 304
 QY 303 IYVILDQVPALENEMVRLKKGGLDVSFKLIVTRILPDAGKTSQNRERISGTHYI 362
 DB 305 VVYILDQVPALENEMVRLKKGGLDVSFKLIVTRILPDAGKTSQNRERISGTHYI 364
 QY 363 LRVFENNGLKMWISRDVWPLYETFAEDAGELAELOGTPTTIGNYSDGNVAST 422
 DB 365 IRVFPENNGILAKWISRDVWPLYETFYEDVSSLEKEMQAPDLIGNSGNVAST 424
 QY 423 LSKVGIITQCNIAHALEKTYKPSDIFWKAFDEKHPSCQFTADIIAMNADFIITSTYQ 482
 DB 425 LAHKGVTOCTIAHALEKTYKPSDIFWKAFDEKHPSCQFTADIIAMNADFIITSTYQ 484
 QY 483 ELAGSKNTVGOVESHAFITLPGLYRVHGDVDPKFNIVSPGADMSIYPPHTEKARLT 542
 DB 485 ELAGSKNTVGOVESHAFITLPGLYRVHGDVDPKFNIVSPGADMSIYPPHTEKARLT 544
 QY 543 SLHGSIENTIYDEPCNDDEHIGLDDRSKPTLFSMARLDRKNTGTGVEAFKACAKRELY 602
 DB 545 AFHPELBELIYSVENSEHFVKDKKKPTLFSMARLDRKNTGTGVEAFKACAKRELY 604
 QY 603 NLVAVAGVYVNSKURBEIAIEKHEMLIKTNLFGQPFMISAQTNRAENGELYYRIAD 662
 DB 605 NLVAVAGVYVNSKURBEIAIEKHEMLIKTNLFGQPFMISAQTNRAENGELYYRIAD 663
 QY 663 THGAFVQPALYEFGLITVEAMTCGLPTATLHGSGAEIIEHGVSGHIDPHYEQAVNL 722
 DB 664 THGAFVQPALYEFGLITVEAMTCGLPTATLHGSGAEIIEHGVSGHIDPHYEQAVNL 723
 QY 723 MADFDRCKODPDHWNISGAGLQRIYKTYKWTXLYSERLMTLAGVYGFMYVSKLEPLET 782
 DB 724 LVNFPKCKADPEYWBISGGGLQRIYKTYKWTXLYSERLMTLAGVYGFMYVSKLEPLET 783
 QY 783 RRYLEMFYILKREELAKTVPLAID 806
 DB 784 RRYLEMFYILKREELAKTVPLAID 807

RESULT 10
 US-10-425-114-53965
 ; Sequence 53965, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 53965
 ; LENGTH: 811
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLM017136B11_FLI.pep
 US-10-425-114-53965

Query Match 70.9%; Score 3011.5; DB 12; Length 811;

Best Local Similarity 70.0%; Pred. No. 9.4e-269;
Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;

```

QY 3 APLINRNASIRSDVEDTLHAHRELVALLSKYVKKGGIIQPHHLLADLDEVOGSSGRAL 62
DB 11 AALULTRHSTRERLGAIFSSHPELILFSTRYVQSGKMLQRIQLAEFLAEDSDCKEY 70
QY AEGPFLDVLRSQAQEAIVLPFVAIAVRPRGWYEVVNVHLSVEQLTVSEYLRFKEEL 122
DB 71 A--PFEDILRAAOEAIVLPFVAIAVRPRGWYDVRVNVSELAVELSSEILAFKEQL 128
QY 123 VDSQNDPVLLELDEPPFNVSVPKRRSSISGVQFLNRHLSIMFRNDCLEPLIDFL 182
DB 129 VDSQNSNMFLELDEPPFNVSVPKRRSSISGVQFLNRHLSIMFRNDCLEPLIDFL 188
QY 183 RGRHKGWVMMNDRIQSLGRLOSILTKAEHLSKLPADTPYSQFAKFOEMGLEKMGD 242
DB 189 KANVYGTMMNDRIQSLGRLOSILTKAEHLSKLPADTPYSQFAKFOEMGLEKMGD 248
QY 243 TAGHVLMTLHLLDIIQAPDPSTLEKFLGRIPMIFNVVVVSPHGFQANVGLPDTGG 302
DB 249 TAKRVLDLHLLDLEAPDPANLEKFLGRTYGFNVVILSPHGFQANVGLPDTGG 308
QY 303 IYVILIDVPALNEMVTLKKGQDVSPEKILVTRILIPAKGTSCNQLRISGTQHTYI 362
DB 309 VYVILIDVPALNEMVTLKKGQDVSPEKILVTRILIPAKGTSCNQLRISGTQHTYI 368
QY 363 LKVPFENNGILKKMISRFDPVPLETFPADAAGELIAELQSTPDTLIGNSQGNVLS 422
DB 369 IAVPFRNENGILKKMISRFDPVPLETFPADAAGELIAELQSTPDTLIGNSQGNVLS 428
QY 423 LSYKMGITQCNIAHALKTKYPSDIFMKNFDEKHFSCQFTADILAMNADPILITSTY 482
DB 429 LAHKLGVTGCTIAHALKTKYPSDIFMKNFDEKHFSCQFTADILAMNADPILITSTY 488
QY 483 ELAAGSNVTVGQYESHTAFPLPGYRVVAGIDVDPKENVISPGADMSIYFPHTEKAKLT 542
DB 489 ELAAGSNVTVGQYESHTAFPLPGYRVVAGIDVDPKENVISPGADMSIYFPHTEKAKLT 548
QY 543 SLHGSIENTIYDPEONDEHIGHLDRSKPILSMAILDVKNITGIVLVEAFKAKARELV 602
DB 549 AHPREIELIYDPEONDEHIGHLDRSKPILSMAILDVKNITGIVLVEAFKAKARELV 608
QY 603 NLVVAYGVNDVYKSKOREELIAELKEMHILKTNHFGQFRMISAQNRARNGELIYVIA 662
DB 609 NLVIYAG--DHGKSKOREELIAELKEMHILKTNHFGQFRMISAQNRARNGELIYVIA 667
QY 663 THGATVQPALYFAFGITVVEAMTCGLPTFATLHGGPAITIEHGVSGFHIDPHPEQAVNL 722
DB 669 THGATVQPALYFAFGITVVEAMTCGLPTFATLHGGPAITIEHGVSGFHIDPHPEQAVNL 727
QY 723 MADPFRCKODPDHWNISGAGLQRIYKTYTWKISERIMTLAGVYGFMYSKLERLE 782
DB 728 LVNPFDKCADPSYMDKISQSGGLQRIYKTYTWKISERIMTLAGVYGFMYSKLERLE 787
QY 783 RRYLEMFYILKFRILAKTVPLAID 806
DB 788 RRYLEMFYILKFRILAKTVPLAID 811

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RESULT 11

US-10-425-114-53296

; Sequence 53296, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingsong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 53296

LENGTH: 823

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700451030_FLI pep

US-10-425-114-53296

Query Match

Best Local Similarity 70.7%; Score 3001; DB 12; Length 823;

Matches 563; Conservative 106; Mismatches 128; Indels 3; Gaps 3;

```

QY 6 LBNASIRSDVEDTLHAHRELVALLSKYVKKGGIIQPHHLLADLDEVOGSSGRAL 61
DB 17 LSRHLSVREIRIGSLSHHPELVAVFTRKLGKGMQRIQLAEVNNALPEAR---EK 73
QY 62 LAEGPFLDVLRSQAQEAIVLPFVAIAVRPRGWYEVVNVHLSVEQLTVSEYLRFKEE 121
DB 74 LKDAFEDVLRAAOEAIVLPFVAIAVRPRGWYEVVNVSELAVELSSEILAFKEEQ 133
QY 122 VDSQNDPVLLELDEPPFNVSVPKRRSSISGVQFLNRHLSIMFRNDCLEPLIDFL 181
DB 134 VDSQNSNMFLELDEPPFNVSVPKRRSSISGVQFLNRHLSIMFRNDCLEPLIDFL 193
QY 182 RGRHKGWVMMNDRIQSLGRLOSILTKAEHLSKLPADTPYSQFAKFOEMGLEKMGD 241
DB 189 KANVYGTMMNDRIQSLGRLOSILTKAEHLSKLPADTPYSQFAKFOEMGLEKMGD 253
QY 242 TAGHVLMTLHLLDIIQAPDPSTLEKFLGRIPMIFNVVVVSPHGFQANVGLPDTGG 301
DB 249 TAKRVLDLHLLDLEAPDPANLEKFLGRTYGFNVVILSPHGFQANVGLPDTGG 313
QY 303 IYVILIDVPALNEMVTLKKGQDVSPEKILVTRILIPAKGTSCNQLRISGTQHTYI 361
DB 309 VYVILIDVPALNEMVTLKKGQDVSPEKILVTRILIPAKGTSCNQLRISGTQHTYI 373
QY 363 LKVPFENNGILKKMISRFDPVPLETFPADAAGELIAELQSTPDTLIGNSQGNVLS 421
DB 369 IAVPFRNENGILKKMISRFDPVPLETFPADAAGELIAELQSTPDTLIGNSQGNVLS 433
QY 423 LSYKMGITQCNIAHALKTKYPSDIFMKNFDEKHFSCQFTADILAMNADPILITSTY 481
DB 429 LAHKLGVTGCTIAHALKTKYPSDIFMKNFDEKHFSCQFTADILAMNADPILITSTY 493
QY 483 ELAAGSNVTVGQYESHTAFPLPGYRVVAGIDVDPKENVISPGADMSIYFPHTEKAKLT 541
DB 489 ELAAGSNVTVGQYESHTAFPLPGYRVVAGIDVDPKENVISPGADMSIYFPHTEKAKLT 553
QY 543 SLHGSIENTIYDPEONDEHIGHLDRSKPILSMAILDVKNITGIVLVEAFKAKARELV 601
DB 549 AHPREIELIYDPEONDEHIGHLDRSKPILSMAILDVKNITGIVLVEAFKAKARELV 613
QY 603 NLVVAYGVNDVYKSKOREELIAELKEMHILKTNHFGQFRMISAQNRARNGELIYVIA 661
DB 609 NLVIYAG--DHGKSKOREELIAELKEMHILKTNHFGQFRMISAQNRARNGELIYVIA 672
QY 663 THGATVQPALYFAFGITVVEAMTCGLPTFATLHGGPAITIEHGVSGFHIDPHPEQAVNL 721
DB 669 THGATVQPALYFAFGITVVEAMTCGLPTFATLHGGPAITIEHGVSGFHIDPHPEQAVNL 732
QY 723 MADPFRCKODPDHWNISGAGLQRIYKTYTWKISERIMTLAGVYGFMYSKLERLE 781
DB 728 LVNPFDKCADPSYMDKISQSGGLQRIYKTYTWKISERIMTLAGVYGFMYSKLERLE 792
QY 783 RRYLEMFYILKFRILAKTVPLAID 806
DB 788 RRYLEMFYILKFRILAKTVPLAID 817

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QY 482 QETASGKNTVYQYQESHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYPPHTKAKRL 541
DQ 494 QETASGKNTVYQYQESHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYPPHTKAKRL 553
QY 542 TSHGSIENLIYDEQNDENHIGLIDRSKPTLSMARLDVKNITGLVEAFKCAKREL 601
DQ 554 TSHGSIENLIYDEQNDENHIGLIDRSKPTLSMARLDVKNITGLVEAFKCAKREL 613
QY 602 VNLVAVGYNDVNSKQREELAEIEMHKLITNLSGQFPMISACTRANRANGELRYIA 661
DQ 614 VNLVAVGYNDVNSKQREELAEIEMHKLITNLSGQFPMISACTRANRANGELRYIA 672
QY 662 DTHGAFVQPAFYEFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGPHIDPYHBOAVN 721
DQ 673 DTHGAFVQPAFYEFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGPHIDPYHBOAVN 732
QY 722 LMADFPKCKODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERLE 781
DQ 733 LMADFPKCKODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERLE 792
QY 782 TRRYLEMFYILKRELAKTVPPLAD 806
DQ 793 TRRYLEMFYILKRELAKTVPPLAD 817

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RESULT 14
US-10-425-114-72813
Sequence 72813, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 2003-04-28
SEQUENCE ID NO: 72813
LENGTH: 823
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4172-051-C3_Flt.pep
US-10-425-114-72813

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Query Match 70.7%; Score 3001; DB 12; Length 823;
Best Local Similarity 69.9%; Pred. No. 9e-268;
Matches 563; Conservative 106; Mismatches 128; Indels 8; Gaps 3;

QY 6 INNASIRDRVEDTLAHNRNELVALSKYVNGKGIOPHIL---DALDEWQSGSVRA 61
DQ 17 LSLHLSVREIRIGSLSHRPHLVAVTRRLKULSKMIOPIQIILAEYNNALPEAR--EK 73
QY 62 LAGPFLDLVRSAGEAIVLPFVAIAVRPPGVMEYVNVVHLSVQLTVSEYLRKEE 121
DQ 74 LKDGAFEDVLRAGEAIVLPFVAIAVRPPGVMEYVNVVHLSVQLTVSEYLRKEE 133
QY 122 LVNCGNDPVTVELDEPPRVSVPRPKRSSISNGVQFLMRHSSIMFRKDCLEPLDR 181
DQ 134 LVEEGPNNVVELDEPPRVSVPRPKRSSISNGVQFLMRHSSIMFRKDCLEPLDR 193
QY 182 LKGRHKGVMNDRIOSLRQSVYTKAEHLSKLPATTPYQAPYKFOEWGLKGMG 241
DQ 194 LKGRHKGVMNDRIOSLRQSVYTKAEHLSKLPATTPYQAPYKFOEWGLKGMG 253
QY 242 DTAGHVLMIHLLDITCADPSTLEKFLGRIPMIVNVVSVHGVFGQANVLGLDPTGG 301

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DQ 254 DCARAOETIHLILLDLEAPDPSTLEKFLGTIPMFVNVVILSPHGYFAQANVLAGYDPTGG 313
QY 302 QIVVITLOVRLEEMETRLKXOGLDVSPKLIITRLIPDAKSGCNRLEISTORTY 361
DQ 314 QIVVITLOVRLEEMETRLKXOGLDVSPKLIITRLIPDAKSGCNRLEISTORTY 373
QY 362 ILRVPFNRNGIILKMWISRPVWPYLETFAADAGEIAAEIQTGDFITIGNSDDNLVAS 421
DQ 374 ILRVPFNRNGIILKMWISRPVWPYLETFAADAGEIAAEIQTGDFITIGNSDDNLVAS 433
QY 422 LLSYMGITQCNIAHAEKTYRPSDIFWKNFDEKHYSCOPTADIIMANNADFITITSY 481
DQ 434 LLAHKGVTCTIAHAEKTYRPSDILYKKFBDHYHSCOPTADILMANNADFITITSY 493
QY 482 QETASGKNTVYQYQESHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYPPHTKAKRL 541
DQ 494 QETASGKNTVYQYQESHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYPPHTKAKRL 553
QY 542 TSHGSIENLIYDEQNDENHIGLIDRSKPTLSMARLDVKNITGLVEAFKCAKREL 601
DQ 554 TSHGSIENLIYDEQNDENHIGLIDRSKPTLSMARLDVKNITGLVEAFKCAKREL 613
QY 602 VNLVAVGYNDVNSKQREELAEIEMHKLITNLSGQFPMISACTRANRANGELRYIA 661
DQ 614 VNLVAVGYNDVNSKQREELAEIEMHKLITNLSGQFPMISACTRANRANGELRYIA 672
QY 662 DTHGAFVQPAFYEFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGPHIDPYHBOAVN 721
DQ 673 DTHGAFVQPAFYEFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGPHIDPYHBOAVN 732
QY 722 LMADFPKCKODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERLE 781
DQ 733 LMADFPKCKODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERLE 792
QY 782 TRRYLEMFYILKRELAKTVPPLAD 806
DQ 793 TRRYLEMFYILKRELAKTVPPLAD 817

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RESULT 15
US-10-424-599-258404
Sequence 258404, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 2003-04-28
SEQUENCE ID NO: 258404
LENGTH: 805
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MR13847_75363C.1.pep
US-10-424-599-258404

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Query Match 70.6%; Score 2999.5; DB 12; Length 805;
Best Local Similarity 69.5%; Pred. No. 1.12e-267;
Matches 560; Conservative 115; Mismatches 130; Indels 1; Gaps 1;

QY 1 MSAPKLRNASIRDRVEDTLAHNRNELVALSKYVNGKGIOPHILDALDEWQSGSVR 60
DQ 1 MATDRLRVRSIRDRVEDTLAHNRNELVALSKYVNGKGIOPHILDALDEWQSGSVR 60
QY 61 ALAEGPFLDLVRSAGEAIVLPFVAIAVRPPGVMEYVNVVHLSVQLTVSEYLRKEE 120
DQ 61 KLTGSAFGEVLRAGEAIVLPFVAIAVRPPGVMEYVNVVHLSVQLTVSEYLRKEE 120

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QY 121 EIVDGOHNDYVLELDEFPFNVSVPBPNSST:GNGVOFLNRHLSIFRNDCLEPLD 180
DB 121 EIVDSSNGNFTLELDEFPFNNA:FPPTANKS:IGNVOFLNRHLSAKL:PHDKS:HPLE 180
QY 181 FURGRHAKGHVMMLANDRISLQSLVLYKAEBHLSKLPADTPYSQFAYKFOEMGLEKGM 240
DB 181 FURHSHVKGKTMNDRIQNPDALQHVLRKABEYLGTVPETPYSSEHKFOEIGLERGM 240
QY 241 SDTAGHVEMLHLLDIIQAPDPSTIEKLGRI:PMI:FNVYVVS:PHGYEQANYLG:PDPTG 300
DB 241 GNAERVESIQLL:DLLEAPDECTLETLGRI:PMVFNVVIIS:PHGYFAQDNYLG:PDPTG 300
QY 301 GOIVYLLDQVRALENEXYLRLKKGGLDVSPKIL:IVTRL:IPDAKGS:CNQSLERISGTCAT 360
DB 301 GOVYVLLDQVRALENEXYLRLKKGGLDVSPKIL:IVTRL:IPDAVGTTCQRLKGVSTERS 360
QY 361 YLRVFPFNENGILKKMISRPDVPYLETFAADAGE:AAELQGTPTDPIIGYSDGNLYA 420
DB 361 HILRVFPRIEKGIVKMKISRFVWPYLETETEDVAHELAKELQKPDILVGNVSDGNLYA 420
QY 421 SFLSYMGITOCNIAHLEKTYPPSDIFPKNFDEKXHSQCFADITAMNADPIITST 480
DB 421 SLAHKLGVTCTIAHLEKTYPPSDIYWKLEBRYHFSQCFADIFAMNHTDPIITST 480
QY 481 YOEIAGSXNTVGOYESHTAFTL:PGHYRVVHGIDVFDPKENIYSPGADWSIYEPHTEKAKR 540
DB 481 FOEIGSKDVTGQYESHTAFTL:PGHYRVVHGIDVFDPKENIYSPGADQTIYEFHETSRR 540
QY 541 LTSHGSIENLIYDEQONDER:IGHLDNRSKPILFPMARLDRVKNITGLVEASAKCAKLE 600
DB 541 LTSFHPRIEELIYSSVENNEH:CYLXDRSKPIIFTMARLDRVKNITGLVEWYGNKAKLE 600
QY 601 LYNLVVAGYNVNKSDREELAELEKMEELIKTNLFGQFHWISAQTRANGELXRYI 660
DB 601 LYNLVVWVAG-DRRKSKDLBEKAEKMKMGIL:ETYLKNGQFRWISSQMNVRNNGELXRYI 659
QY 661 ADTHGAFYQPALYEAFGITVEAMTCGLPTFAITHGSEALIEHGVSGFHIDPYHPEQAV 720
DB 660 CDTREAFYQPAVEAFGLITVEAMTCGLPTFAICNGSPALIEVHGKSGFHIDPYHGDRA 719
QY 721 NIMADFPDRCODPDHWNISAGLQRIYEXYTKIYSERLMTLAGVYGFWRYSKLEBL 780
DB 720 DLVYDFPEKCKLDPHMDKISKAGLQRIEEXYTKQIYSQRLTLTGAVYGFWRHVSNDRR 779
QY 781 FTRRYLEMFTYIKREELAKTVPLAD 806
DB 780 ESRRYLEMFTYAKYKRLAESVPLAE 805

Search completed: May 24, 2004, 11:38:09
Job time : 44.6803 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:35:47 ; Search time 7009.39 Seconds

(without alignments)
16924.423 Million cell updates/sec

Title: US-10-080-114A-1

Perfect score: 2737

Sequence: 1 gtcgaccacgcgtccgagc.....aaaaaaaaagggcgccgc 2737

Scoring table: **ORIGO_NUC**

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size: 50

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

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1:  gb_da:*
2:  gb_hg:*
3:  gb_in:*
4:  gb_lm:*
5:  gb_lm:*
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41: gb_lm:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2710	99.0	2710	AY059416	AY059416 Zea mays
2	2138	78.1	2837	AY124703	AY124703 Zea mays
3	192	7.0	297	AX756452	AX756452 Sequence
4	191	7.0	258	AX756409	AX756409 Sequence
5	122	4.5	265	AR246503	AR246503 Sequence
6	103	3.8	221	BV079817	BV079817 sc1180_P3
7	103	3.8	225	BV079815	BV079815 sc1180_P3
8	103	3.8	234	BV079813	BV079813 sc1180_P3
9	103	3.8	239	BV079812	BV079812 sc1180_P3
10	103	3.8	239	BV079814	BV079814 sc1180_P3
11	103	3.8	239	BV079819	BV079819 sc1180_P3
12	72	2.6	240	BV079818	BV079818 sc1180_P3
13	69	2.5	234	BV079820	BV079820 sc1180_P3
14	69	2.5	246	BV079821	BV079821 sc1180_P3

ALIGNMENTS

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RESULT 1
AY059416
LOCUS       AY059416                2710 bp    mRNA    linear    PLN 07-NOV-2001
DEFINITION  Zea mays sucrose synthase mRNA, partial cds.
ACCESSION   AY059416
VERSION     AY059416.1
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE   1 (bases 1 to 2710)
  AUTHORS   Carlson,S.J., Chourey,P.S., Helentjaris,T. and Datta,R.
  TITLE     Gene expression studies on developing kernels of maize sucrose
  JOURNAL   Plant Mol. Biol. (2001) In press
  PUBLISHED 2 (bases 1 to 2710)
  AUTHORS   Helentjaris,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-2001) Agronomic Traits/T&T, Pioneer Hi-Bred,
  PUBLISHED 7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA
  FEATURES  Location/Qualifiers
            1..2710
               /organism="Zea mays"
               /mol_type="mRNA"
               /db_xref="taxon:4577"
               /chromosome="1"
               /map="bin .04, between IG15100 and JC208"
               /tissue_type="worm-infested roots, vs"
               /note="fibred B73"
            <1..2393
               /codon_start=3
               /product="sucrose synthase"
               /protein_id="AAL27096.1"
               /db_xref="GI:16797785"
               /translation="DRVDFTHAHNRNELLVALLSKYVKKGGKILGPHHILDLBVOGS
               GGRALAGPFLDIKRSQENIYLPFAIYVPRPGWYRYRVVHLSYQLVSEY
               LRFRELVQDQNDPVYELDFEPNVSVPPNKSSTIGKGVQFLNHLSTIFRNRD
               CLPPLDLFLGHRHKGVMMLNDRIQSLGSLQSVLYTAERHLSLPADVPVSPAYNK
               QEWGLKSGMDTAGHVEMLHLADIIQADPSTLEKFLIPMIFVWVVSPPKYGK
               QANVLEGLPRTGGQIVYLIDOVRALENMVLRLKQGLDVSPEKILIVRLIPDAKTSK
               NORLERSGQHTYILRVPRNENGILKXWISPRDVPYLETFAEDAGETAAELQGT
               PDRILGNSDGNVVASLSYKMGITQCNIAHAEKTKYPPSDIFMKRPDKYHSCQF
               TADILANRNDPITITSTYORFASKNTVGGFESHATFLRLRVAGIVDFPKENI
               VSPGADWSITFPTERAKRLTSLHGSLENIIDPEONDERIHGLDRSKPLFSMARL

```

CDS

ORIGIN

DRVNITGLVEAFKACAKLRELVNLYVAVGVNDVNSKDRBE:ABIEKHEB:IKTHNL
FOFBNITNOTRANRSELYRYIADPHGA.FVQ.PALYEAAGLTVMEKGL:PEPFAITH
GGPAE:IEB:GVGFHID:YHP:EPDAVXIMAD:PFDRCKOD:PDHVN:ISGAGL:QET:YKTY
KATYSEIRMTLAVGVFMYKVS:KLEIRLETRYEMFY:ILKRELA:TVPLA:IDPQ*

Query Match 99.0%; Score 2710; DB 8; Length 2710;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GCGACCGCTGAGAGACCCCTTCCAGCCGACCCGCAAGAGCTGTGGCCCTCTGTGCA 77
DB 1 GCGACCGCTGAGAGACCCCTTCCAGCCGACCCGCAAGAGCTGTGGCCCTCTGTGCA 60

QY 78 AGTACGTGAACAAGGGGAAAGGGGATCTCTGAGCCGCAACAATCTCTGAGCCGCTGAG 137
DB 61 AGTACGTGAACAAGGGGAAAGGGGATCTCTGAGCCGCAACAATCTCTGAGCCGCTGAG 120

QY 138 AGGTCCAGGGCTCCGGGGGCGCGGCTAGCCGAGGGAGCCCTTCTCTGAGCTCTGAGCT 197
DB 121 AGGTCCAGGGCTCCGGGGGCGCGGCTAGCCGAGGGAGCCCTTCTCTGAGCTCTGAGCT 180

QY 198 CCGCGAGAGAGCGATCGTCTGCGCCGCTTCTGTGCAATCGCGATGCGCCGCGCCG 257
DB 181 CCGCGAGAGAGCGATCGTCTGCGCCGCTTCTGTGCAATCGCGATGCGCCGCGCCG 240

QY 258 GAGTTGGGAGTACGTCGCGCGTCAAGTTTCAAGAGCTGAGCTGAGAGAGCTCAAGTCT 317
DB 241 GAGTTGGGAGTACGTCGCGCGTCAAGTTTCAAGAGCTGAGCTGAGAGAGCTCAAGTCT 300

QY 318 CGGAGTACCTCGCTTCAAGGAGAGCTGTGAGCCGAGCCAGACAAATGATCTCTAGCTTC 377
DB 301 CGGAGTACCTCGCTTCAAGGAGAGCTGTGAGCCGAGCCAGACAAATGATCTCTAGCTTC 360

QY 378 TCGAGCTTACCTTGAAGCCGTTCAATGTCTCACTCCAGCCGCAATCGCTCATCTTA 437
DB 361 TCGAGCTTACCTTGAAGCCGTTCAATGTCTCACTCCAGCCGCAATCGCTCATCTTA 420

QY 438 TGGGAAACGGTGGGAGTTCTTCAACGCACTTGTCTTCAATGATCTTCCGAAAGAG 497
DB 421 TGGGAAACGGTGGGAGTTCTTCAACGCACTTGTCTTCAATGATCTTCCGAAAGAG 480

QY 498 ATTGCTGAGAGCCCTGTGGAATTTCTCGTGGGCAACCGGCAAGGGCATGTTATGA 557
DB 481 ATTGCTGAGAGCCCTGTGGAATTTCTCGTGGGCAACCGGCAAGGGCATGTTATGA 540

QY 558 TCGTTATGATGATACAAAGCTTGGGAGCTTCACTGTGTGTGCAACCAAGCTGAG 617
DB 541 TCGTTATGATGATACAAAGCTTGGGAGCTTCACTGTGTGTGCAACCAAGCTGAG 600

QY 618 AGCACTGTCAAGAGCCCTGTGAGCAACCATACCTCAATCTTGTATTAATTTCAAG 677
DB 601 AGCACTGTCAAGAGCCCTGTGAGCAACCATACCTCAATCTTGTATTAATTTCAAG 660

QY 678 AGTGGGAGCTGAGAAAGTTGGGGTGAACAAGAGAGATGTTTGAAGATGATCATC 737
DB 661 AGTGGGAGCTGAGAAAGTTGGGGTGAACAAGAGAGATGTTTGAAGATGATCATC 720

QY 738 TCTCTTGAACATCAATTCAGGCGCAGAGCCCACTTACCTTGAAGAAATTTGGGAGGA 797
DB 721 TCTCTTGAACATCAATTCAGGCGCAGAGCCCACTTACCTTGAAGAAATTTGGGAGGA 780

QY 798 TCCCACTGATTTTAAAGTTGTGTGTATCCCTCACTGATGATCTTGTGCAAGCTPATG 857
DB 781 TCCCACTGATTTTAAAGTTGTGTGTATCCCTCACTGATGATCTTGTGCAAGCTPATG 840

QY 858 TATTAGGCTTGCAGACACAGAGAGACAGATGCTATATATATGACCAAGTCCGTGAC 917
DB 841 TATTAGGCTTGCAGACACAGAGAGACAGATGCTATATATGACCAAGTCCGTGAC 900

QY 918 TAGAAATGATGATGCTTCTGCTTTAAAGAAACAGGGCTGATGTTTCCCAAGATTC 977
DB 901 TAGAAATGATGATGCTTCTGCTTTAAAGAAACAGGGCTGATGTTTCCCAAGATTC 960

QY 978 TCATTGTTACTGGCTGATACAGATGCAAGAAAGAACATCATGATCAAGGGCTTGAGA 1037
DB 961 TCATTGTTACTGGCTGATACAGATGCAAGAAAGAACATCATGATCAAGGGCTTGAGA 1020

QY 1038 GAATTAGTGAACACAGCATACTTACATATTAAGAGTCTCTTCAAGAAATGAATGGGA 1097
DB 1021 GAATTAGTGAACACAGCATACTTACATATTAAGAGTCTCTTCAAGAAATGAATGGGA 1080

QY 1098 TACTTAAGAAATGATATACAGATTTGATGTGTGGCAATCTGGAACATTTGCTGAG 1157
DB 1081 TACTTAAGAAATGATATACAGATTTGATGTGTGGCAATCTGGAACATTTGCTGAG 1140

QY 1158 ATGCTGTGTGAATTTGCTGTGATTTCAAGGTACTCAGACTCATATATGGAATCT 1217
DB 1141 ATGCTGTGTGAATTTGCTGTGATTTCAAGGTACTCAGACTCATATATGGAATCT 1200

QY 1218 ACAGTATGAAATCTTGTGGCGTCAATGCTATCTTAACAAGATGGAAATTAACAGTGA 1277
DB 1201 ACAGTATGAAATCTTGTGGCGTCAATGCTATCTTAACAAGATGGAAATTAACAGTGA 1260

QY 1278 ACATTGCTATGCTCTGGAAGAGCTTACATGATTCAGATTCAGACATATTTGGAAGAT 1337
DB 1261 ACATTGCTATGCTCTGGAAGAGCTTACATGATTCAGATTCAGACATATTTGGAAGAT 1320

QY 1338 TCGATGAGAGTACATTTCTCTGCGCATGCTAGTATATATTTGCTATGAAACATG 1397
DB 1321 TCGATGAGAGTACATTTCTCTGCGCATGCTAGTATATATTTGCTATGAAACATG 1380

QY 1398 CTGATTTTATCATCACAGACATATACAAAGAAATTCCTGGAAGCAAAATACTGTTGAC 1457
DB 1381 CTGATTTTATCATCACAGACATATACAAAGAAATTCCTGGAAGCAAAATACTGTTGAC 1440

QY 1458 AGTATGAGAGTATATCTGCTTTACTCTGCTGTGTCTGTAACGAGTGTGCAATGGATCG 1517
DB 1441 AGTATGAGAGTATATCTGCTTTACTCTGCTGTGTCTGTAACGAGTGTGCAATGGATCG 1500

QY 1518 ATGTCTGATTCGAAGTTCAATATATATGTCTCTCTGAGCGTGAATGCAATATCTTC 1577
DB 1501 ATGTCTGATTCGAAGTTCAATATATATGTCTCTCTGAGCGTGAATGCAATATCTTC 1560

QY 1578 CACATACGAGAGAGCCGCAAGCCGACTCACTCTTCAATGTTCAATGAAATTTGATTT 1637
DB 1561 CACATACGAGAGAGCCGCAAGCCGACTCACTCTTCAATGTTCAATGAAATTTGATTT 1620

QY 1638 ATGACCCGAGCAAAAAGATGAACAATGGGATCTGATGTAACGGATCAAGCCATCC 1697
DB 1621 ATGACCCGAGCAAAAAGATGAACAATGGGATCTGATGTAACGGATCAAGCCATCC 1680

QY 1698 TCTTCTCAATGGCAAGCTGACAGGGTGAAGAACATTAACAGGGCTGTGAAAGCTTTG 1757
DB 1681 TCTTCTCAATGGCAAGCTGACAGGGTGAAGAACATTAACAGGGCTGTGAAAGCTTTG 1740

QY 1758 CTAAATGCTTAAGCTTGAAGAGCTGTGTAACCTTGTGTGTGTGCGGGTACATGATG 1817
DB 1741 CTAAATGCTTAAGCTTGAAGAGCTGTGTAACCTTGTGTGTGTGCGGGTACATGATG 1800

QY 1818 TCAACAGTCCAGAGCAAGGAGAGATGCGGAGATGAGAGAAATGATCAATCACTCA 1877
DB 1801 TCAACAGTCCAGAGCAAGGAGAGATGCGGAGATGAGAGAAATGATCAATCACTCA 1860

QY 1878 AGACCCACAACTTGTGTGGGAGTTCGCTGATCTTCCGACAGACAAACAGGGCCGCTA 1937
DB 1861 AGACCCACAACTTGTGTGGGAGTTCGCTGATCTTCCGACAGACAAACAGGGCCGCTA 1920

QY 1938 ACAGGAGCTTATGCTTACATGCTGATATCCATGATGCTTTGTATACGGCGCTTGT 1997
DB 1921 ACAGGAGCTTATGCTTACATGCTGATATCCATGATGCTTTGTATACGGCGCTTGT 1980

QY 1998 ATGAGAGTTCGATTCACAGCTGTTGAGGCAATGACCTGTGGCTTCTTACTTTCGGA 2057
DB 1981 ATGAGAGTTCGATTCACAGCTGTTGAGGCAATGACCTGTGGCTTCTTACTTTCGGA 2040

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DB 2101 CGTACCCGCCCCGAGCAGGCTTTATCTGATGAGCCGACTTTTGTGACCGGTCGACGACAG 2160
QY 2178 ACCGAGTCACTGAGTATATCTGAGAGCGGCTGACGCGCATATACGAGAGTACA 2237
DB 2161 ACCGAGTCACTGAGTATATCTGAGAGCGGCTGACGCGCATATACGAGAGTACA 2220
QY 2238 CATGAGAGATATATCTGAGAGGTTGATGACACTGCGCGGGCTTACGCTTCTGAGAGT 2297
DB 2221 CATGAGAGATATATCTGAGAGGTTGATGACACTGCGCGGGCTTACGCTTCTGAGAGT 2280
QY 2298 ACCGTCGAGAGCTGAGAGGCTGAGACGAGCGCTTACTTGAGATGTTCTCATCTGTA 2357
DB 2281 ACCGTCGAGAGCTGAGAGGCTGAGACGAGCGCTTACTTGAGATGTTCTCATCTGTA 2340
QY 2358 AGTTCGCGAGCTGCGGAGACCGCTGCGCTTGCATTTGACCAACGCGAGAGCTTGCAG 2417
DB 2341 AGTTCGCGAGCTGCGGAGACCGCTGCGCTTGCATTTGACCAACGCGAGAGCTTGCAG 2400
QY 2418 AACTGCGACTGCGGAGCACTTGTGACAAAGCTGAAACCTGAGAGACCTTCACTAATTAG 2477
DB 2401 AACTGCGACTGCGGAGCACTTGTGACAAAGCTGAAACCTGAGAGACCTTCACTAATTAG 2460
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DB 2521 TAATGCGAGATTAACAATAATTTACTGAGAGGAGTGGCTTGCATGTTGTTGTTGTTACTG 2580
QY 2598 TTTACTGATTAATGTCAGAGCTGTCGCTGCAATTTCTTTGTCGACAGCGGACGACCTG 2657
DB 2581 TTTACTGATTAATGTCAGAGCTGTCGCTGCAATTTCTTTGTCGACAGCGGACGACCTG 2640
QY 2658 GTGAGAGCTGAGTAATCATCATTTCTGTTGACCTGTGAAAAAATTTTTTTTTTTTTTT 2717
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QY 2718 AAAAAAAAAA 2727
DB 2701 AAAAAAAAAA 2710

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RESULT 2
LOCUS AY124703 2837 bp mRNA linear PLN 05-AUG-2002
DEFINITION Zea mays sucrose synthase 3 mRNA, complete cds.
ACCESSION AY124703
VERSION AY124703.1 GI:22121989
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

```

REFERENCE 1 (bases 1 to 2837)

AUTHORS Holtegraw, D.L., Scholz, A., Altmann, B. and Winter, H.

JOURNAL Unpublished

AUTHORS Holtegraw, D.L., Scholz, A., Altmann, B. and Winter, H.

TITLE Direct Submission

FEATURES Submitted (20-JUN-2002) BioLOGY, University of Osnabrueck, Barbara

Strasse 11, Osnabrueck 49076, Germany

Location/Qualifiers

1.2837

CDS

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/organism="Zea mays"
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/EC_number="2.4.1.13"
/notes="SUS3; sucrose-UDP glucosyltransferase"
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polysite

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Query Match 78.1%; Score 2138; DB 8; Length 2837;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 158 GCGACCGCTGCGAGACACCTTCCACCGCACCGCAACGAGCTGTCGCTCTCTGTCGA 217
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DB 218 AGTACGGAACAAAGGGGAGGGGACATCTGACACCGGACCAACATCTGACACCGCTGACAG 277
QY 138 AGGTCCAGGAGCTCCGGGGGCGCGCGCTAGCGGAGGACCTTCTCTGACGCTCCGCT 197
DB 278 AGGTCCAGGAGCTCCGGGGGCGCGCGCTAGCGGAGGACCTTCTCTGACGCTCCGCT 337
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QY 258 GAGTTGGAGTACGTGCGCGCTGACAGCTTCAAGAGCTCAGGTCGAGACAGTCAAGCT 317
DB 398 GAGTTGGAGTACGTGCGCGCTGACAGCTTCAAGAGCTCAGGTCGAGACAGTCAAGCT 457
QY 318 CGGAGTACTCCGCTTCAAGAGAGGCTTTCAGAGGCGCAGCAACATGATCCTACGTT 377
DB 458 CGGAGTACTCCGCTTCAAGAGAGGCTTTCAGAGGCGCAGCAACATGATCCTACGTT 517
QY 378 TCGAGCTTGAAGCTTGAAGCGCTTCAAGTTCACAGCGCCCAATGCGTCAATCTTA 437
DB 518 TCGAGCTTGAAGCTTGAAGCGCTTCAAGTTCACAGCGCCCAATGCGTCAATCTTA 577
QY 438 TTGGAACCGTGGAGAGTTCCTCAACGCACTTGTCTCAATATGTTGCGAACAGAG 497
DB 578 TTGGAACCGTGGAGAGTTCCTCAACGCACTTGTCTCAATATGTTGCGAACAGAG 637
QY 498 ATTGCTTGAGAGCCCTGTTGATTTCTCGGTGCGCACCGGCAACAGGGGATGTATGA 557
DB 638 ATTGCTTGAGAGCCCTGTTGATTTCTCGGTGCGCACCGGCAACAGGGGATGTATGA 697
QY 558 TGCTTAATGATTAATCAAGCTTGGGGAGGCTTGAAGTGTGCTGACCAAGGTGAGG 617
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QY 618 AACACTGTCAAGAGTCCCTGCTGACACACCACTACCTACCAATTTGCTATTAATTTCAAG 677
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 Db 1538 CTGATTTTATCATCACACAGACATACCAAGAAATTTCTGGAAGCAAAATTTACTTTGAC 1597
 QY 1458 AGTATGAGAGTCACTACGCTTTACTCTGCTGCTGTGTACAGAGTGTCAATGGATG 1517
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 QY 1518 ATGCTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1577
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QY 1698 TCTTCTCAATGAG 1757
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 QY 1758 CTAAGTGCCTTAAGCTGAG 1817
 Db 1898 CTAAGTGCCTTAAGCTGAG 1957
 QY 1818 TCAACAGTCCAAAG 1877
 Db 1958 TCAACAGTCCAAAG 2017
 QY 1878 AGACCAAGCTTGTGCGGAG 1937
 Db 2018 AGACCAAGCTTGTGCGGAG 2077
 QY 1938 ACGGAGCTTAATGCTGATACATGCTGATATCCATGATGCTTGTGATACAGCGGCTTGT 1997
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 Db 2138 ATGAAAGCTTGTGCTCACTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2197
 QY 2058 CGCTCCATGAG 2117
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 QY 2118 CGTACACCCCGAG 2177
 Db 2258 CGTACACCCCGAG 2317
 QY 2178 ACCCAATGATGAG 2237
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 QY 2238 CATTGAAGATTAATCTGAG 2297
 Db 2378 CATTGAAGATTAATCTGAG 2437
 QY 2298 ACGTGTGAG 2357
 Db 2438 ACGTGTGAG 2497
 QY 2358 AGTTCGAG 2410
 Db 2498 AGTTCGAG 2550

RESULT 3
 AX756452/c
 LOCUS AX756452 297 bp DNA linear PAT 23-JUN-2003
 DEFINITION Sequence 1191 from Patent WO03000905.
 ACCESSION AX756452
 VERSION AX756452.1 GI:32168583
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 1
 REFERENCE
 AUTHORS Zhu, T., Cheng, M., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
 Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Ristic, D.
 TITLE Identification and characterization of plant genes
 JOURNAL Patent: WO 03000905-A 1191 03-JAN-2003;
 SynGenea Participations AG (CH)
 FEATURES
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 /organism="Zea mays"
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 ORIGIN

Query Match 7.0%; Score 192; DB 6; Length 297;
 Best Local Similarity 99.6%; Pred. No. 2.2e-90;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1373 GCTGATATTAATGCTATGAACAAATGCTGATTTTATCATCAACGACACATACCAAGAAAT 1432
 DB 243 GCTGATATTAATGCTATGAACAAATGCTGATTTTATCATCAACGACACATACCAAGAAATC 184

QY 1433 GCTGGAAGCAAAATATCTGTGTGACATATGAGCATATCTACTGCTTACTCTCTGCT 1492
 DB 183 GCTGGAAGCAAAATATCTGTGTGACATATGAGCATATCTACTGCTTACTCTCTGCT 124

QY 1493 CTGTACCAAGCTTGTCCATGGGACCGATGTCTGTGATCCAAAGTTCATATAGTCTCTCT 1552
 DB 123 CTGTACCAAGCTTGTCCATGGGACCGATGTCTGTGATCCAAAGTTCATATAGTCTCTCT 64

QY 1553 GGAAGCTGACATGTTCATATATCTTCCACATACCGAAGGCGCAAGCACTCCTCTCT 1612
 DB 63 GGAAGCTGACATGTTCATATATCTTCCACATACCGAAGGCGCAAGCACTCCTCTCT 4

QY 1613 CAT 1615
 DB 3 CAT 1

RESULT 4
 AX756409/c 258 bp DNA linear PAT 24-JUN-2003
 LOCUS AX756409 Sequence 1148 from Patent WO03000905.
 DEFINITION AX756409
 ACCESSION AX756409
 VERSION AX756409.1 GI:32168540
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays
 Sukariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1
 AUTHORS Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Noughamer, T.,
 Glazebrook, K., Katagiri, F., Kreps, J., Provart, N. and Rieke, D.
 Identification and characterization of plant genes
 Patent: WO 03000905-A 1148 03-JUN-2003;
 JOURNAL Syngenta Participations AG (CH)
 FEATURES location/Qualifiers
 source 1..258
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ORIGIN

Query Match 7.0%; Score 191; DB 6; Length 258;
 Best Local Similarity 100.0%; Pred. No. 7.5e-90;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GCCGAGGGAACCCCTCTCGAGCTCTCCGCGCGCGGAGGAGGCGATGTCGCGCGG 226
 DB 258 GCCGAGGGAACCCCTCTCTCGAGCTCTCCGCGCGCGGAGGAGGCGATGTCGCGCGG 199

QY 227 TTGCTGGCCATCGCGGATCGCGCGCGCGGAGTTTGGAGTACGTCGCGGTCAAGCTT 286
 DB 198 TTGCTGGCCATCGCGGATCGCGCGCGCGGAGTTTGGAGTACGTCGCGGTCAAGCTT 139

QY 287 CACGAGCTCAGCGCTGACGACACTCAAGTCTCGAGTACCTCCGTTCAAGAGAGAGTT 346
 DB 138 CACGAGCTCAGCGCTGACGACACTCAAGTCTCGAGTACCTCCGTTCAAGAGAGAGTT 79

QY 347 GTCCAGGCGCA 357
 DB 78 GTCCAGGCGCA 68

RESULT 5

AR246503
 LOCUS AR246503 265 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 1862 from patent US 6476212.
 ACCESSION AR246503
 VERSION AR246503.1 GI:27294377
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 265)
 AUTHORS Lajudi, R.V., Ito, L.Y. and Sherman, B.K.
 TITLE Polynucleotides and polypeptides derived from corn ear
 JOURNAL Patent: US 6476212-A 1862 05-NOV-2002;
 FEATURES location/Qualifiers
 source 1..265
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 Query Match 4.5%; Score 122; DB 6; Length 265;
 Best Local Similarity 100.0%; Pred. No. 4.3e-53;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 564 ATGATAGATACAAAGCTGGGAGGCTTCAAGTCTGTGCTGACCAAGCTGAGGACT 623
 DB 110 ATGATAGATACAAAGCTGGGAGGCTTCAAGTCTGTGCTGACCAAGCTGAGGACT 169

QY 624 TGTCAAGCTCCCTGCTGACACACCATATCTACAAATTTGCTATTAATTCAAGAGTGG 683
 DB 170 TGTCAAGCTCCCTGCTGACACACCATATCTACAAATTTGCTATTAATTCAAGAGTGG 229

QY 684 GC 685
 DB 230 GC 231

RESULT 6
 BV079817 221 bp DNA linear SRS 30-SEP-2003
 LOCUS BV079817
 DEFINITION sc1180_p3 Mol17 Zea mays Mol17 Zea mays SRS genomic, sequence tagged
 site.
 ACCESSION BV079817
 VERSION BV079817.1 GI:37051474
 KEYWORDS SRS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE 1
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 221)
 McMillen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
 JOURNAL MPZ-UCI Joint SNP Discovery
 COMMENT Unpublished (2003)

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: GAGCGCTACCTGAGATGTCGA
 Primer B: ATTATCAGCACTTACCACTGGC
 Protocol: PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Tag Polymerase: RedTag (Sigma)
 Total Vol: 10 uL
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplified DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

FEATURES

PHRED/PHRAP Quality Scores 62 53 60 59 86 86 80 80 82 30 82 82 82
81 81 77 77 79 73 83 90 90 90 88 88 62 68 50 59 57 73
68 75 84 84 83 83 89 82 79 79 87 87 90 81 81 87 87 83 80 84 84
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/dev_stage="seedling"
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ORIGIN

Query Match 3.8%; Score 103; DB 11; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GCGGAGACCGTGCCTGCAATTGACCAACCGAGTAGCTTGCACACTGCGACTGCG 2430
DB 119 GCGGAGACCGTGCCTGCAATTGACCAACCGAGTAGCTTGCACACTGCGACTGCG 178
QY 2431 TAGCACTTGTTCAGACTGAACTGAAAGGACCTTCACTAAT 2473
DB 179 TAGCACTTGTTCAGACTGAAAGGACCTTCACTAAT 221

RESULT 7
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LOCUS sc1180.p3 CML322 Zea mays CML322 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079815
VERSION BV079815.1 GI:37051472
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 225)
McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATACGACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 20 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle

Sequencing ready reaction with amplified DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

FEATURES

PHRED/PHRAP Quality Scores 47 44 40 34 66 61 63 63 82 82 80 82 82
87 81 85 85 81 77 76 81 84 80 73 73 88 90 90 82 70 73 85 81 90
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Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="CML322"
/db_xref="taxon:4577"
/clone_lib="Zea mays CML322"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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ORIGIN

Query Match 3.8%; Score 103; DB 11; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GCGGAGACCGTGCCTGCAATTGACCAACCGAGTAGCTTGCACACTGCGACTGCG 2430
DB 123 GCGGAGACCGTGCCTGCAATTGACCAACCGAGTAGCTTGCACACTGCGACTGCG 182
QY 2431 TAGCACTTGTTCAGACTGAACTGAAAGGACCTTCACTAAT 2473
DB 183 TAGCACTTGTTCAGACTGAAAGGACCTTCACTAAT 225

RESULT 8
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LOCUS sc1180.p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079813
VERSION BV079813.1 GI:37051470
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 234)
McMillen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATACGACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 20 uL
Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 37 44 40 29 29 29 42 42 44 77 73 60
55 51 58 58 82 82 82 82 82 82 85 85 80 76 77 77 77 75 73 90
90 90 83 63 63 62 71 83 90 77 81 87 82 84 81 81 83 86 81 90 90
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FEATURES

Location/Qualifiers

1..234
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CML333"
/db_xref="taxon:4577"
/clone_lib="Zea mays CML333"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>234

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 234;
Best Local Similarity 100.0%; Pred.No.5.6e-43;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGGAGACCGTGGCGCTTGCAATTGACCAACCGAGTAGCTTGGCACTGGCG 2430

Db 132 GGGAGACCGTGGCGCTTGCAATTGACCAACCGAGTAGCTTGGCACTGGCG 191

QY 2431 TAGCACTTGTACAGACTGAACCTGAAGAGACCTTCAGTAT 2473

Db 192 TAGCACTTGTACAGACTGAACCTGAAGAGACCTTCAGTAT 234

RESULT 9
BV079812 239 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Kull11 Zea mays STS genomic, sequence
DEFINITION tagged site.

ACCESSION BV079812 GI:37051469
VERSION BV079812.1
KEYWORDS STS.

SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT

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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCATTCCACAGTGC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL

Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 32 32 28 28 56 70 74 67 67 63 75 61
75 81 77 76 62 60 54 67 62 90 88 84 82 82 90 81 90 87 82 81 76 81
81 77 77 77 83 90 79 71 71 79 83 79 90 90 89 84 84 89 84
80 80 80 86 90 87 87 87 90 79 79 87 86 82 90 90 81 81 7.

FEATURES

Location/Qualifiers

1..239
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Kull11"
/db_xref="taxon:4577"
/clone_lib="Zea mays Kull11"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>239

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred.No.5.6e-43;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGGAGACCGTGGCGCTTGCAATTGACCAACCGAGTAGCTTGGCACTGGCG 2430

Db 137 GGGAGACCGTGGCGCTTGCAATTGACCAACCGAGTAGCTTGGCACTGGCG 196

QY 2431 TAGCACTTGTACAGACTGAACCTGAAGAGACCTTCAGTAT 2473

Db 197 TAGCACTTGTACAGACTGAACCTGAAGAGACCTTCAGTAT 239

RESULT 10
BV079814 239 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
DEFINITION site.

ACCESSION BV079814 GI:37051471
VERSION BV079814
KEYWORDS STS.

SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT

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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCATTCCACAGTGC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)

Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 32 29 34 33 48 37 33 28 44 33 37
44 48 48 46 42 34 25 33 31 42 42 44 42 42 44 48 35 35 35
13 13 13 42 35 66 73 58 68 71 77 73 79 82 76 73 76 73 76 76
75 75 75 80 85 82 90 88 92 90 79 90 90 78 88 88 73 73 6.
FEATURES
Location/Qualifiers
1..239

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Oh43"
/db_xref="taxon:4577"
/clone_1ib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: Leaf; genomic DNA from inbred line"
<1..>239

ORIGIN
STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGCGAGACCGTGGCCCTGGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGC 2430
DB 137 GGCGAGACCGTGGCCCTGGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGC 196
QY 2431 TAGCACTTGTACAGACTGAAGCTGAAGACCTTCAGTAAT 2473
DB 197 TAGCACTTGTACAGACTGAAGCTGAAGACCTTCAGTAAT 239

RESULT 11
LOCUS BV079819 239 bp DNA linear STS 30-SEP-2003
DEFINITION sc1180_p3 M37W Zea mays M37W Zea mays STS genomic, sequence tagged
site.
ACCESSION BV079819 GI:37051476
VERSION BV079819.1
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATACGACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM

Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 31 28 28 52 66 59 59 57 52 63 57
75 77 73 75 75 67 61 67 65 82 82 84 84 82 90 90 86 86 82 81 82
90 80 76 76 76 87 89 90 90 82 88 84 90 82 83 90 82 77 74 75 80
85 80 80 82 79 79 77 80 86 84 82 82 90 87 83 79 81 81 81 7.
FEATURES
Location/Qualifiers
1..239

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="M37W"
/db_xref="taxon:4577"
/clone_1ib="Zea mays M37W"
/dev_stage="seedling"
/note="Organ: Leaf; genomic DNA from inbred line"
<1..>239

ORIGIN
STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGCGAGACCGTGGCCCTGGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGC 2430
DB 137 GGCGAGACCGTGGCCCTGGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGC 196
QY 2431 TAGCACTTGTACAGACTGAAGCTGAAGACCTTCAGTAAT 2473
DB 197 TAGCACTTGTACAGACTGAAGCTGAAGACCTTCAGTAAT 239

RESULT 12
LOCUS BV079818 240 bp DNA linear STS 30-SEP-2003
DEFINITION sc1180_p3 Ky21 Zea mays Ky21 Zea mays STS genomic, sequence tagged
site.
ACCESSION BV079818 GI:37051475
VERSION BV079818.1
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 240)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATACGACTTCACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM

dnTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliflag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 46 42 34 34 56 73 64 63 61 71 61 66
63 67 75 74 66 74 76 85 73 90 90 90 90 82 77 90 87 87 81 80
82 80 73 73 88 90 90 82 82 71 85 85 74 90 90 84 84 77 75 75
77 72 77 85 80 79 81 84 86 90 85 85 84 84 85 90 90 87 7.

FEATURES

source

1. .240
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>240

ORIGIN

STS

Query Match 2.6%; Score 72; DB 11; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2402 CCGGAGTAGCTTGGCGAAGCTGCGAGCTGAGCACTTGGTACAAAGACTGAACCTGAAGG 2461
DB 169 CCGGAGTAGCTTGGCGAAGCTGCGAGCTGAGCACTTGGTACAAAGACTGAACCTGAAGG 228
QY 2462 ACCTTCAGTAAT 2473
DB 229 ACCTTCAGTAAT 240

RESULT 13
BV079820 234 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Hp301 Zea mays Hp301 Zea mays STS genomic, sequence
DEFINITION
tagged site.
ACCESSION BV079820
VERSION BV079820.1 GI:37051477
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 234)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS
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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAATGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng

Primer: each 0.5 uM
dnTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliflag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 66 62 61 67 65 61 61 61 69 71 73 63
66 64 72 72 87 87 88 84 80 80 80 85 84 81 76 77 80 71 73 84
79 79 79 78 78 67 81 85 90 81 85 83 77 72 69 69 77 75 75 85 80
79 90 90 90 90 81 81 84 84 82 90 79 77 70 75.

FEATURES

source

1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Hp301"
/db_xref="taxon:4577"
/clone_lib="Zea mays Hp301"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>234

ORIGIN

STS

Query Match 2.5%; Score 69; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 7.2e-25;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2405 CAGTAGCTTGGCGAAGCTGCGAGCTGAGCACTTGGTACAAAGACTGAACCTGAAGACC 2464
DB 166 CAGTAGCTTGGCGAAGCTGCGAGCTGAGCACTTGGTACAAAGACTGAACCTGAAGACC 225
QY 2465 TTTCAGTAAT 2473
DB 226 TTTCAGTAAT 234

RESULT 14
BV079821 246 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 CM247 Zea mays CM247 Zea mays STS genomic, sequence
DEFINITION
tagged site.
ACCESSION BV079821
VERSION BV079821.1 GI:37051478
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAATGCC
Protocol:
PCR amplification of genomic DNA

Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: Redtaq (Sigma)
 Total Vol: 10 uL
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 Redtaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 37 34 34 42 42 42 42 42 42 26 26 26
 26 37 35 34 34 52 50 61 57 82 73 78 71 71 77 70 82 82 79 66 58 58
 58 55 63 63 80 80 84 75 70 66 61 56 61 67 67 84 84 79 79 90 83
 81 87 77 81 81 79 82 82 87 77 82 90 82 82 84 79 77 77 83 81 71
 83 83 71 66 60.

FEATURES

Location/Qualifiers
 1..246
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /catalyze="CML247"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays CML247"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
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ORIGIN

Query Match 2.5%; Score 69; DB 11; Length 246;
 Best Local Similarity 100.0%; Pred.No. 7.2e-25;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2405 CAGTAGCTGGCGAAGCTGCGACTGCGTACGACCTGTTGTTACAGACTGAACTGAGAGACC 2464
 DB 178 CAGTAGCTGGCGAAGCTGCGACTGCGTACGACCTGTTGTTACAGACTGAACTGAGAGACC 237
 QY 2465 TTGAGTAAT 2473
 DB 238 TTGAGTAAT 246

Search completed: May 26, 2004, 06:45:30
 Job time : 7016.39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 53.7325 Seconds
(without alignments)
4254.056 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247
Sequence: 1 MSAPEKLNRASTRDRVEDTL.....YIAKFEELAKTYALIDPQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4247	100.0	809	5	AAE28502	Aae28502 Corn Sus3
2	4177	98.4	802	5	AAE28499	Aae28499 Corn suscr
3	3485	82.1	809	5	ABR92810	Abbr92810 Herbicida
4	3158	74.4	766	2	AAE66222	Aae66222 Sucrose-s
5	3129	73.7	797	6	ABR39586	Abbr39586 A. thaliana
6	3108.5	73.2	805	5	ABR93752	Abbr93752 Herbicida
7	3108.5	73.2	805	6	ABR39585	Abbr39585 A. thaliana
8	3060.5	72.1	773	5	AAE28503	Aae28503 Maize suc
9	3011.5	70.9	802	5	AAE28500	Aae28500 Corn suscr
10	3006.5	70.8	808	3	AAE28564	Aae28564 Rice suscr
11	2997	70.6	816	5	AAE28501	Aae28501 Corn suscr
12	2985	70.3	816	7	ADCC07856	Adcc07856 Rice prot
13	2985	70.3	816	7	ADCC08209	Adcc08209 Rice prot
14	2976.5	70.1	815	7	ADCC68460	Adcc68460 Lolium pe
15	2972	70.0	806	5	AAU97898	Aau97898 Cotton su
16	2972	70.0	814	7	ADCC68366	Adcc68366 Lolium pe
17	2947	69.4	816	7	ADCC68367	Adcc68367 S. arund
18	2942.5	69.3	808	7	ADCC68459	Adcc68459 Lolium pe
19	2938.5	69.2	808	7	ADCC68364	Adcc68364 Lolium pe
20	2934.5	69.1	808	5	ABG69063	Abg69063 Amino aci
21	2934.5	68.9	808	7	ADCC68365	Adcc68365 S. arundi
22	2914.5	68.6	771	7	AAE85666	Aae85666 PS3 prot
23	2905.5	68.4	808	5	ABR92501	Abbr92501 Herbicida
24	2892.5	68.1	805	3	AAE16282	Aae16282 Eucalyptu
25	2892.5	68.1	805	3	AAE16336	Aae16336 Eucalyptu

26	2892.5	68.1	805	3	AAE28141	Aae28141 Sucrose s
27	2892.5	68.1	805	5	AAU80759	Aau80759 Eucalyptu
28	2867.5	67.5	808	5	ABR93562	Abbr93562 Herbicida
29	2763.5	65.1	777	7	ADCC8297	Adcc8297 Rice prot
30	2763.5	65.1	777	7	ADCC07858	Adcc07858 Rice prot
31	2353.5	55.4	942	5	ABR91573	Abbr91573 Herbicida
32	2319.5	54.6	786	7	ADCC07862	Adcc07862 Rice prot
33	2295	54.0	843	5	ABR93633	Abbr93633 Herbicida
34	2260.5	53.2	798	7	ADCC07860	Adcc07860 Rice prot
35	2005	47.2	514	7	ADCC07854	Adcc07854 Rice prot
36	1833	43.2	806	2	AAW53103	Aaw53103 Andraena
37	1692.5	39.9	395	5	ABG69054	Abg69054 Amino aci
38	1212	28.5	348	3	AAE16313	Aae16313 Pinus rad
39	802.5	18.9	225	5	ABG69052	Abg69052 Amino aci
40	709	16.7	149	3	AAE16309	Aae16309 Eucalyptu
41	651	15.3	217	3	AAE16312	Aae16312 Pinus rad
42	639	15.0	198	3	AAE85667	Aae85667 Plant col
43	633	14.9	204	7	ABW73686	Abw73686 DNA clone
44	622	14.6	158	3	AAE16284	Aae16284 Pinus rad
45	587	13.8	139	3	AAE16314	Aae16314 Pinus rad

ALIGNMENTS

RESULT 1

AAE28502 standard; protein; 809 AA.

AAE28502; 29-AUG-2003 (revised)

DT 27-DEC-2002 (first entry)

DE Corn Sus3-Sorghum EST chimeric protein.

XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KW cellulose; corn; Sus3; chimeric.

XX Zea mays.
OS Sorghum propinquum.
OS Chimeric.

XX Key location/Qualifiers

FT Region 1..13 /note= "Sorghum propinquum EST DNA encoded peptide"

FT Region 14..809 /note= "Corn Sus3 protein"

PN W0200267662-A1.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002MO-US005137.

PR 22-FEB-2001; 2001US-0270777P.

PA (PTON-) PIONEER HI-BRED INT INC.

PI Dhuga KS, Helentjaris TG, Niu X;

XX WPI; 2002-691625/74.

DR N-PSDB; AAD45856.

XX New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.

PS Claim 12; Page 120-121; 125pp; English.

XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC

CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 CC acids. The polynucleotide, or its encoded protein, is useful for
 CC modulating the level of sucrose synthase in a transgenic plant,
 CC increasing cellulose production in the stalk tissue of a transgenic
 CC plant, or increasing the concentration of cellulose in the tissues of a
 CC seed of a transgenic plant. This is particularly useful in plant (e.g.
 CC maize or soybean) breeding, especially for e.g. improving stalk length in
 CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is Corn Sus3-Sorghum Est chimeric protein. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX Sequence 809 AA;

Query Match 100.0%; Score 4247; DB 5; Length 809;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAPFLANRNASIRDEVEPTLHAHRNELVALLSKYNNKGKGLQPHHIDALDEVQSSGVR 60
 DB 1 MSAPFLANRNASIRDEVEPTLHAHRNELVALLSKYNNKGKGLQPHHIDALDEVQSSGVR 60
 QY 61 ALAEGPFLDVRSAGQALVLPPEVALAVRPRGWEYVRVNVHLSVEQLTVSEYLAREKE 120
 DB 61 ALAEGPFLDVRSAGQALVLPPEVALAVRPRGWEYVRVNVHLSVEQLTVSEYLAREKE 120
 QY 121 ELYVQGNDDPYLLELDEEPFNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLD 180
 DB 121 ELYVQGNDDPYLLELDEEPFNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLD 180
 QY 121 ELYVQGNDDPYLLELDEEPFNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLD 180
 DB 121 ELYVQGNDDPYLLELDEEPFNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLD 180
 QY 181 FLRGHRHGHVWMLNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKGM 240
 DB 181 FLRGHRHGHVWMLNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKGM 240
 QY 181 FLRGHRHGHVWMLNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKGM 240
 DB 181 FLRGHRHGHVWMLNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKGM 240
 QY 241 GDTAGHLEMLHLLDIIQAPDSTLEKEFLGRIPIFNVVVVSHPGFCQANVLGLPDTG 300
 DB 241 GDTAGHLEMLHLLDIIQAPDSTLEKEFLGRIPIFNVVVVSHPGFCQANVLGLPDTG 300
 QY 241 GDTAGHLEMLHLLDIIQAPDSTLEKEFLGRIPIFNVVVVSHPGFCQANVLGLPDTG 300
 DB 241 GDTAGHLEMLHLLDIIQAPDSTLEKEFLGRIPIFNVVVVSHPGFCQANVLGLPDTG 300
 QY 301 GOIVYVILDOVRALNEMVTALKKQGLDVSFKLITVTRLLPDAKGTSCNQLRISGTQHT 360
 DB 301 GOIVYVILDOVRALNEMVTALKKQGLDVSFKLITVTRLLPDAKGTSCNQLRISGTQHT 360
 QY 361 YLLARPERENGILKKKWSIRPDMFPLTEFADAGEIAAEIOGTDPITGVNSDQNLVA 420
 DB 361 YLLARPERENGILKKKWSIRPDMFPLTEFADAGEIAAEIOGTDPITGVNSDQNLVA 420
 QY 361 YLLARPERENGILKKKWSIRPDMFPLTEFADAGEIAAEIOGTDPITGVNSDQNLVA 420
 DB 361 YLLARPERENGILKKKWSIRPDMFPLTEFADAGEIAAEIOGTDPITGVNSDQNLVA 420
 QY 421 SLSLYMGITQCNIAHAEKTYEPDSDFWKNPDEKTHFSQPTADIIAMNNADFTITST 480
 DB 421 SLSLYMGITQCNIAHAEKTYEPDSDFWKNPDEKTHFSQPTADIIAMNNADFTITST 480
 QY 421 SLSLYMGITQCNIAHAEKTYEPDSDFWKNPDEKTHFSQPTADIIAMNNADFTITST 480
 DB 421 SLSLYMGITQCNIAHAEKTYEPDSDFWKNPDEKTHFSQPTADIIAMNNADFTITST 480
 QY 481 YGEIAGSKTVQGYSEHTAFTPLGLYRVVHGIDVPRKNIVTSFGADMSTYEPHTEKAR 540
 DB 481 YGEIAGSKTVQGYSEHTAFTPLGLYRVVHGIDVPRKNIVTSFGADMSTYEPHTEKAR 540
 QY 481 YGEIAGSKTVQGYSEHTAFTPLGLYRVVHGIDVPRKNIVTSFGADMSTYEPHTEKAR 540
 DB 481 YGEIAGSKTVQGYSEHTAFTPLGLYRVVHGIDVPRKNIVTSFGADMSTYEPHTEKAR 540
 QY 541 LNSLGSITNLLYDPQNDENHIGLDDRKPLIFSMARIDRVNITGLVEAFKCAKARE 600
 DB 541 LNSLGSITNLLYDPQNDENHIGLDDRKPLIFSMARIDRVNITGLVEAFKCAKARE 600
 QY 541 LNSLGSITNLLYDPQNDENHIGLDDRKPLIFSMARIDRVNITGLVEAFKCAKARE 600
 DB 541 LNSLGSITNLLYDPQNDENHIGLDDRKPLIFSMARIDRVNITGLVEAFKCAKARE 600
 QY 601 LYNLVVAGYNDVNSKQREELIAEIKHMEILKTNHLFGQFWRISAGTNRAAGELYYRI 660
 DB 601 LYNLVVAGYNDVNSKQREELIAEIKHMEILKTNHLFGQFWRISAGTNRAAGELYYRI 660
 QY 601 LYNLVVAGYNDVNSKQREELIAEIKHMEILKTNHLFGQFWRISAGTNRAAGELYYRI 660
 DB 601 LYNLVVAGYNDVNSKQREELIAEIKHMEILKTNHLFGQFWRISAGTNRAAGELYYRI 660
 QY 661 AOTHAQFVQPAIYEAAGLTVVAMTCGLTFATIHGGPAEITIEHGVSGHIDPYHEQAV 720
 DB 661 AOTHAQFVQPAIYEAAGLTVVAMTCGLTFATIHGGPAEITIEHGVSGHIDPYHEQAV 720
 QY 661 AOTHAQFVQPAIYEAAGLTVVAMTCGLTFATIHGGPAEITIEHGVSGHIDPYHEQAV 720
 DB 661 AOTHAQFVQPAIYEAAGLTVVAMTCGLTFATIHGGPAEITIEHGVSGHIDPYHEQAV 720
 QY 721 NLMADPDRCKODPDHWNVISGAGLQRIYEKTYTWKYSERIMTLAGVYFWKXVSLRETL 780
 DB 721 NLMADPDRCKODPDHWNVISGAGLQRIYEKTYTWKYSERIMTLAGVYFWKXVSLRETL 780
 QY 781 ETRRYLEMFYILKRELAKTVPALDOPQ 809
 DB 781 ETRRYLEMFYILKRELAKTVPALDOPQ 809

RESULT 2
 AAE28499
 ID AAE28499 standard; protein; 802 AA.

XX AAE28499;

XX 27-DEC-2002 (first entry)

DB Corn sucrose synthase (Sus3).

XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 XX cellulose; corn; Sus3.

XX Zea mays.

XX WO200267662-A1.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US005137.

XX 22-FEB-2001; 2001US-0270777P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Dhurga KS, Helentjaris TG, Niu X;

XX MPI; 2002-691625/74.

XX N-PSDB; AAD45849.

XX New polynucleotide and its encoded sucrose synthase, useful for
 XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
 XX or soybean) to improve stalk length, reduce grain breakage, or improving
 XX plant or grain strength.

XX Claim 12; Page 103-104; 125pp; English.

XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
 XX acids. The polynucleotide, or its encoded protein, is useful for
 XX modulating the level of sucrose synthase in a transgenic plant,
 XX increasing cellulose production in the stalk tissue of a transgenic
 XX plant, or increasing the concentration of cellulose in the tissues of a
 XX seed of a transgenic plant. This is particularly useful in plant (e.g.
 XX maize or soybean) breeding, especially for e.g. improving stalk length in
 XX maize, reducing grain breakage during combining, transport or movement
 XX into storage, or improving plant or grain strength. The present sequence
 XX is corn Sus3 protein

XX Sequence 802 AA;

Query Match 98.4%; Score 4177; DB 5; Length 802;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 DREVECTLHAHRNELVALLSKYNNKGKGLQPHHIDALDEVQSSGVRALABGFLDVLR 73
 DB 7 DREVECTLHAHRNELVALLSKYNNKGKGLQPHHIDALDEVQSSGVRALABGFLDVLR 73
 QY 74 AOEALVLPPEVALAVRPRGWEYVRVNVHLSVEQLTVSEYLRFKBLVDGQHNDEYVL 133
 DB 67 AOEALVLPPEVALAVRPRGWEYVRVNVHLSVEQLTVSEYLRFKBLVDGQHNDEYVL 126
 QY 134 ELDFEFPNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLDPLFLGHRKRYMM 193
 DB 127 ELDFEFPNVSVPRRNSSISGVQVPLNRHLSIMFRNDDCLEPLLDPLFLGHRKRYMM 186
 QY 194 LNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKMGDTAGVLEMLHL 253
 DB 187 LNDRIOSLGRLOSVLTKAEHLSKLPADTPYSQFAFKFOEMGLEKMGDTAGVLEMLHL 246

QY 254 LLDIIQAPPSTSEKFLGRIPMIFNVVVS PHGYFGQAVNLGPPJGQGVITVLLDQVRAL 313
 XX |||||
 DB 247 LLDIIQAPPSTSEKFLGRIPMIFNVVVS PHGYFGQAVNLGPPJGQGVITVLLDQVRAL 306
 QY 314 ENEMVRLKKQGGIDVSPKILVTRLIPDAKGTSCNQLERISGTQHTYLLRVPFRNENGI 373
 XX |||||
 DB 307 ENEMVRLKKQGGIDVSPKILVTRLIPDAKGTSCNQLERISGTQHTYLLRVPFRNENGI 366
 QY 374 LKKWIRPFWPVLTEFPAEPAAGEIAAELOGTPTDITIGNSDGNVVAALSTYMGITQCN 433
 DB 367 LKKWIRPFWPVLTEFPAEPAAGEIAAELOGTPTDITIGNSDGNVVAALSTYMGITQCN 426
 QY 434 IAALEKTYPPSDIFMKNPDEKHYHSCOPTADIIAMNNADFIITSTYGHISAGKNTVQG 493
 DB 427 IAALEKTYPPSDIFMKNPDEKHYHSCOPTADIIAMNNADFIITSTYGHISAGKNTVQG 486
 QY 494 YESHTAFTLPGLYRVVHGIDVDPKXENIVSPGADMSIYPHTEKAKRLTSLHGSINLLY 553
 DB 487 YESHTAFTLPGLYRVVHGIDVDPKXENIVSPGADMSIYPHTEKAKRLTSLHGSINLLY 546
 QY 554 DEQONDEHGHLDDBSKPILFPMARLDRYKNTGLVYEAFAKCAKRELNVLVVYAGYNDV 613
 DB 547 DEQONDEHGHLDDBSKPILFPMARLDRYKNTGLVYEAFAKCAKRELNVLVVYAGYNDV 606
 QY 614 NKSKESEIAETEKMEHLIKTNLFGQEFWISAQTRARNGELYRYTIADTHGAFVOPALY 673
 DB 607 NKSKESEIAETEKMEHLIKTNLFGQEFWISAQTRARNGELYRYTIADTHGAFVOPALY 666
 QY 674 EAPGLTVVAMTGTGLTFPATLHGSPAEIIEHGVSGPHIDYHBEQAVNIMADFFDCKOD 733
 DB 667 EAPGLTVVAMTGTGLTFPATLHGSPAEIIEHGVSGPHIDYHBEQAVNIMADFFDCKOD 726
 QY 734 PPHWVVISAGLORITEXTKTKIYSEKRLTLAGVYGMKVSGLBELETRRYIEMYYILK 793
 DB 727 PPHWVVISAGLORITEXTKTKIYSEKRLTLAGVYGMKVSGLBELETRRYIEMYYILK 786
 QY 794 PRELAKTVELAIDPOQ 809
 DB 787 PRELAKTVELAIDPOQ 802

RESULT 3
 ABB92810
 ID ABB92810 standard; protein; 809 AA.
 XX
 AC ABB92810;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DB Hericidially active polypeptide SEQ ID NO 2021.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN MO200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 28-AUG-2001; 2001MO-EP009892.
 XX
 PR 28-AUG-2001; 2001MO-EP009892.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Tietjen K, Weidler M;
 XX
 DR WPI; 2002-26310/1.
 XX
 PT Identifying plant target proteins for herbicidially active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.
 XX
 PS Claim 5; SEQ ID NO 2021; 261pp + Sequence Listing: English.
 XX
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidially active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 CC
 XX
 SQ Sequence 809 AA;
 QY
 DB
 QY 1 MSAPKLNKASIRDRVEDTAAHNEIYALSKYVNGKGILOPHHILDADEVQSGS- 58
 DB 1 MAMPKTRVLTSDRVQDTLSARHNEIYALSRVYDQSGILOPHHILDADEVQSGS- 60
 QY 59 VRALAESEFLDVRSQAEALVLPPEFVALAVRPPGVMEYRVNVHELSEVQLTVSEYLRF 118
 DB 61 KKSLSGPEGEILKSMAMEALVPEFVALAVRPPGVMEYRVNVHELSEVQLTVSEYLRF 120
 QY 119 KEELVDSQHNDPVYELDEFEPPNVSVPRNRSSISGVQVFLNHLSSIMFRDCLPEL 178
 DB 121 KEELVDSQNDPVYELDEFEPPNVSVPRNRSSISGVQVFLNHLSSIMFRDCLPEL 180
 QY 179 LDFLRGHRHGHMMNDRIQSILGRLOSVLTKAEHSKLPADPTYSQFAKPEQMGLEK 238
 DB 181 LDFLRVHKYGHPLMNDRIQSILGRLOSVLTKAEHSKLPADPTYSQFAKPEQMGLEK 240
 QY 239 GWDGTAGVLEMLHLLDIIQAPPSTSEKFLGRIPMIFNVVVS PHGYFGQAVNLGPPD 298
 DB 241 GWDGTAGVLEMLHLLDIIQAPPSTSEKFLGRIPMIFNVVVS PHGYFGQAVNLGPPD 300
 QY 299 TGGQIVITLDQVRALENEMVRLKKQGGIDVSPKILVTRLIPDAKGTSCNQLERISGTQ 358
 DB 301 TGGQIVITLDQVRALENEMVRLKKQGGIDVSPKILVTRLIPDAKGTSCNQLERISGTQ 360
 QY 359 HTYLLRVPFRNENGIKKWIRPFWPVLTEFPAEPAAGEIAAELOGTPTDITIGNSDGNL 418
 DB 361 HTYLLRVPFRNENGIKKWIRPFWPVLTEFPAEPAAGEIAAELOGTPTDITIGNSDGNL 420
 QY 419 VASLSTYKMGITQONTAALEKTYPPSDIFMKNPDEKHYHSCOPTADIIAMNNADFIIT 478
 DB 421 VASLSTYKMGITQONTAALEKTYPPSDIFMKNPDEKHYHSCOPTADIIAMNNADFIIT 480
 QY 479 STYGHISAGKNTVQGHESHTAFTLPGLYRVVHGIDVDPKXENIVSPGADMSIYPHTEKA 538
 DB 481 STYGHISAGKNTVQGHESHTAFTLPGLYRVVHGIDVDPKXENIVSPGADMSIYPHTEKA 540
 QY 539 KR.TSLHGSTENLIYDPEONDEHGHLDDBSKPILFPMARLDRYKNTGLVYEAFAKCAKL 598
 DB 541 KR.TSLHGSTENLIYDPEONDEHGHLDDBSKPILFPMARLDRYKNTGLVYEAFAKCAKL 600
 QY 599 RELVNLVVVAGYNDVNSKDRSEIAETEKMEHLIKTNLFGQEFWISAQTRARNGELYR 658
 DB 601 RELVNLVVVAGYNDVNSKDRSEIAETEKMEHLIKTNLFGQEFWISAQTRARNGELYR 660
 QY 659 YIADTHGAFVOPALYEAFTGLVYEAFTGLVYEAFTGLVYEAFTGLVYEAFTGLVYEAFT 718
 DB 661 YIADTHGAFVOPALYEAFTGLVYEAFTGLVYEAFTGLVYEAFTGLVYEAFTGLVYEAFT 720
 QY 719 AVNIMADFFRCKODPDHWVVISAGLORITEXTKTKIYSEKRLTLAGVYGMKVSGLBE 778
 DB 721 AVNIMADFFRCKODPDHWVVISAGLORITEXTKTKIYSEKRLTLAGVYGMKVSGLBE 780
 QY 779 RLETRRYIEMYYILKPRELAKTVELAID 806

CC cofactors, and enzymes in microorganisms and plants. Additionally, the
CC LMP nucleic acid and protein may be used in identifying an organism as
CC being Arabidopsis thaliana, as markers for specific regions of the
CC genome, and in evolutionary and protein structural studies. Sequences
CC ABR3572-587 represent A. thaliana LMP sequences

XX Sequence 797 AA;

Query Match 73.74; Score 3129; DB 6; Length 797;
Best Local Similarity 74.14; Pred. No. 5e-272;
Matches 580; Conservative 192; Mismatches 99; Indels 2; Gaps 2;

```

QY 27 LVALLSKYVKKGKILQPHILIDA-IDEVQSGG-VRALAEGPFLDVRSAQEAIVLPPEV 84
D 14 LVIVTPIRYVAQGGKILQSHQLIDFELKTVKVDGTLIDLNKSPFMKVLQSAEKAIVLPPEV 73
QY 85 AIAVRRPGVWEYVYVNVHLSVEQLTVSEYLFKSELYDQNDPYVLEDEPPNVSV 144
D 74 ALAIRBPGVREVYVNVVELSVDELTVSEYLFKSELYVGHANGDYLLLELDEPPNATL 133
QY 145 PPRNRSSISGNGVQFLNRHLSIMFRNRDCLPEFLDLGRHKGHVMMLNDRIGSLGR 204
D 134 PPRNRSSISGNGVQFLNRHLSIMFRNRKSMELFLERLTHKHDGRPMMLNDRIGSLGR 193
QY 205 QSVLTKAEELSKLADTPYSGPAKFEQEWLEKMGDITAGHYLEMILHLLDITIQAPDS 264
D 194 QGALARAEELSKLPLATPYSEFELOQMGFERMGDTQAKVSEMHLLDITIQAPDS 253
QY 265 TLEKFLGRIPMTNVYVYVPHGFFGQANVLGLPDTGGQIVYIILDORALENEVALLKQ 324
D 254 VLETFGRIPMTNVYVYVPHGFFGQANVLGLPDTGGQIVYIILDORALENEVALLKQ 313
QY 325 GLDVSKILITVTLIDAGKTSQNOPLERISGTOHTYTLVPRNENKILKKMISRPDW 384
D 314 GLDVSKILITVTLIDAGKTSQNOPLERISGTOHTYTLVPRNENKILKKMISRPDW 373
QY 385 PYLETAEADAGEIAELQSTPDIIGNVSDGNLVASLSTYKMTQCNIAHALKTKYP 444
D 374 PYLETAEADAGEIAELQSTPDIIGNVSDGNLVASLSTYKMTQCNIAHALKTKYP 433
QY 445 DSDIFMKNFDEKTHSCQFTADILIMANNADPITSTYQAGSKNNTYGGYESTAFLLPG 504
D 434 ESDIFMKNFDEKTHSCQFTADILIMANNADPITSTYQAGSKNNTYGGYESTAFLLPG 493
QY 505 LRVYVAGIVDFDKEKIVSPGADMSIYFPHTEKAPLTSIHSLNLIYDEGNDEIGH 564
D 494 LRVYVAGIVDFDKEKIVSPGADMSIYFPHTEKAPLTSIHSLNLIYDEGNDEIGH 553
QY 565 LDDRSXPILFEMARLDRVKNITGLVEAFKACAKLRELVNLVYVAGYNDVYKSKOREIAE 624
D 554 LDDRSXPILFEMARLDRVKNITGLVEAFKACAKLRELVNLVYVAGYNDVYKSKOREIAE 613
QY 625 TEMMELLKTHNLPGCFRMTSAQTNBARKNGELRYIADOTGAVOPALYAEGLTYEAM 684
D 614 IOMHSLLEQYDLHGFEFRWIAQMNRAKNGELRYIADOTGAVOPALYAEGLTYEAM 673
QY 685 TCOLPFEATLHGGPAILIEHVGSGFIIDPYHPQAVNLMAFDKCGKODPDHVNISGAG 744
D 674 TCOLPFEATLHGGPAILIEHVGSGFIIDPYHPQAVNLMAFDKCGKODPDHVNISGAG 733
QY 745 LQRIYKRYTAKLYSEBLMTLAGYGFVKVSKLERLETRRYLTMFYILKRELAQVPLA 804
D 734 LKRIYKRYTAKLYSEBLMTLAGYGFVKVSKLERLETRRYLTMFYILKRELAQVPLA 793
QY 805 TDQ 807
D 794 TDE 796

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RESULT 6
ABR33752
ID ABR33752 standard; protein; 805 AA.
XX

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AC ABR33752;
XX
XX 31-MAY-2002 (first entry)
DT
XX
XX Herbicidally active polypeptide SEQ ID NO 2963.
DE
XX Herbicidal; plant; agriculture; herbicide.
XX
XX Arabidopsis thaliana.
XX
XX W0200210210-A2.
XX
XX 07-FEB-2002.
XX
XX 28-AUG-2001; 2001MO-EP009892.
XX
XX 28-AUG-2001; 2001MO-EP009892.
XX
XX (FARB ) BAYER AG.
XX
XX Tietjen K, Weidler M;
XX
XX WPI; 2002-269010/31.
XX
XX Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms.
XX
XX Claim 5; SEQ ID NO 2963; 261pp + Sequence Listing; English.
XX
XX
XX The invention relates to identifying target proteins (ABR90790-ABR94016)
XX for herbicidally active compounds, comprising aligning and comparing
XX nucleic acid or amino acid sequences from plant with nucleic acid or
XX amino acid sequences from non-plant organisms using suitable search
XX parameters, where plant sequences having an E-value greater by a factor
XX of 3 than the E-value of most similar non-plant sequences are selected.
XX The polypeptides or nucleic acids encoding them are useful for
XX identifying modulators. The identified modulators are useful as
XX herbicides
XX
XX Sequence 805 AA;
XX
XX
XX Query Match 73.24; Score 3108.5; DB 5; Length 805;
XX Best Local Similarity 74.34; Pred. No. 3.6e-270;
XX Matches 579; Conservative 98; Mismatches 97; Indels 5; Gaps 3;
QY 31 LSKYVKKGKILQPHILIDA-IDEVQSGG-VRALAEGPFLDVRSAQEAIVLPPEV 88
D 29 LRVYVAGKGIILQSHQLIDFELKTVKVDGTELDLNKSPFMKVL--QEAIVLPPEV 85
QY 89 RPRPGVWEYVYVNVHLSVEQLTVSEYLFKSELYDQNDPYVLEDEPPNVSVPRN 148
D 86 RPRPGVWEYVYVNVHLSVEQLTVSEYLFKSELYDQNDPYVLEDEPPNVSVPRN 145
QY 149 RSSISGNGVQFLNRHLSIMFRNRDCLPEFLDLGRHKGHVMMLNDRIGSLGR 208
D 146 RSSISGNGVQFLNRHLSIMFRNRKSMELFLERLTHKHDGRPMMLNDRIGSLGR 205
QY 209 TKAEEHLSKLPADTPYSGPAKFEQEWLEKMGDITAGHYLEMILHLLDITIQAPDS 268
D 206 TKAEEHLSKLPADTPYSGPAKFEQEWLEKMGDITAGHYLEMILHLLDITIQAPDS 265
QY 269 FLGRIPMTNVYVYVPHGFFGQANVLGLPDTGGQIVYIILDORALENEVALLKQ 328
D 266 FLGRIPMTNVYVYVPHGFFGQANVLGLPDTGGQIVYIILDORALENEVALLKQ 325
QY 329 SPKILITVTLIDPAKTSQNOPLERISGTOHTYTLVPRNENKILKKMISRPDW 388
D 326 IPKILITVTLIDPAKTSQNOPLERISGTOHTYTLVPRNENKILKKMISRPDW 385
QY 389 TPAEDAGETIAALQSTPDIIGNVSDGNLVASLSTYKMTQCNIAHALKTKYP 448
D 389 TPAEDAGETIAALQSTPDIIGNVSDGNLVASLSTYKMTQCNIAHALKTKYP 448

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Dc 386 TEADNASNEISAELOGVNLLIGNYSDGNLVASLLASKLGVIOCNIAHALEKTKYPSDI 445
Qy 449 FKNPDEKXHSOCOTADIIAMNNADFIITSTYOEIAGSKNVGVGESHATATLLEGLRV 508
Db 446 YWRNEDKXHSFSSQFTADIIAMNNADFIITSTYOEIAGSKNVGVGESHATATLLEGLRV 505
Qy 509 VHGIVFDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSIEMLIYDPEONDEHIGLDDR 568
Db 506 VHGIVFDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSIEMLIYDPEONDEHIGLDDR 565
Qy 569 SKPIIFSMARLDKRVNLTGLVEAFKACAKLRELVLVAVVAGYNDVNSKDRBEIAIEKM 628
Db 566 SKPIIFSMARLDKRVNLTGLVEAFKACAKLRELVLVAVVAGYNDVNSKDRBEIAIEKM 625
Qy 629 HELIKTHNLFGQFRMISAQTRARANGELYRYTADTHGAFVOPALYEAFLTYVEANTCG 688
Db 626 HSLIEQYDLHGFRFWIAQOMNRRANGELYRYTADTHGAFVOPALYEAFLTYVEANTCG 685
Qy 689 PFEATLHGAPALIEHGVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 748
Db 686 PFEATLHGAPALIEHGVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 745
Qy 749 YERYTWKLYSERLMTLAGVYGFVKVYSKLELRETRRYLEMFIYILKRELAKTVPLAIDQ 807
Db 746 YERYTWKLYSERLMTLAGVYGFVKVYSKLELRETRRYLEMFIYILKRELAKTVPLAIDQ 804

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RESULT 7

ABR39585

ABR39585 standard; protein; 805 AA.

AC ABR39585;

DT 12-JUN-2003 (first entry)

DE A. thaliana lipid metabolism protein (LMP)-clone ID PK118.

KM Lipid metabolism protein; LMP; seed storage; plant; transgenic.

OS Arabidopsis thaliana.

PN W02C03014376-A2.

PD 20-FEB-2003.

PR 12-AUG-2002; 2002W0-US025586.

PR 10-AUG-2001; 2001US-0311414P.

PA (BADI) BASF PLANT SCI GMBH.

PI Miltendorf V, Haertel H, Cäpurs P;

DR WPI, 2003-256595/25.

DR N-PSDB; A3276371.

XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 XX producing transgenic plants, for modulating seed storage compounds, e.g.
 XX lipid or fatty acid, in plants, and for evolutionary and protein
 XX structural studies.

PS Claim 2; Fig 12B; 108pp; English.

XX The invention relates to isolated lipid metabolism proteins (LMP) and
 XX polynucleotides. The LMP functions as a modulator of seed storage
 XX compound in a plant. The LMP nucleic acid and protein are useful in
 XX producing transgenic plants and in modulating the levels of seed storage
 XX compounds. These are used to modify or increase lipids and fatty acids,
 XX cofactors, and enzymes in microorganisms and plants. Additionally, the
 XX LMP nucleic acid and protein may be used in identifying an organism as
 XX being Arabidopsis thaliana, as markers for specific regions of the
 XX genome, and in evolutionary and protein structural studies. Sequences
 XX ABR39572-587 represent A. thaliana LMP sequences

XX Sequence 805 AA;
 SQ

Query Match 73.2%; Score 3108.5; DB 6; Length 805;
 Best Local Similarity 74.3%; Pred. No. 3.6e-270;
 Matches 579; Conservative 98; Mismatches 97; Indels 5; Gaps 3;

```

Qy 31 LSKYNNKKGKGLIOPHHILDA-LDEVQSGC-YKALAEGLPDLVRSKQAVIYPPFVAIAV 88
Db 29 LVRIYAQKGKGLIOPHHILDA-LDEVQSGC-YKALAEGLPDLVRSKQAVIYPPFVAIAV 85
Qy 89 RRPFGVMEYVRVNVNHELVEQLTVSEYLRFKEELVDGQNDPVLDELFPFNVSVPRN 148
Db 86 RRPFGVMEYVRVNVNHELVEQLTVSEYLRFKEELVDGQNDPVLDELFPFNVSVPRN 145
Qy 149 RASSTGNGVQPLNRLHSSIMFERNRCLEPDLPLAGHKKGVNMLNDISQISGRQSVL 208
Db 146 RASSTGNGVQPLNRLHSSIMFERNRCLEPDLPLAGHKKGVNMLNDISQISGRQSVL 205
Qy 209 TKAEBHLKLPADPTYSOPAYKFOEMGLEKMGDTAGHVLNMLHLLDILIOAPDPSTLAK 268
Db 206 TKAEBHLKLPADPTYSOPAYKFOEMGLEKMGDTAGHVLNMLHLLDILIOAPDPSTLAK 265
Qy 269 FLGRIPMLNENNVVSPHGVFGQANYLGLPDTGQIVYILDOYRA-ENENWVRLKKGGLDY 328
Db 266 FLGRIPMLNENNVVSPHGVFGQANYLGLPDTGQIVYILDOYRA-ENENWVRLKKGGLDY 325
Qy 329 SPKILIVTRLIPDAKGTSCNORLEBISGQHTYILRPVRNENGLKMKISRPDWPYLE 388
Db 326 SPKILIVTRLIPDAKGTSCNORLEBISGQHTYILRPVRNENGLKMKISRPDWPYLE 385
Qy 389 TEADNASNEISAELOGVNLLIGNYSDGNLVASLLASKLGVIOCNIAHALEKTKYPSDI 448
Db 386 TEADNASNEISAELOGVNLLIGNYSDGNLVASLLASKLGVIOCNIAHALEKTKYPSDI 445
Qy 449 FKNPDEKXHSOCOTADIIAMNNADFIITSTYOEIAGSKNVGVGESHATATLLEGLRV 508
Db 446 YWRNEDKXHSFSSQFTADIIAMNNADFIITSTYOEIAGSKNVGVGESHATATLLEGLRV 505
Qy 509 VHGIVFDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSIEMLIYDPEONDEHIGLDDR 568
Db 506 VHGIVFDPKFNIVSPGADMSIYPPHTEKAKRLTSLHGSIEMLIYDPEONDEHIGLDDR 565
Qy 569 SKPIIFSMARLDKRVNLTGLVEAFKACAKLRELVLVAVVAGYNDVNSKDRBEIAIEKM 628
Db 566 SKPIIFSMARLDKRVNLTGLVEAFKACAKLRELVLVAVVAGYNDVNSKDRBEIAIEKM 625
Qy 629 HELIKTHNLFGQFRMISAQTRARANGELYRYTADTHGAFVOPALYEAFLTYVEANTCG 688
Db 626 HSLIEQYDLHGFRFWIAQOMNRRANGELYRYTADTHGAFVOPALYEAFLTYVEANTCG 685
Qy 689 PFEATLHGAPALIEHGVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 748
Db 686 PFEATLHGAPALIEHGVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 745
Qy 749 YERYTWKLYSERLMTLAGVYGFVKVYSKLELRETRRYLEMFIYILKRELAKTVPLAIDQ 807
Db 746 YERYTWKLYSERLMTLAGVYGFVKVYSKLELRETRRYLEMFIYILKRELAKTVPLAIDQ 804

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RESULT 8

AAE28503

AAE28503 standard; protein; 773 AA.

AC AAE28503;

DT 27-DEC-2002 (first entry)

DE Maize sucrose synthase consensus protein.

XX Sucrose synthase; shrunken-1; SH1; constitutive sucrose synthase; Su1;
 XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 XX cellulose; maize.

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XX Zea mays.
OS
XX MO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helemtjaris TG, Nin X;
XX
XX WPI; 2002-691625/74.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Example 9; Fig 8; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Susi) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is maize sucrose synthase consensus protein
XX
XX Sequence 773 AA;
XX
XX Query Match 72.1%; Score 3060.5; DB 5; Length 773;
XX Best Local Similarity 76.7%; Pred. No. 7e-266;
XX Matches 614; Conservative 72; Mismatches 86; Indels 29; Gaps 21;
XX
XX 6 LNRNASTIRDPVEPTLHAHNEELVALSKYVNGKGILOPHHITDALDEVGSGVRLAEG 65
XX 1 LSRHLSLRERIGTGLSAHPNEELVALSKRYN-GKGMLOPHQILAEFDADAC--RSLKDG 57
XX
XX 66 PFLDVLRSAGQEAIVLPPFAIAVAPRGVWEYRVVNHLSVQELTVSEYLRKEELVDG 125
XX 58 PFEDVLRAGQEAIVLPPWALAIRPRGVWEYRVVNSVLAELSVSEYL-FKEQLVDG 116
XX
XX 126 QHNDPVYLEIDFPEPVSVPRENKSISNGVOFLNRHLSLIMFARNDCLEPLDPLRGH 185
XX 117 QNN--FVLEIDFPEPVASPRPSLSKISNGVOFLNRHLSKLF-DESLYPLINFLRAH 173
XX
XX 186 RHNGHYVMANDRIQSLGLOSVLTKAEHNSKLPADPYGSAFYKFOEMLEKMGDPDAG 245
XX 174 RYNG-TMELNDRIQSLA-LQSALRKAEHNSLPADPYSEF-HRQGLGLEKMGDPDAG 230
XX
XX 246 HYLEMTHLLDIIQADPSTLEKFLGRIPMIFNVVVVSPRGYEQANVLGLPDTGGQIVY 305
XX 231 RYLETHLLDLEADPSTLEKFLGRIPMIFNVVVVSPRGYEQANVLGLPDTGGQIVY 290
XX
XX 306 ILDQYALRENMRLKQGLDVSPTLITRLIPDAKGSQORLERISGTOHTYLRV 365
XX 291 ILDQYALRENMRLKQGLDITPKLITRLIPDA-GTTCORLEKVGISTHTHLRV 349
XX
XX 366 PFENKNGILKKWISREFDVWYLETFAEDAGETAAELQGPDPFLIGYSGNIVASLISY 425
XX 350 PFENKNGILKKWISREFDVWYLETYEDVA-ETAAELQ-APDLIGYSGNIVASLISAH 407
XX
XX 426 KMGITQCNIAALEKTKYRPSDIFMKNFDEKYPHSCQFTADIIAMNADPITSTYQRIA 485
XX 408 KMGVTOCTIAHALEKTKYRPSDIYWKKFD-YHPSQCFADLIAMNADPITSTFOBIA 466

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XX 486 GSKNTGYOYESHAFITLPGLYRVVHGIWVDEPKENIVSPGADMSIYEPHTEKARLTSLH 545
XX 467 GSKDTYGQYESHAFITLPGLYRVVHGIWVDEPKENIVSPGADMSIYEPHTEKARLTSLH 525
XX
XX 546 GSIEENLYDPEONDEHIGLIDRSKPLISGMARLDKVNITGLVEAFKAKALBELVNLV 605
XX 526 PATEHILY--SENSEKFLVD--RKPIIPSMARLDKVNITGLVEAFKAKALBELVNLV 581
XX
XX 606 VVAGINDVMSKORBEIAIEKHELIKTHNLFGQFRMISAQTRKANGELIYRIADTGH 665
XX 582 VVAGDHC---SKDRERQAEFKQKHDLI-DYNL-GHIRMISAQMRVANGELIYRIADTGH 636
XX
XX 666 AFVQAPAYEAPGLTVQAMTCGLPTFATLKGPAEIIIEHGVSGFHIDPYHDKAA--LIVD 725
XX 637 AFVQAPAYEAPGLTVQAMTCGLPTFAT-HQGPABIIIVHGVSGFHIDPYHDKAA--LIVD 693
XX
XX 726 FPDRCQDDPDHWNISGAGLQRIYEKTYKISERLMTLAGVYGFMYKYSKLELERTRY 785
XX 694 FPDRCQDDPDHWN--IQGGIQRIVYEKTYKISERLMTLAGVYGFMYKYSKLELERTRY 751
XX
XX 786 LEMFYTLKREELAKTYPLAID 806
XX 752 LEMFYTLKREELAKTYPLAID 772
XX
XX RESULT 9
XX AAE28500
XX ID AAE28500 standard; protein; 802 AA.
XX
XX AAE28500;
XX
XX 21-DEC-2002 (first entry)
XX
XX Corn sucrose synthase shrunken-1 (Sh1) protein.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; chromosome 9.
XX
XX Zea mays.
XX
XX MO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helemtjaris TG, Nin X;
XX
XX WPI; 2002-691625/74.
XX
XX N-PSDB; AAD45851.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Example 9; Page 108-110; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Susi) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement

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CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sh1 protein. Corn Sh1 gene is located at chromosome 9
 XX
 SQ Sequence 802 AA;

Query Match 70.9%; Score 3011.5; DB 5; Length 802;
 Best Local Similarity 70.0%; Pred. No. 1,9e-261;
 Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;

```

QY 3 APLNNASIRDRVEDTTHAARELVALLSKYNNKKGILLPHHLLDALDEVQSGVRL 62
DB 2 AAKLFTLSRLRGATFSSHPNELTALSRYVHQKMLQHRQLAEPDALFDSDEKX 61
QY 63 AAGPLDVRSAOEAIVLPFVALAPRPGVWERYVNVVHLSNEQLVSEYLRKEEL 122
DB 62 A--PEEDILRAOEAIVLPFVALAPRPGVWDYIRVNVSELSVSEYLRKEEL 119
QY 123 VDGQNDPYVLELDEEPFNASVPRPSSSIGNGVOFLNRHLSIMFNRCLEPLDPL 182
DB 120 VDGQNSNRYVLELDEEPFNASVPRPSSSIGNGVOFLNRHLSKLFQKESYIPILNLT 179
QY 183 RGRHKGHWMLNDRIQSLGRLQSVITKAEHLSKLPADTPYSQPAKYKQEMGLEKMGD 242
DB 180 KAHNYKGTMTMDRIQSLRGLOSSIRKAEYLLSVPODTPYSEFNRHFOELGLEKMGD 239
QY 243 TAGHVLMTHTLDDIQAAPPSTLEKELGRIPMEVNVVSPHGYGQANVLGLPTGGQ 302
DB 240 TAKRVLDITHTLDDLEAPDPANLEKFLGTIPMEVNVVLSFNGYKQSVGLPTGGQ 299
QY 303 IYVILDOVRALNEMVLRKKGQGLDVSPKILVTRLLIPDAKTSQNRLEISGTOHYI 362
DB 300 VYIILDOVRALNEMVLRKKGQGLDITPILVITRLPDAAGTCGQRLKXVIGTHETDI 359
QY 363 IAVPRNENKILKMWISRPDWPVYLTFAEDNAGETIAELQSTPDPIIGNSDGNVSL 422
DB 360 IAVPRNENKILKMWISRPDWPVYLTETEDVSEIMKEMQAKPDILIGNSDGNVSL 419
QY 423 LSYKQGITQCNLAHALEKTKYPSDIPFMNPFDEKVFSCQFADIIAMNADPIITSTQ 482
DB 420 LNAKRGVTOCTLAHALEKTKYPSDIPFMNPFDEKVFSCQFADIIAMNADPIITSTQ 479
QY 483 ELASGNVYQYSESHAFITLPGLYRVVHGIDVDPKYNVSPGADMSIYFPHTEKAKRL 542
DB 480 ELASGNVYQYSESHAFITLPGLYRVVHGIDVDPKYNVSPGADMSIYFPHTEKAKRL 539
QY 543 SLHGSITENLIYDEQNDHEHIGLDRSKPILSMANLDKRYKNTGLVZAFKCAKARELY 602
DB 540 AEPHEIEELIYSDVENSEHKEFVLRKDKKPIIFSMARLDKRYKNTGLVEMGXARLEDA 599
QY 603 NIVVAVGVNDVYNSKDRSEIASEIERKHELIKTNHLSGQFPMISAOITNRAANGELYIAD 662
DB 600 NIVVAVGVNDVYNSKDRSEIASEIERKHELIKTNHLSGQFPMISAOITNRAANGELYIAD 658
QY 663 TGAFAVQAPALYEAFTLVEAMTCGLPTATLHGGAELIIEHVSQPHIIDPYHPEQAVNL 722
DB 659 TGAFAVQAPALYEAFTLVEAMTCGLPTATLHGGAELIIEHVSQPHIIDPYHPEQAVNL 718
QY 723 MADPFRCKQCPDRHVNITSGAGIQRIYKKTWKIYSESLMTLAGVGFPMKYYSKLERLE 782
DB 719 LVYFFPKACADPBYWEISQGGIQRIYKKTWKIYSESLMTLAGVGFPMKYYSKLERLE 778
QY 783 RRYLEMEYILKPEELAKVPLAID 806
DB 779 RRYLEMEYILKPEELAKVPLAID 802

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RESULT 10

AA85664
 AA85664 standard; protein; 808 AA.

AC AA85664;
 XX
 DT 13-FEB-2001 (first entry)

XX Rice sucrose synthase amino acid sequence.
 DB
 XX Cold resistance; transgenic plant; sucrose decomposition; rice;
 KM sucrose synthase.
 XX

OS Oryza sativa.

PN JP2000245279-A.

PD 12-SEP-2000.

PF 01-MAR-1999; 99JP-00052102.

PR 01-MAR-1999; 99JP-00052102.

XX (MITA) MITSUI CHEM INC.

DR WPI; 2000-675173/66.

DR N-PSDB; AAC66090.

PT Novel method for the reinforcement of cold resistance in a plant
 PT comprising introducing a vector encoding an enzyme that decomposes
 PT sucrose into the plant.

PS Disclosure; Page 8-11; 22pp; Japanese.

CC This invention relates to a method for the reinforcement of cold
 CC resistance in a plant, comprising introducing an expression vector having
 CC a DNA encoding an enzyme for decomposing sucrose connected downstream to
 CC a promoter expressible in the plant, and expressing the enzyme in the
 CC plant body. Included in the invention are an expression vector used in
 CC the method; a transformed plant carrying the expression vector; and a
 CC transformed rice carrying the above expression vector. The method is used
 CC for reinforcing cold resistance in a plant. The present sequence
 CC represents a sucrose synthase protein used in the method
 XX

SQ Sequence 808 AA;

Query Match 70.8%; Score 3006.5; DB 3; Length 808;
 Best Local Similarity 69.8%; Pred. No. 5,5e-261;
 Matches 565; Conservative 103; Mismatches 127; Indels 15; Gaps 3;

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QY 3 APLNNASIRDRVEDTTHAARELVALLSKYNNKKGILLPHHLLDALDEVQSGVRL 62
DB 2 AAKLFTLSRLRGATFSSHPNELTALSRYVHQKMLQHRQLAEPDALFDSDEKX 61
QY 63 A--PEEDILRAOEAIVLPFVALAPRPGVWERYVNVVHLSNEQLVSEYLRKEEL 116
DB 62 A--PEEDILRAOEAIVLPFVALAPRPGVWDYIRVNVSELSVSEYLRKEEL 113
QY 117 RPKKEELVDSQNDPVTLELDEEPFNASVPRPSSSIGNGVOFLNRHLSIMFNRCLE 176
DB 114 APEQULVDGHTNSFVLELDEEPFNASVPRPSSSIGNGVOFLNRHLSIMFNRCLE 173
QY 177 PLIDFLRGHKGHWMLNDRIQSLGRLQSVITKAEHLSKLPADTPYSQPAKYKQEMGLE 236
DB 174 PLNFTKANHNGKTMMDRIQSLGRLQSVITKAEHLSKLPADTPYSQPAKYKQEMGLE 233
QY 237 EKMGWDTAGHYLEMTHTLDDIQAAPPSTLEKELGRIPMEVNVVSPHGYGQANVL 296
DB 234 EKMGWDTAGHYLEMTHTLDDIQAAPPSTLEKELGRIPMEVNVVSPHGYGQANVL 293
QY 297 PDGGOVYIILDOVRALNEMVLRKKGQGLDVSPKILVTRLLIPDAKTSQNRLEISG 356
DB 294 PDGGOVYIILDOVRALNEMVLRKKGQGLDVSPKILVTRLLIPDAKTSQNRLEISG 353
QY 357 TQHTYILRVPRNENKILKMWISRPDWPVYLTFAEDNAGETIAELQSTPDPIIGNSD 416
DB 354 TQHTYILRVPRNENKILKMWISRPDWPVYLTFAEDNAGETIAELQSTPDPIIGNSD 413
QY 417 NIVASLSTKMGITQCNLAHALEKTKYPSDIPFMNPFDEKVFSCQFADIIAMNADPI 476

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D5 414 KMWATLAAHLGVTQCTIAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNATDFI 473
QY 477 TSTVOELAGSKNTGQGYSHTAFTPGIYRYVHGIDVCDPKNTYSPADMSIYPHPE 536
DB 474 TSTVOELAGSKNTGQGYSHTAFTPGIYRYVHGIDVCDPKNTYSPADMSIYPHPE 533
QY 537 KAKRLTSLGSGTBNLYDPEONDEHGHLDSSKPIIFPMARLDRYONTGTGVEAFKCA 596
DB 534 AKKRLTAFFPELBEILYSVEENDEHFPVLKDKNKPIIFSYARLDRYONTGTGVEAFKCA 593
QY 597 KLRLEYNLVVAGYNDVYKSDREELAEIEKMHLEIKTNLFGQFPMISAQTNRAANGEL 656
DB 594 HRDLANLIVYVG-DHGNQSKOREBAEFKKMYGGLDQYKMKHINWISAQNMRYANGEL 652
QY 657 YRIADTGAFTQPALYEAFGLTVYEAATCGLPTATLHGPAETIEHVSGFHIDPHYE 716
DB 653 YRICTKGVFVQPAYEAFGLTVYEAATCGLPTATLHGPAETIEHVSGFHIDPHYE 712
QY 717 EDAVNLMADEFRCODPDHWNISGAGLQRIYEKTYKTIYSERLMTLAGVYGFMYKYSK 776
DB 713 DKAADLVNPFCKODSTYMDNISGGLORIYEKTYKTIYSERLMTLAGVYGFMYKYSK 772
QY 777 LRLLETRRYLMEFYLIKEREIAKTVPDLAID 806
DB 773 LRRERTRRYLMEFYLIKEREIAKTVPDLAID 802

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RESULT 11
AAE28501 standard; protein; 816 AA.

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ID AAE28501 standard; protein; 816 AA.
AC AAE28501;
DT 27-DEC-2002 (first entry)
DE Corn sucrose synthase (Sus1).
XX Sucrose synthase; shrunken-1; SH1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; chromosome 9.
XX Zea mays.
XX MO200267662-A1.
PD 06-SEP-2002.
XX 21-FEB-2002; 2002WC-TS005137.
XX 22-FEB-2001; 2001US-0270777P.
PA (PION-) PIONEER HI-BRED INT INC.
PI Dhauga KS, Helentjaris TG, Niu X;
XX WPI; 2002-691625/74.
XX N-PSDB; AAD45852.
XX New polynucleotide and its encoded sucrose synthase, useful for
PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT or soybean) to improve stalk length, reduce grain breakage, or improving
PT plant or grain strength.

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Example 9; Page 114-115; 125pp; English.

The invention relates to two sucrose synthases, shrunken-1 (Sh1) and constitutive sucrose synthase (Sus1) and their corresponding nucleic acids. The polynucleotide, or its encoded protein, is useful for modulating the level of sucrose synthase in a transgenic plant, increasing cellulose production in the stalk tissue of a transgenic plant, or increasing the concentration of cellulose in the tissues of a seed of a transgenic plant. This is particularly useful in plant (e.g. maize or soybean) breeding, especially for e.g. improving stalk length in

CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is corn Sus1 protein. Corn Sus1 gene is located at chromosome 9
XX
SQ Sequence 816 AA;

Query Match 70.6%; Score 2997; DB 5; Length 816;
Best local similarity 69.8%; Pred. No. 4e-260;
Matches 562; Conservative 107; Mismatches 128; Indels 8; Gaps 3;

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QY 6 LKRNASIRDRVEDTTLAHNRNELVALISKYNNKSGILQPHHIL---DALDEVOGSCVRA 61
DB 10 LSRHSVRRIIGDLSLAHPELVAFAVFTRLNLSKGMLOPHQIIAEYNNALPEAER---EK 66
QY 62 LAGPFLDYIRSAQOEAIVLPZFYAIVAPRPQGWYVYVNVNHLSTVQGLVSEYLRKEE 121
DB 67 LKGAPEDEVYRAQOEAIVLPZFYAIVAPRPQGWYVYVNVNHLSTVQGLVSEYLRKEE 126
QY 122 LVDSQHNDFVYELDEPEPEVSVPRPSSSINGVOFLNRHLSTLMFRNRDCLPELDF 181
DB 127 LVDSQHNDFVYELDEPEPEVSVPRPSSSINGVOFLNRHLSTLMFRNRDCLPELDF 186
QY 182 LRGRHKGVMMLNDRISQISGLQSVITKAEELSKLPADTPYSQPAKYQEWGLEKMG 241
DB 187 LRANHYKGMTMMLNDRISQISGLQSVITKAEELSKLPADTPYSQPAKYQEWGLEKMG 246
QY 242 DTGAGVLEMTHTLDDIIOADPSTLEKEGRIIMIYVNVVSVPHGYGQANVGLPPTGG 301
DB 247 DCKRAQETHHLDDLEADPSTLEKEGRIIMIYVNVVSVPHGYGQANVGLPPTGG 306
QY 302 QIVYILDQVRLNEMWLRKQGLDVSFKILVTRLLIPAKGTSNQRERISGTOHTY 361
DB 307 QVYIILDQVRLNEMWLRKQGLDVSFKILVTRLLIPAKGTSNQRERISGTOHTY 366
QY 362 ILRVPFRNENGILKKWISRPDVPYLTFABDAAAGETAAELQSTPDTILGYSNGNLVAS 421
DB 367 ILRVPFRNENGILKKWISRPDVPYLTFABDAAAGETAAELQSTPDTILGYSNGNLVAS 426
QY 422 LLSYKMGITQCNLAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNADFLITSTY 481
DB 427 LLAHKGAVTHCTIAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNADFLITSTY 486
QY 482 QELAGSKNTGQGYSHTAFTPGIYRYVHGIDVCDPKNTYSPADMSIYPHPEKAKRL 541
DB 487 QELAGSKNTGQGYSHTAFTPGIYRYVHGIDVCDPKNTYSPADMSIYPHPEKAKRL 546
QY 542 TSLHGSTENTLYDPEONDEHGHLDSSKPIIFPMARLDRYONTGTGVEAFKCAKAREL 601
DB 547 TSLHPEIEELLYSQTEHTEHGFVLDNRNKPIIFPMARLDRYONTGTGVEAFKCAKAREL 606
QY 602 VNLVYVAGYNDVYKSDREELAEIEKMHLEIKTNLFGQFPMISAQTNRAANGELYRYIA 661
DB 607 VNLVYVAGYNDVYKSDREELAEIEKMHLEIKTNLFGQFPMISAQTNRAANGELYRYIA 665
QY 662 DTGAFVQPALYEAFGLTVYEAATCGLPTATLHGPAETIEHVSGFHIDPHYEQAQVN 721
DB 666 DTGAFVQPALYEAFGLTVYEAATCGLPTATLHGPAETIEHVSGFHIDPHYEQAQVN 725
QY 722 LMADEFRCODPDHWNISGAGLQRIYEKTYKTIYSERLMTLAGVYGFMYKYSGLDELE 781
DB 726 LMADEFRCODPDHWNISGAGLQRIYEKTYKTIYSERLMTLAGVYGFMYKYSGLDELE 785
QY 782 TRRYLMEFYLIKEREIAKTVPDLAID 806
DB 786 TRRYLMEFYLIKEREIAKTVPDLAID 810

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RESULT 12
ADC07856 standard; protein; 816 AA.

ID ADC07856
AC ADC07856;
XX

18-DEC-2003 (first entry)
 Rice protein sequence Seq ID122 related to grain filling.
 plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 gene; ds; plant.
 Oryza sativa.
 WO200300905-A2.
 03-JAN-2003.
 21-JUN-2002; 2002WO-IB002450.
 22-JUN-2001; 2001US-0300112P.
 26-SEP-2001; 2001US-0325277P.
 20-DEC-2001; 2001US-0342327P.
 (SYGN) SYNGENTA PARTICIPATIONS AG.
 (Zhu T, Briggs W, Briggs S, Cooper B, Goff SA, Moughamer T,
 Gizebrook U, Katagiri F, Kreps J, Provart N, Rieke D;
 WPI; 2003-229341/22.
 N-PSDB; ADC07855.
 New plant genes encoding polypeptides having an activity involved in or
 associated with the synthesis, metabolism or degradation of carbohydrates
 in the plant grain useful in generating plants having improved
 nutritional properties.
 Claim 1; SEQ ID NO 122; 130bp; English.
 This invention, in the area of plant biotechnology, relates to novel
 polynucleotides comprising a nucleotide sequence encoding a protein which
 is involved in or associated with the synthesis, metabolism or
 degradation of carbohydrates in the plant grain and the expression of
 which is up-regulated during grain filling. The plant is selected from
 corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 sugarbeet, wheat, and rice. The invention may be useful for the
 improvement of protein, oil, starch, fibre and moisture content of the
 cereal grains. In addition, carbohydrate levels may be modified to a more
 desirable level using the present invention. The present sequence is the
 amino acid sequence of a rice protein of the invention. Note: The
 sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/publisthedpct_sequences.
 Sequence 8-6 AA;
 Query Match 70.3%; Score 2985; DB 7; Length 816;
 Best Local Similarity 69.7%; Pred. No. 4,8e-259;
 Matches 561; Conservative 107; Mismatches 129; Indels 8; Gaps 3;
 6 INRNASIRDRVDTLHAHNEIYALISKYVKKGKGLQPHHL----DALDEVQSSGVA 61
 10 ISRLHSVRERIGDSIAHNEIYALISKYVKKGKGLQPHHL----DALDEVQSSGVA 66
 62 LAGPPLDYLRSAGEAIVLPFAIVAVRPGWVEYVAVVHLSYEQULTVSEYLAFFKEE 121
 67 LKQGAEDVLRSGQESIVTSPWALAIRPGWVEYVAVVHLSYEQULTVSEYLAFFKEE 126
 122 LVDGQNDPYVLELDEPFNVSVPRNRSSISNGVQFLNRHLSIMFNRDCELEPLDF 181
 127 LVEBGGNNKVELEIDPEFPNASFPRLSKSISNGVQFLNRHLSIMFNRDCELEPLDF 186
 182 LAGHRKGVVYVLTNDRIQSLGRQSVLTAAEHLSTLPADTPYSGAAYVQEWGLKGMG 241
 187 LRAHNYKGMVMTLNDRIQLSLGRQSVLTAAEHLSTLPADTPYSGAAYVQEWGLKGMG 246

242 DTAGVLEMIHLIDLIQAPDPSTLEKELGRIPMIFNVVVSPIGYSQAVNLGPDTCG 301
 247 DCAKRSQETIHLIDLIQAPDPSTLEKELGRIPMIFNVVVSPIGYSQAVNLGPDTCG 306
 302 QIVYILQVRLAEVRLKKGGLDVSFKLLITRLIPDAKGSNORLRISTORTY 361
 307 QVYVILQVRLAEVRLKKGGLDVSFKLLITRLIPDAKGSNORLRISTORTY 366
 362 ILRPFERNENGLIKKTSRFPVWPLYETFEADAGEIAAELOGCTPDPIIGNSDGNLVAS 421
 367 ILRPFERNENGLIKKTSRFPVWPLYETFEADAGEIAAELOGCTPDPIIGNSDGNLVAS 426
 422 LLSYMGITQCNIAHALEKTKYPSDIPWPKFDEKTHSCQPTADIIAMNADPITTSY 481
 427 LLAHMGVTHCTIALALEKTKYPSDIPWPKFDEKTHSCQPTADIIAMNADPITTSY 486
 482 CEIAGSKNTVQYQESHNAFTLPGLYRVHGDVPRPKNTVSGADMSTYPPHTEAKRL 541
 487 CEIAGSKNTVQYQESHNAFTLPGLYRVHGDVPRPKNTVSGADMSTYPPHTEAKRL 546
 542 TSLHGSTENLIYDPEQNDHEIGHLDPRSKPILFSMARLDRVKNITGLVEAFKACALREL 601
 547 TSLHGSTENLIYDPEQNDHEIGHLDPRSKPILFSMARLDRVKNITGLVEAFKACALREL 606
 602 VMLVAVAGYNDVNNKSKREBEIAIEKHEILKTHNLSCQFEMIQAQTNBARNGELYRYIA 661
 607 VMLVAVAGYNDVNNKSKREBEIAIEKHEILKTHNLSCQFEMIQAQTNBARNGELYRYIA 665
 662 LTRGAFVQPALYBAAGLYVYEAATGCLPFAALHAGPAITIHSGVGFHIDPHPQAVN 721
 666 DTKGAFVQPALYBAAGLYVYEAATGCLPFAALHAGPAITIHSGVGFHIDPHPQAVN 725
 722 LMADEPDCOKDPDMVNNISGAGLQRIYETWKIYSEILMTLAGYGFWKVYSKLERE 781
 726 LMADEPDCOKDPDMVNNISGAGLQRIYETWKIYSEILMTLAGYGFWKVYSKLERE 785
 782 TRRYLEMYIILKRELAKTVPLAID 806
 786 TRRYLEMYIILKRELAKTVPLAID 810
 RESULT 13
 ID ADC08209 standard; protein; 816 AA.
 AC ADC08203;
 DT 18-DEC-2003 (first entry)
 DE Rice protein sequence Seq ID514 related to grain filling.
 plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 gene; ds; plant.
 Oryza sativa.
 WO200300905-A2.
 03-JAN-2003.
 21-JUN-2002; 2002WO-IB002450.
 22-JUN-2001; 2001US-0300112P.
 26-SEP-2001; 2001US-0325277P.
 20-DEC-2001; 2001US-0342327P.
 (SYGN) SYNGENTA PARTICIPATIONS AG.
 (Zhu T, Briggs W, Briggs S, Cooper B, Goff SA, Moughamer T;

PI Glazebrook J, Karagiri F, Kreps J, Provart N, Rieke D;
 XX WPI, 2003-229341/22.
 DR N-PSDB; ADC684208.
 XX New plant genes encoding polypeptides having an activity involved in or
 XX associated with the synthesis, metabolism or degradation of carbohydrates
 XX in the plant grain useful in generating plants having improved
 XX nutritional properties.
 XX Claim 34; SEQ ID NO 514; 130bp; English.
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarcane, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wipo.int/pub/publishepct_sequences.
 XX
 XX Sequence 816 AA;
 SQ
 Query Match 70.3%; Score 2985; DB 7; Length 816;
 Best Local Similarity 69.7%; Pred. No. 4.8e-259;
 Matches 561; Conservative 107; Mismatches 129; Indels 8; Gaps 3;
 QY 6 LNBNASIRDRVETTHAHRENEVALSKYKNGKGLIOPHIL---DAIDVOGSGVRA 61
 DB 10 ISRLHSVRERIGDLSAHPVELVAVFTRNLGKGMLOAHQIIAYNNIASEADR--EK 66
 QY 62 LAEGPFLDYRSNOBALVLPFVAIAVRPVGWEYVYRVVHLSYQLVSEYLRPEE 121
 DB 67 LKQAFEDVRSQEGIVLSPWALAIRPRGVWEYVYRVVSEIAVALLVPYLYQKEQ 126
 QY 122 LVDSQNDPVYVLDPEFPVSVPRNRSSISGNGVQFLNRHLSIFNRDCLEPLDLP 181
 DB 127 LVBEGGNNNFVLDPEFPVAFPRPSLSKISGNGVQFLNRHLSIFNRDCLEPLDLP 186
 QY 182 LRGHRHKGAVMLNDRIQSLRQSVLTAKBHSKLPADTPYSQAFYKQWGLKGMG 241
 DB 187 LRAHNYKGMTMLNDRISLSALQALRKAHEHLSGLSADTPYSEFHRROEGLKGMG 246
 QY 242 DTAGHLEMLHLLDIIQADPSTLEKELGRIMFVNVVVSVPGVGOANVGLPTTG 301
 DB 247 DCAKRSOETHHLLDLADPSTLEKELGRIMFVNVVVSVPGVGOANVGLPTTG 306
 QY 302 QIVYIILDOVALENEMVLRLKQGLDVSPKILIVTRILIPDAKTSQNRERISGTQHTY 361
 DB 307 QVYIILDOVALENEMVLRLKQGLDVSPKILIVTRILIPDAKTSQNRERISGTQHTY 366
 QY 362 ILAVPPFNENGLIKKMSRFDVMPYLETFAEDAAAGTAAELQSTPPITIGNSDNVAS 421
 DB 367 ILAVPPFNENGLIKKMSRFDVMPYLETFAEDAAAGTAAELQSTPPITIGNSDNVAS 426
 QY 422 LLSYKMGICCCNLAHLEKTRPSDSEFMKPFDEKHFSCOPFADIIAANNADPILNSTY 481
 DB 427 LLSYKMGICCCNLAHLEKTRPSDSEFMKPFDEKHFSCOPFADIIAANNADPILNSTY 486
 QY 482 QEINAGSKTVGOYESHTAFTPLGLYRVVHSDIVDPKENVISPGADMSIYFPHTEKAKRL 541
 DB 487 QEINAGSKTVGOYESHTAFTPLGLYRVVHSDIVDPKENVISPGADMSIYFPHTEKAKRL 546
 QY 542 TSLHGSTENTLYPEQNDHEHGLDORSKPLTSMALDVKNTGTGYEPAKAKAREL 601
 DB 547 TSLHGSTENTLYPEQNDHEHGLDORSKPLTSMALDVKNTGTGYEPAKAKAREL 606

QY 602 VNLVAVGVNDVKSOREIABEKHELIKTHNLFGOPRMTSAQNRBARNGELYRIA 661
 DB 607 VNLVAVCG-DHGPSKDEKQAEKMFDLBOYINLGHIRWISAQNRVANGELIRYIC 665
 QY 662 DTGAFAVQALYBAFGLTVVEAMTCGLPTEATLHGPAEIIENGVSFHIDPYRBOAVN 721
 DB 666 DTGAFAVQALYBAFGLTVVEAMTCGLPTEATLHGPAEIIENGVSFHIDPYRBOAVN 725
 QY 722 LMADFEPCRKQDPDHRWNISGAGLQRIYKTYTWIYSEBRLMTLAGVYGFMYKSTLELE 781
 DB 726 LMADFEPCRKQDPDHRWNISGAGLQRIYKTYTWIYSEBRLMTLAGVYGFMYKSTLELE 785
 QY 782 TRRYLEFYLIKRFELAKTVPLAID 806
 DB 786 TRRYLEFYLIKRFELAKTVPLAID 810
 RESULT 14
 ID ADC68460 standard; protein; 815 AA.
 XX
 XX ADC68460;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX
 DE Lolium perenne fructan biosynthesis protein SEQ ID NO:170.
 XX
 XX Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
 KM biosynthetic pathway; plant.
 XX
 XX Lolium perenne.
 XX
 XX NO2003040306-A2.
 PN
 XX 15-MAY-2003.
 PD
 XX 07-NOV-2002; 2002MO-NZ000239.
 PF
 XX 07-NOV-2001; 2001US-0337703P.
 PR
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIG-) WRIGHTSON SEEDS LTD.
 XX
 XX Demmer J, Forster RL, Gibson JB, Shenk MA, Norris MG, Glenn M;
 PI Saulsbury KM, Hall C;
 XX WPI; 2003-441544/41.
 DR N-PSDB; ADC68424.
 DR
 XX New polynucleotide encoding polypeptides from Lolium perenne or Festuca
 PT arundinacea, useful for modulating the biosynthesis of lignin, fructan or
 FT tannin in a plant.
 XX
 XX Claim 18; SEQ ID NO 170; 240bp; English.
 PS
 XX The present invention describes isolated polynucleotides (I) encoding
 XX proteins (II) from Lolium perenne and Festuca arundinacea which are
 CC active in lignin, fructan and tannin biosynthetic pathways. Also
 CC described: (1) an isolated oligonucleotide probe or primer comprising at
 CC least 10 contiguous residues complementary to 10 contiguous residues of
 CC (1); (2) a kit comprising the oligonucleotide probe or primer; (3) a
 CC genetic construct comprising (1); (4) a transgenic plant cell comprising
 CC the genetic construct of (3); (5) a plant or its seed, fruit or progeny
 CC comprising the transgenic plant cell of (4); (6) modulating one or more
 CC of the lignin, fructan or tannin compositions of a plant; (7) producing a
 CC plant having one or more of the lignin, fructan or tannin compositions;
 CC and (8) modifying the activity of (II) involved in a lignin, fructan or
 CC tannin biosynthetic pathway in a plant. (I) can be used for modulating
 CC the biosynthesis of lignin, fructan or tannin in a plant. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 815 AA;
 SQ

Query Match 70.1%; Score 2976.5; DB 7; Length 815;
 Best Local Similarity 69.1%; Pred. No. 2.8e-258;
 Matches 556; Conservative 113; Mismatches 127; Indels 9; Gaps 4;

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QY 6 LNRNASIRDEVDITLAHNEILVALLSKYVKKGGIIOPHIIL----DALDEVQSSGYRA 61
DB 10 LSRHSYVERIGDSLASHPNELVAVFTLVNLGKGMLOPHOIIAEVNTAIPBAER---EK 66
QY 62 LAEPFLDVLRSAGEALVLPFPVAIAVRPRGVWEYVAVNVNHELSEVQLTSEYLRPEE 121
DB 67 LKDAFEDVLAAGEALVISPVALAIRPRGVWEYVAVNVNSELAVELSVPEYLQFEQ 126
QY 122 LVDSQNDPVYELDEFPENVSVPKRNSSIGNGVCFINRLSSIMFRNDCLEPLTDF 181
DB 127 LVBSQND- FVLELDEFPENVSFPKRNSSIGNGVCFINRLSSIMFRNDCLEPLTDF 185
QY 182 LRGHRHGHVMTLNDRIQSLGRLQSVLTAEELSKLPADTPYSQFAVKEQEWELKMG 241
DB 186 LRANVYKGMWMMNDVRSLSALQALRKAEELSGLPADTPYSDFHRRFQELGELKMG 245
QY 242 DTAGHVLMTLDDITQAPDPTLEKFLRIPMIENNVVVSPPHGYFGQAVNLGPDGTG 301
DB 246 DCARAGDTLHLLDLLEADPSTLEKFLGSLPMVENVVLSPPHGYFGQAVNLGPDGTG 305
QY 302 QIVVYILDQVRALBNEMVLRKKQGLDVSPLIIVTRLIPDAKGISCNQRLERISQTHY 361
DB 306 QIVVYILDQVRALBNEMVLRKKQGLDITPRILITRLIPDAKGTTCGRLKVGTEHTH 365
QY 362 ILRVFPNENGIILKWTISRPDVPYLETFAEDAGEIAELQGPDPITIGNSDGNLVAS 421
DB 366 ILRVFPNENGIILKWTISRPDVPYLETFAEDAGEIAELQGPDPITIGNSDGNLVAC 425
QY 422 LLSYMGITQCNINAALEKTYPOSDFWKEDEKYESCOETDIIMNNAADFTISTY 481
DB 426 LLAHMGVTHCTIHALEKTYPNSDLWKKEBDHYHSCOPTDILMNHADFTISTY 485
QY 482 QEIGSKRTVQGYSHTAFTLPGYRVVHGIDVDPKKNIVSPGADSIYEPHTEKARL 541
DB 486 QEIGNKQVQGYSHAFWPGMYRVVHGIDVDPKKNIVSPGADSIYEPHTEKARL 545
QY 542 TSLHGSIENTLYDEQNDHEITGHLDRSKPLIFSMARLDVKNITGLVAEPAKCAKREL 601
DB 546 TSLHGSIENTLYDEQNDHEITGHLDRSKPLIFSMARLDVKNITGLVAEPAKCAKREL 605
QY 602 VNVVWVGYMNVKSKDEETABIERKMEHILKTNLFCQFPMISAQVRAANGELYRTIA 661
DB 606 VNLVWVCG-DHGNPSKDEBOEFKQMPDLIEQYINLNGHIRKITSQMRVNAELIRYIC 664
QY 662 DTHGAFVQPALYEAAGLTVEAMTGLPTFATLHGAPARILIEHVSGFHIDPYHDEQAVM 721
DB 665 DTHGAFVQPALYEAAGLTVEAMTGLPTFATLHGAPARILIEHVSGFHIDPYHDEQAVM 724
QY 722 LMAEFPDRCODPDHMTVINISGAGLQRIYKTYMKLYSERLMTLAQVGPWKVSLTEBLE 781
DB 725 LVEPEKCOGDHSHMTKISLQGLQRIEYKTYMKLYSERLMTLTQVYGVKWSYSLERRE 784
QY 782 TRRYTEMFYILKRELAKTVPLAID 806
DB 785 TRRYTEMFYILKRELAKTVPLAID 809

```

RESULT 15

AAU97898 standard; protein; 806 AA.

AAU97898;

13-AUG-2002 (first entry)

Cotton sucrose synthase Susy protein.

Cotton; Sucrose synthase; Susy; fibre; seed; transgenic; plant; enzyme.

XX

Goesypium hirsutum.

Location/Qualifiers

Misc-difference 414

/label= Unknown

/note= "Encoded by NAC"

MO200245485-A1.

13-JUN-2002.

07-DEC-2001; 2001WO-A0001580.

08-DEC-2000; 2000AU-00001975.

08-DEC-2000; 2000US-0251852P.

(CSIR) COMMONWEALTH SCT & IND RES ORG.

Llwelllyn D, Furbank R, Ruan Y;

MPI; 2002-463779/49.

N-Psdb; ABK52880.

Altering fibre development or properties of a fibre producing plant by

modulating sucrose synthase activity and/or expression in such plants,

useful for enhancing fibre yield and quality and for increasing seed

size.

Claim 5; Page 57-60; 62pp; English.

This invention relates to a novel method for altering fibre development

or properties of a fibre producing plant by modulating sucrose synthase

(Susy) activity and/or expression in such plants. The invention also

comprises a fibre producing plant comprising a chimaeric gene in its

genome, the seeds of the plant and fibre isolated from the plant. The

method is useful for altering fibre development or properties of a fibre

producing plant like cotton plant. Therefore, the method is useful for

enhancing fibre yield, enhancing fibre quality and for increasing seed

size in a fibre producing plant. The present sequence represents the

cotton sucrose synthase (Susy) protein used to create the transgenic

plant of the invention

Sequence 806 AA;

Query Match 70.0%; Score 2972; DB 5; Length 806;

Best Local Similarity 69.4%; Pred. No. 6.9e-258;

Matches 559; Conservative 113; Mismatches 131; Indels 2; Gaps 2;

1 MSAPLNRNASTIRDEVDITLAHNEILVALLSKYVKKGGIIOPHIILDALDEVQSSGYR 60

1 MAERALTFRVHSIRKRLDITLAHNEILVALLSIRIGKGGIIOHIIISFEALPERNEK 60

61 ALAEPFLDVLRSAGEALVLPFPVAIAVRPRGVWEYVAVNVNHELSEVQLTSEYLRPEE 120

61 KLANAEFEVLAAGEALVISPVALAIRPRGVWEYVAVNVNSELAVELSVPEYLQFEQ 120

121 ELVDQNDPVYELDEFPENVSVPKRNSSIGNGVCFINRLSSIMFRNDCLEPLTDF 180

121 ELVDSSSGNFTLELDEFPENVSFPKRNSSIGNGVCFINRLSSIMFRNDCLEPLTDF 180

181 FLRGHRHGHVMTLNDRIQSLGRLQSVLTAEELSKLPADTPYSQFAVKEQEWELKMG 240

181 FLRVHCHGKMMMLNDRIQNLALQHVLRKAEYLGTPPTCAFEHRFOEIGLERGM 240

241 GDTAGHVLMTLDDITQAPDPTLEKFLRIPMIENNVVVSPPHGYFGQAVNLGPDGTG 300

241 GDTARVYEMTQLLDLLEADPSTLEKFLGSLPMVENVVLSPPHGYFGQAVNLGPDGTG 300

301 QIVVYILDQVRALBNEMVLRKKQGLDVSPLIIVTRLIPDAKGISCNQRLERISQTHY 360

301 QGVVYILDQVRALBNEMVLRKKQGLDITPRILITRLIPDAKGTTCGRLKVGTEHTH 360

361 YLRVFPNENGIILKWTISRPDVPYLETFAEDAGEIAELQGPDPITIGNSDGNLV 415

Db 351 DLRVPEFTEKGIYRKNIISREFEKWPYLETYTEVVAHEISKELHGTDDLIGNXSDGNTY 420
QY 420 ASLSYKMGITQCNIAHALEKTYPPDSJFWKNFDEKYNHSCQFTADIIAMNADFIITS 479
Db 421 ASLHAKKLGVTOCTIAHALEKTYPPDSJYWKLEBKYNHSCQFTADLFAMNHDPIITS 480
QY 480 TYQELAGSKYVQYQYSHHTAFILPGIYRVYHGSDVPDEKNIYVSGADMSIYFPHTEKAK 539
Db 481 TFOELAGSKDYVQYQYSHHTAFILPGIYRVYHGSDVPDEKNIYVSGADMEIYFPHYEEKR 540
QY 540 RLTSLSHGSJENLIYDPEONDEHIGLDDRSK2ILFSMARLDRYKNITGLVEAFACAKLR 599
Db 541 RLKHPHPELBDLLTYKVENEBHLCVLNDNRK2ILFTMPRLDRYKNUJGLVWCGKNPKLR 600
QY 600 ELVNLVVVAGYNDVNSKXDRBILAELEKMHETLKHNLFGQFRMISAQTNRANGELXYR 659
Db 601 ELANLVVVGSDRRKSKDLEKAKEMKMPBELDKYNLNGQFRMISQNMRIINVELXYR 659
QY 660 IADTHGAFYQPALYEAFFGLTVVAMTCGLPTFATLHGGPAEIIHGVSGFHIDPYHBCA 719
Db 660 ICDYKGAFFQPALYEAFFGLTVVAMTCGLPTFATLHGGPAEIIHGVSGFNIIDPYHBCA 719
QY 720 VNLMAJFDRCKODPDHMTNISGAGLQRIYEKTYAKIYSERLMTLAGVYGFMYSKLER 779
Db 720 ADLIVDFEFCKKODPSHMDKISQGGILRIEKTWKIYSERLMTLAGVYGFMYKHSNLER 779
QY 780 IETRYLEMFYILKPRELAKTVPLA 804
Db 780 RESRYLEMFYALKYRKIAESVPLA 804

Search completed: May 24, 2004, 11:27:21

Cod time : 55.7325 secs

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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 19.5847 seconds

(without alignments)
2132.550 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247

Sequence: 1 MSARKLNNSIRSRVEDTL.....YIKREIAKTVPLIDPQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 3%
Maximum Match 100%

Listing first 45 summaries

Database :
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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3158	74.4	766	2	US-08-553-436A-8
2	2892.5	68.1	806	4	US-09-598-401C-77
3	1833	43.2	806	4	US-08-684-325-2
4	467.5	11.0	720	4	US-09-394-272-14
5	466.5	11.0	1083	4	US-09-394-272-11
6	450	10.6	1056	4	US-09-394-272-12
7	447.5	10.5	963	4	US-09-394-272-13
8	447.5	10.5	963	4	US-09-394-272-13
9	445	10.5	1059	4	US-09-394-272-5
10	444	10.5	1068	2	US-08-429-054A-11
11	444	10.5	1068	2	US-08-718-777-7
12	444	10.5	1068	3	US-09-051-341-7
13	444	10.5	1068	3	US-09-394-272-8
14	441.5	10.4	1045	2	US-08-553-436A-6
15	441.5	10.4	1045	2	US-09-394-272-7
16	438	10.3	1054	1	US-08-356-354-4
17	438	10.3	1054	2	US-08-356-354-4
18	436.5	10.3	1053	4	US-09-394-272-6
19	425	10.0	1054	4	US-09-394-272-3
20	420	9.9	1059	4	US-09-697-367-16
21	414	9.7	1057	4	US-09-697-367-23
22	414	9.7	1057	3	US-09-394-272-2
23	408.5	9.6	1081	4	US-08-853-948B-2
24	401.5	9.5	1084	4	US-09-394-272-9
25	396	9.3	846	1	US-08-356-354-2
26	396	9.3	846	2	US-08-356-354-2
27	396	9.3	846	2	US-08-778-656-2

28	355	8.4	125	4	US-09-598-401C-76	Sequence 76, Appl
29	351	8.3	1049	4	US-09-394-272-10	Sequence 10, Appl
30	307	7.2	908	1	US-08-356-354-6	Sequence 6, Appl
31	307	7.2	908	2	US-08-778-656-6	Sequence 6, Appl
32	280	6.6	668	4	US-09-697-367-2	Sequence 2, Appl
33	262.5	6.2	343	3	US-09-697-367-24	Sequence 24, Appl
34	256	6.0	343	3	US-08-853-948B-10	Sequence 10, Appl
35	251	5.9	341	3	US-08-853-948B-4	Sequence 4, Appl
36	233.5	5.5	365	4	US-09-697-367-8	Sequence 8, Appl
37	222	5.2	343	3	US-08-853-948B-3	Sequence 3, Appl
38	221	5.2	348	3	US-08-853-948B-5	Sequence 5, Appl
39	186	4.4	59	3	US-09-125-984-2	Sequence 2, Appl
40	172	4.0	210	4	US-09-697-367-10	Sequence 10, Appl
41	161	3.8	507	4	US-09-134-031C-3978	Sequence 3978, Ap
42	160.5	3.8	358	4	US-09-697-367-20	Sequence 20, Appl
43	152.5	3.6	502	4	US-09-134-031C-4511	Sequence 4511, Ap
44	149.5	3.5	369	4	US-09-543-681A-7514	Sequence 7514, Ap
45	148	3.5	393	4	US-09-252-991A-19043	Sequence 19043, A

ALIGNMENTS

RESULT 1
US-08-553-436A-8
Sequence 8, Application US/08553436A
Patent No. 5866730
GENERAL INFORMATION:
APPLICANT: HESSE, Holger
APPLICANT: MULLER-ROBER, Bernd
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Sofien
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,436A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4317596.1
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wellman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-436A-8
Query Match 74.4% Score 3158, DB 2, Length 766;

Best Local Similarity 79.2%; Pred. No. 6.7e-286;
Matches 595; Conservative 73; Mismatches 81; Indels 2; Gaps 2;

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QY 58 GVALAEGPELDVRSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLR 117
DB 3 SKQLSDGPESEVARSAGEAIVPFPVAIAVRPRGWEYVRVNVHLSVEQLVSEYLR 62
QY 118 FKEELVDSKADHYVLEIDFEPFNESVPRPSSISGVQPLNHLSSMFCNDCELP 122
DB 63 FKEELVDSKADHYVLEIDFEPFNESVPRPSSISGVQPLNHLSSMFCNDCELP 122
QY 178 LIDFELRGHKGHWMLNDRIQSLQSLVLTAKAEHLSKLPATPYSAQFAKFGEMGLE 237
DB 123 LIDFELRGHKGHWMLNDRIQSLQSLVLTAKAEHLSKLPATPYSAQFAKFGEMGLE 182
QY 238 KGMWDTAGVLEMLHLLDITIOAPDPSTLEKFLGRIPIFNVVVSPPHIGQANVGLP 297
DB 183 KGMWDTAGVLEMLHLLDITIOAPDPSTLEKFLGRIPIFNVVVSPPHIGQANVGLP 242
QY 298 DTGGQIVVILDOVRLEHMTLRIKKQGLDVSFKLITRLIPDAKGSQNRLEIRISGT 357
DB 243 DTGGQIVVILDOVRLEHMTLRIKKQGLDVSFKLITRLIPDAKGSQNRLEIRISGT 302
QY 358 QHTVILRVPFRNENGILKKWISRPDWPYLETFAEDAGELAAELQGPDPFIIGNYSQGN 417
DB 303 QHTVILRVPFRNENGILKKWISRPDWPYLETFAEDAGELAAELQGPDPFIIGNYSQGN 362
QY 418 LVASLSTRKMGITTCNIAALEKTYPPSDIPKMFDEKTHPSCOPTADITAMNADPFI 477
DB 363 LVASLSTRKMGITTCNIAALEKTYPPSDIPKMFDEKTHPSCOPTADITAMNADPFI 422
QY 478 TSTVOELGSKXTVQOYESHTAFPLPGLYRVVHGIDVPDKENIYSPGADMSIYPPHTEK 537
DB 423 TSTVOELGSKXTVQOYESHTAFPLPGLYRVVHGIDVPDKENIYSPGADMSIYPPHTEK 482
QY 538 AKRITSLHSGSIENLIYDPEQNDENHGHLDNRKPEILFSMARDRYKNTITGLVEAFKCA 596
DB 483 AKRITSLHSGSIENLIYDPEQNDENHGHLDNRKPEILFSMARDRYKNTITGLVEAFKCA 542
QY 597 KLSLAVLVVAGYNDVNSKQREBIAELKMHLEIKTNLFGQRFWISAGQNRANENGL 656
DB 543 KLSLAVLVVAGYNDVNSKQREBIAELKMHLEIKTNLFGQRFWISAGQNRANENGL 602
QY 657 YRYIADTGAFVOPALYEAFFGLTYVEAMTCGLPTFATLHGPAEIIIEHGVSGEHIDPYHP 716
DB 603 YRYIADTGAFVOPALYEAFFGLTYVEAMTCGLPTFATLHGPAEIIIEHGVSGEHIDPYHP 662
QY 717 EQAVNIMADFPDRCKODPDHWNISGAGLQRIYKTYKTYSRMLTLAGVYGFMYKYSK 776
DB 663 EQAVNIMADFPDRCKODPDHWNISGAGLQRIYKTYKTYSRMLTLAGVYGFMYKYSK 721
QY 777 LERLETRRLMEFYLIKRELAQTVPLADQ 807
DB 722 LERLETRRLMEFYLIKRELAQTVPLADQ 752

```

RESULT 2

US-09-598-401C-77
Sequence 77, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Pereira, C. Zanjan
APPLICANT: Bagleton, Clare
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1036c2
CURRENT APPLICATION NUMBER: US/09/598.401C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 805
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-598-401C-77

Query Match 68.1%; Score 2892.5; DB 4; Length 805;
Best Local Similarity 66.9%; Pred. No. 4.7e-261;
Matches 540; Conservative 120; Mismatches 144; Indels 3; Gaps 2;

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QY 1 MSAPLNANASTRODVEPTLHAHREIVALLSKYVKNKGGLIOPHIIDALDEVOQSGVR 60
DB 1 MADRLTSHSRKREKIDELSHARDIVAFISVRPAKGGKILQRIQTFEPFELISSESA 60
QY 61 ALAEGPFLDVRSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLRPEK 120
DB 61 KLLDGAPEGLKSTDEALVSPFWALAVRPRGWEHIVNVHVALVLEJAEVAYLAFPE 120
QY 121 ELVDQENDPVYLEIDFEPFNESVPRPSSISGVQPLNHLSSIMFRNDCELPILD 180
DB 121 ELVDQENDPVYLEIDFEPFNESVPRPPTLSKISGVQPLNHLSSIMFRNDCELP 180
QY 181 FLRGHKGHWMLNDRIQSLQSLVLTAKAEHLSKLPATPYSAQFAKFGEMGLEKGM 240
DB 181 FLRGHKGHWMLNDRIQSLQSLVLTAKAEHLSKLPATPYSAQFAKFGEMGLEKGM 240
QY 241 GDTAGVLEMLHLLDITIOAPDPSTLEKFLGRIPIFNVVVSPPHIGQANVGLPDTG 300
DB 241 GDTAGVLEMLHLLDITIOAPDPSTLEKFLGRIPIFNVVVSPPHIGQANVGLPDTG 300
QY 301 GQIVVILDOVRLEHMTLRIKKQGLDVSFKLITRLIPDAKGSQNRLEIRISGTHT 360
DB 301 GQIVVILDOVRLEHMTLRIKKQGLDVSFKLITRLIPDAKGSQNRLEIRISGTHT 360
QY 361 YLYRVPFRNENGILKKWISRPDWPYLETFAEDAGELAAELQGPDPFIIGNYSQGN 420
DB 361 YLYRVPFRNENGILKKWISRPDWPYLETFAEDAGELAAELQGPDPFIIGNYSQGN 420
QY 421 SLLSYKMGITTCNIAALEKTYPPSDIPKMFDEKTHPSCOPTADITAMNADPFIIT 480
DB 421 SLLSYKMGITTCNIAALEKTYPPSDIPKMFDEKTHPSCOPTADITAMNADPFIIT 480
QY 481 YQELIAGSKOTVQOYESHNAFTLPGLYRVVHGIDVPDKENIYSPGADMSIYFAITQDER 540
DB 481 YQELIAGSKOTVQOYESHNAFTLPGLYRVVHGIDVPDKENIYSPGADMSIYFAITQDER 540
QY 541 LYSINGSIENLIYDPEQNDENHGHLDNRKPEILFSMARDRYKNTITGLVEAFKCAKLR 600
DB 541 LYSINGSIENLIYDPEQNDENHGHLDNRKPEILFSMARDRYKNTITGLVEAFKCAKLR 600
QY 601 LYNLVVAGYNDVNSKQREBIAELKMHLEIKTNLFGQRFWISAGQNRANENGLYR 659
DB 601 LYNLVVAGYNDVNSKQREBIAELKMHLEIKTNLFGQRFWISAGQNRANENGLYR 658
QY 659 IADTGAFVOPALYEAFFGLTYVEAMTCGLPTFATLHGPAEIIIEHGVSGEHIDPYHP 719
DB 659 IADTGAFVOPALYEAFFGLTYVEAMTCGLPTFATLHGPAEIIIEHGVSGEHIDPYHP 718
QY 719 LERLETRRLMEFYLIKRELAQTVPLAD 806
DB 719 LERLETRRLMEFYLIKRELAQTVPLAD 805

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RESULT 3

US-08-684-005-2

Db 255 LIALSLSPDRKRNHKLIAVAGSPQQAQANIVTAG-----NRDITDLQCPRE 306
QY 627 KMEHLKT--HNIFGCFRMTISAQTNRAH-GEIYRIADTHGAFVOPALYEAGLTWVE 682
Db 307 VLTDLTLITDRYDLGKVAAY--PKONQAEVYALFRLTALSOGVFINPALTEPFGTLTIB 364
QY 683 AMTCGLPFLTHGCPHAEIIEHVSGFHIDPYHEGCAVNMADPFDCCKODPDHVMVNSG 742
Db 365 AAAGGVIVATGDDGVPDILIKNGCYLIMELSDV---IADKLKLVANDKQOQFPLSE 420
QY 743 AGLORIEKTYWKIYSERIMTAGVGFWMKYVSKLEBLETFRYLEMPY 790
Db 421 SGLGVRKHYSWESHVSY--LBAINALTQOTSLVLRKSDLKRRRTIVY 466

RESULT 5
US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-11

Query Match 11.0%; Score 466.5; DB 4; Length 1083;
Best Local Similarity 24.3%; Pred. No. 3.8e-34;
Matches 184; Conservative 130; Mismatches 285; Indels 159; Gaps 32;

QY 118 EKEELVDG-QHNDPVYELDEPPENVSVPRNRSSSI-----GNGVOPL 160
Db 67 FVEEVVNSFDESDDYKTKWIKYATATNTERSRNLENIQRIWMLARKKKQIYMDGVLS 126
QY 161 NRHLSSINFRRDCEPLIDEL-RGHRHKGHVMNDRIOSLGRLOSULTAEHLSKLP 219
Db 127 KRRIREGGRN-DAEEDILSELSEBKDK-----NDGEKESVYVTLIAPRDMPIR 179
QY 220 ADTPYSQPAKKFQEWGLEKGMGDTAGHYLEMITHLIDIIQAPDPSLTLEKFLGRIMFNV 279
Db 180 SE-----VQISED-----DKSR-----NLVIVIRQVEIGFSDLF-----VVFNM 216
QY 280 VV-----VSPHGYF-GQANVLGL-PTGGQIYIILDOVALNEMLRLKK 323
Db 217 LVGLTMCYLYPFCFTGCSHGILVRGENNELGRSDPTGGQVKKVYVLAIRALAN-----T 269
QY 324 QGLDVSPTKLIYTRLIIPDAK-GTSCNORLERIS-----GTQH--TYILRVFPFNENGILKK 376
Db 270 EGVH--RVDLITRQISPEVDVSYGEPEVEMLSCPRESSDSGSGIIRIPC-----GSRDK 322
QY 377 WISREDVMPYLETFPAEDAGAIYA-----ELQG-----TPDFIIGNYSQNLVASLSLSY 425
Db 323 YIPKESLWPHIPELFDGALNHNIVSTARSLGEQVNGKPIWYVYIGHVYADAGEVAHLAG 382
QY 426 KMGITQCNIAHELEKTY-----PDSDFIKNDPEKTHSCOPTADIIAMNNADFIITSTY 481
Db 383 ANAVMVLVILGHSLGNKKEQOLLOQGRITEDIIDRYTKIRIIEABEQSLDAAEYVYVSTR 442
QY 482 QELIASKVTVGQYEHHTATFLPGCYRVYHGIDV-----FDEPKNIV 522
Db 443 QSID-----AQM-----GLY-----LGFIDIKERKIRVRRKRGVSLGIVYPMYVI 484
QY 523 SPGADMSIYFPH--TEKARLTLSHGSIENLIYDPEQN--DEHIGLDRSKRPILFSMAR 578

Db 485 PRGMDPSYVLTODSQEODZDLKSLIGDRNOIKKPEVPIWSEIRPFPSNPKPTLLALS 544
QY 579 LCMVRNITGLVEAFKCAKLRELVNLVWVAGYDVNSKDEEIAIEKMBLITKRNLF 638
Db 545 PBEKQNTTILVKAAGECOPLRELANVLIIQNRDIEHMRSSSVLMNVKLTIDQYLY 604
QY 639 GQFRMTISAQTNRAHGEIYRIADTHGAFVOPALYEAGLTWVEAMTCGLPFLTHGCP 698
Db 605 GQVAY-PKHNGSEVPIYRLAAKTGVFINPALVEPFGTLIEMAAVGLPIVATRNQGP 663
QY 699 AEIIEHGVSGFHIDPYHEGCAVNMADPFDCCKODPDHVMVNSAGLORIEKTYWKIYS 758
Db 664 VDIYKALNNGILVDP-HDQQA1--SDALJLKVANKHLMABCRKGLKNIH-RFSWPERC 718
QY 759 ERLMTLAGVGFWMKYVSKLEBLETFRYLEMPYILKPRE 796
Db 719 R-----NYLSHVEHCRRHRHPTSSIDIKVPE 744

RESULT 6
US-09-394-272-11
; Sequence 1, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-394-272-11

Query Match 10.6%; Score 450; DB 4; Length 1056;
Best Local Similarity 26.4%; Pred. No. 1.3e-32;
Matches 145; Conservative 97; Mismatches 218; Indels 90; Gaps 18;

QY 279 VVWVSPHGYF-GQANVLGL-PTGGQIYIILDOVALNE-----MTLRKQGLDV 328
Db 176 VVLSIHGILRGENNELGRSDPTGGQVKKVYVLAIRALAGMPGVYRVDLITRQVSAPGVDM 235
QY 329 S---PKIIVTRLIIPDAKGTSCNORLERISGTHYIIRVPRNENGILKKWISREDVMP 385
Db 236 SYGEP-----TEMLSSRNSNSTEQIGSSG--AYIIRIP-----GPKQKIVAKELMP 283
QY 386 YLETFPAEDAG-----EIAELQGTPTDFIIGNYSQNLVASLSYNGITQCN 434
Db 284 YIEPEVDGALSHIKQMSKYLSEQIGGLPWYASVSHGHADAGDSALSLGALNVMPFT 343
QY 435 AVALERKTK-----YPPDSDFIKNDPEKTHSCOPTADIIAMNNADFIITSTYOEIASKYT 490
Db 344 GHSIRGDKLDQOLKQGRLSREVDATYKIMRIRABELCLDASKEIYITSTROBIEBO-- 400
QY 491 VQGYRSHAFLLPGIYRVYHGIDV-----POKFNIVSPGADMSIY 531
Db 401 -----WQLYHGFVLTERKLRAMRRGVSCHGFRMPRMAKIPKGMFPNHI 445
QY 532 PFTEKAKLTLSHGSIE-NLIYDPEQNDHEIHLDRSKPILFSNARLDVKNITGLVE 590
Db 446 AP--EDALMDTDIDHKKESNANPDVYIWEIRFESNGRKMPTIALARPPKKNLTLVX 503
QY 591 AFAKCAKRELVNLVWVAGYDVNSKDEEIAIEKMBLITKRNLFQCFRMTISAQTN 650
Db 504 AFGECEPFLRELANLTIIQNRDIDEMSTSSVLSIILKLTIDKYLYGQVAY-PKHNGK 562
QY 651 ANGBELYRIADTHGAFVOPALYEAGLTVEAMTCGLPFLTHGCPAEIIEHGVSGPH 710

Db 563 SVPPDIYRLAAKTKGFINPAPLEPPGLLLEAAANGLPVATKNGSPVDIIIGVNDGLL 622
Qy 711 IDPYHEQAVNLMADEFRCODPDHWNISAGLQRIYEKTYW---KIYSERLMTLAG 766
Db 623 IDP-HDQKSI---ADALIKLVADKHELMTCRQNGLNKH-LESPHECHKNYLSRIASCP 677
Qy 767 VYGFYKTVSK 776
Db 678 RQPNWQRIDE 687

RESULT 7

US-09-394-272-12
; Sequence 12, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-12

Query Match 10.5%; Score 447.5; DB 4; Length 963;
Best Local Similarity 25.7%; Pred. No. 1.9e-32;
Matches 167; Conservative 103; Mismatches 252; Indels 127; Gaps 26;
Qy 182 LRGHRKHGVMNDRIOSIGRLQSV-----LTAKBHSKLPADETPYSGFAVYKQ- 232
Db 67 MRSRRSHALBNVTMTIMNLARKKKEFEKSEACRLSKROPEKTRADATAMSEDLFEG 126
Qy 233 EWGLEKSG---WGD-TAGHVLMIHLLDIIQAPDSTLEKFLGRIPMIFNVVVSPIHG 286
Db 127 EKGEDGDSPVAAGDSTTG-----SSPKTSSIDKLY-----IVLISLHG 165
Qy 287 YF-QQANVIGL-PTGQGIYIILDQVRALENEMVLKKGGLVSP---KILVTR----- 337
Db 166 LVRGEMMELGRSDTGGQVYVVELAKALSS-----SPGVYRVDLLTROILA 212
Qy 338 -----LIPAKGTSQNRLEISGQHTYTLRVFERNENGILKKMISRPDWP 385
Db 213 PNFDRSYGPAELIVSTSGKSKQKGENSG---ATITRIIPF---GPKDKYLAKHEHLP 265
Qy 386 YLETFADNAGEIA-----AEIQGT-----PDFIIGNYSDGMLVASLISYKMGITQCN 434
Db 266 FIEFVDGALSHIVRSKAIGETGRGHPVPSVIGHYASAGIAAALLGALNLPMAFT 325
Qy 435 AAALAEKTK---YPPDSIEFKNDEKTHFSCQFTADIIAMNADFIITSTYQELAGSKNT 490
Db 326 GHFLGDKLEGLIKQGRQTRQINMTYKIMCRLEAEELSIDASEIVLASTROKIBEQMNL 385
Qy 491 VGGYESTHTFTPLGLRVVYHIDV---FDPKFNIVSGADMSTYFPTEKAKRLTSLH-- 545
Db 386 YDGFETVILARKLRA--RVKRGANCYGRFMRMVIIPPGV---FGHI-----IHDF 431
Qy 546 ---GSLEN---LIYPEDNDENHIGLDDRSKPIIFSMARLDRVKNITGLVEAFKCAKLR 599
Db 432 DMGGEENPSPASBDPIWQIMRFETNPARKMILAVARPYPEKNITTLVAKAGECPELR 491
Qy 600 ELVNLVVAGYNDVNSKDEBEIAIEKHEMLIKTHLFGQFRMISQTNARANGELXYR 659
Db 492 ELANLTLTIMGNREAISSYHNMMSAAVLTSVLTLLIDEDYLVQGVAY--PKHKGSEVPDIYRL 550
Qy 660 IADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLHGGAPEIIEHVGSGFIIDPYHPEQA 719
Db 492 ELANLTLTIMGNREAISSYHNMMSAAVLTSVLTLLIDEDYLVQGVAY--PKHKGSEVPDIYRL 550
Qy 660 IADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLHGGAPEIIEHVGSGFIIDPYHPEQA 719

Db 551 AARTKGAFFVNAVYFBQFVTLLEAAANGLPATKNGAPVEINQVNLNGLLVDPHQ--- 607
Qy 720 VNLMADEFRCODPDHWNISAGLQRIYEKTYW---KIYSERLMTL 764
Db 608 -NAIDALYKLSDKQWMSRCREMELTNHQ-FSPHECHKNYLSRIITL 654

RESULT 8

US-09-394-272-13
; Sequence 13, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Saccharum officinarum
US-09-394-272-13

Query Match 10.5%; Score 447.5; DB 4; Length 963;
Best Local Similarity 25.7%; Pred. No. 1.9e-32;
Matches 167; Conservative 103; Mismatches 252; Indels 127; Gaps 26;
Qy 182 LRGHRKHGVMNDRIOSIGRLQSV-----LTAKBHSKLPADETPYSGFAVYKQ- 232
Db 67 MRSRRSHALBNVTMTIMNLARKKKEFEKSEACRLSKROPEKTRADATAMSEDLFEG 126
Qy 233 EWGLEKSG---WGD-TAGHVLMIHLLDIIQAPDSTLEKFLGRIPMIFNVVVSPIHG 286
Db 127 EKGEDGDSPVAAGDSTTG-----SSPKTSSIDKLY-----IVLISLHG 165
Qy 287 YF-QQANVIGL-PTGQGIYIILDQVRALENEMVLKKGGLVSP---KILVTR----- 337
Db 166 LVRGEMMELGRSDTGGQVYVVELAKALSS-----SPGVYRVDLLTROILA 212
Qy 338 -----LIPAKGTSQNRLEISGQHTYTLRVFERNENGILKKMISRPDWP 385
Db 213 PNFDRSYGPAELIVSTSGKSKQKGENSG---ATITRIIPF---GPKDKYLAKHEHLP 265
Qy 386 YLETFADNAGEIA-----AEIQGT-----PDFIIGNYSDGMLVASLISYKMGITQCN 434
Db 266 FIEFVDGALSHIVRSKAIGETGRGHPVPSVIGHYASAGIAAALLGALNLPMAFT 325
Qy 435 AAALAEKTK---YPPDSIEFKNDEKTHFSCQFTADIIAMNADFIITSTYQELAGSKNT 490
Db 326 GHFLGDKLEGLIKQGRQTRQINMTYKIMCRLEAEELSIDASEIVLASTROKIBEQMNL 385
Qy 491 VGGYESTHTFTPLGLRVVYHIDV---FDPKFNIVSGADMSTYFPTEKAKRLTSLH-- 545
Db 386 YDGFETVILARKLRA--RVKRGANCYGRFMRMVIIPPGV---FGHI-----IHDF 431
Qy 546 ---GSLEN---LIYPEDNDENHIGLDDRSKPIIFSMARLDRVKNITGLVEAFKCAKLR 599
Db 432 DMGGEENPSPASBDPIWQIMRFETNPARKMILAVARPYPEKNITTLVAKAGECPELR 491
Qy 600 ELVNLVVAGYNDVNSKDEBEIAIEKHEMLIKTHLFGQFRMISQTNARANGELXYR 659
Db 492 ELANLTLTIMGNREAISSYHNMMSAAVLTSVLTLLIDEDYLVQGVAY--PKHKGSEVPDIYRL 550
Qy 660 IADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLHGGAPEIIEHVGSGFIIDPYHPEQA 719
Db 551 AARTKGAFFVNAVYFBQFVTLLEAAANGLPATKNGAPVEINQVNLNGLLVDPHQ--- 607
Qy 720 VNLMADEFRCODPDHWNISAGLQRIYEKTYW---KIYSERLMTL 764

Db 608 -NALADALYKLSXQXMSRCREGLTINHQ-FSPHECKNYLRILT 654

RESULT 9
US-03-394-272-5
Sequence 5, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haigler, Cardace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 5
LENGTH: 1059
TYPE: PAT
ORGANISM: Vicia faba
US-09-394-272-5

Query Match 10.5%; Score 445; DB 4; Length 1059;
Best Local Similarity 27.4%; Pred. No. 3,7e-32;
Matches 148; Conservative 92; Mismatches 222; Indels 78; Gaps 22;

Qy 279 VVVVSPHGYF-GQANVGL-PDTGGQIVYLDOVALENEM-----VLRKKQGLDVP 330
Db 169 IVLISIHGLIGENNELGRSDPTGGQVKKVVELARALGMPGVYVDLITRQVSSPDVDM 228
Qy 331 KILIVTRILPAKSGSCNORLERISGQHTYILRPFRNENGLKKWISRPDVPYLETE 390
Db 229 SYGPEPTMLAPRNTDFDQMGESG---AYTIRLPFGRN---KYLPEKELMPYITEF 281
Qy 391 AEDAGEI-----AAELOGT-----PDIIGNYSDGNLVASLSTYKMGITQCNIAHLE 439
Db 282 VDGANGHILQMSKALGEQIGSHAWPVALHGHYADAGSALLGALNVPMIFGHSIG 341
Qy 440 KTK---YPSDIFWKNFDEKTHFSCQFTAD-IAMNADFIITSTYQBIAGSKNTVGQYE 495
Db 342 RDKLEQLKQGRSLSTDEINSTYKIMRIEAEELADGETVITSTRQIE-----EQWR 395
Qy 446 SHTAFTLPLGYRVHVG-----IDVDPKFNIVSPGADMSIYEPHTEKAKRLTSLGSS 547
Db 396 LYNQFD-PVLERKIPARIRRNVSQYGRYVPMWSVIPGME-----FHH-----IAPLDGD 444
Qy 548 I-----ENLIYDEQND-----EHIGLIDRSKPILEFMSARLDKVKITGLVEAFKACAL 598
Db 445 IETPEGLIDHPAPQDPPIMSEIMPFSPKPFVILALARPDKKXITTLVKAFGECRPL 504
Qy 599 RELVNVVVVAGYNDVYKSKOREELAEIERKHELIKTHNIFGQFEMISACTNPARNGELYR 658
Db 505 RELANUTLITMGRDQIDEMSSSTSSVLISVLKIDKIDYQGVAV-FKHKKSQDPDIYR 563
Qy 653 YIADTHGAFVQALYEAEGITVVEAMTCGLPFATLHGGPAILIEGV--SGPHIDPVPYR 716
Db 564 IAAKRGVFINPAFIEPGLTLEAAAYGLPVAATKNGSPVDI--HVVADNGLLDP-HD 620
Qy 717 EOVAVIMADFFRCQODPDHWNVISGAGHQR-VEKXTY---KIYSERLMTLAGYGVFMK 772
Db 621 EKSI---ADALLKIVSNKQJAKKQNGIKXTH-LFSWPEHCKTYSKATQPRHPQWQ 676

RESULT 10
US-08-429-054A-11
Sequence 11, Application US/08429054A
Patent No. 597126
GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),

TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN AND MUSELLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429,054A

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 842,337

FILING DATE: 20-March-1992

APPLICATION NUMBER: PCT/FR 91/00593

FILING DATE: 18-July-1991

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: French 90402094.9

FILING DATE: 20-July-1990

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Charles A. Musellian

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 146,1137

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1068

TYPE: Amino acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-429-054A-11

Query Match 10.5%; Score 444; DB 2; Length 1068;
Best Local Similarity 25.2%; Pred. No. 4,7e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

Qy 241 GDTAGVLEMIHLADIIOAPDPSTLEKFIAGRIPMI-----FNVVVVSPHGYF- 288
Db 141 GDTIGEL-----APVETTKKQFQRFSDLTWMSDDKKEKKYIVLISVAGLVR 188
Qy 289 GQANVGL-PDTGGQIVYLDOVALENEMVLRKKQGLDVP--KILIVTLLI--PD- 341
Db 189 GENMEIGSDSDTGGQVKKVVELARA-----MSMGEYRVVLDFTKQVSSPDV 235
Qy 342 -----AKGTSCNORLERISGQHTYILRPFRNENGLKKWISRPDVPYLETE 390
Db 236 DMSYGEPTMLCAQSDGEGMESG---AYTIRLPFGRN---KYLPEKELMPYITEF 281
Qy 391 AEDAGEI-----AAELOGT-----PDIIGNYSDGNLVASLSTYKMGITQCNIAHLE 439
Db 289 VDGANGHILQMSKALGEQIGSHAWPVALHGHYADAGSALLGALNVPMIFGHSIG 341
Qy 440 KTK---YPSDIFWKNFDEKTHFSCQFTAD-IAMNADFIITSTYQBIAGSKNTVGQYE 495
Db 446 SHTAFTLPLGYRVHVG-----IDVDPKFNIVSPGADMSIYEPHTEKAKRLTSLGSS 547
Qy 495 RELVNVVVVAGYNDVYKSKOREELAEIERKHELIKTHNIFGQFEMISACTNPARNGELYR 658
Db 505 RELANUTLITMGRDQIDEMSSSTSSVLISVLKIDKIDYQGVAV-FKHKKSQDPDIYR 563
Qy 653 YIADTHGAFVQALYEAEGITVVEAMTCGLPFATLHGGPAILIEGV--SGPHIDPVPYR 716
Db 564 IAAKRGVFINPAFIEPGLTLEAAAYGLPVAATKNGSPVDI--HVVADNGLLDP-HD 620
Qy 717 EOVAVIMADFFRCQODPDHWNVISGAGHQR-VEKXTY---KIYSERLMTLAGYGVFMK 772
Db 621 EKSI---ADALLKIVSNKQJAKKQNGIKXTH-LFSWPEHCKTYSKATQPRHPQWQ 676

QY 537 KAKRLTSLHSGSIENLTYDEQNDHEIG-----HLDKSKPLPSMAR 578
DB 449 -----EDIDGSDVDYDIDVLEGASPKSPPIWAEVRFILNPHKPMIALSR 496
QY 579 LDRVKNITGLVEAFKACAKLRELYNLVVAGYDVNKSXDRBEIAIEKHEILKTHMLF 638
DB 497 PDKPKNITLTVKAFGECPRLRELANLTLIMGNRDDIDDMSAGNASVLTIVLKILDKYDLY 556
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DB 557 GSVAF-PKHNGQADVETIYRLAKKMGVFINPALVEPGLTLEAAHGLPIVATKNGSP 615
QY 699 AEIIEHVSGFHIDYHPHQAIVNLADFPDRCKODPDHWNISGAGLQRIYEKTYKIS 758
DB 616 VDTNALNGLVDPHDQ-----NAIADALIKLVADKNLMQBCRRGNLTH-LYSWPHC 670
QY 759 ERLMT-LAGVYGFWMKYVSKLELETRRYLE 787
DB 671 RYTLTRVAGC-----RLRNPRLK 689

RESULT 11
US-08-718-777-7
; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Landu, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Vcelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE
; TITLE OF INVENTION: SYNTHASE IN PLANTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,777
; FILING DATE: NOT YET ASSIGNED
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,471
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GANE.072.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-777-7

Query Match 10.5%; Score 444; DB 2; Length 1068;
Best Local Similarity 25.2%; Pred. No. 4,7e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGVLEMIHLLDIIQADPSTLEKFLGRIEMI-----ENVVVSPPHYF 288
DB 141 GDTIGEL-----APVETTKKFKQNFPSDLTVMSDNKEXLYIVLSVGLYR 188
QY 289 GQANVGL-PTGGQIVILLDOVRALNEMVRLKKQGLDVP-----KILVRLI--PD- 341
DB 189 GENMEIGRSDSDGGGVKKVVELARA-----MSMPGVYRVDLFRQVSSPDV 235
QY 342 -----AKGTSNORLERISGTOHTYLLRVFNRNGLIKKMSRFDVWPYLETF 390
DB 236 DMSYSEPTMLCAGSNDGMBESG--AYIVRIPC-----GRDXYLKKEBALMPYLOEF 288
QY 391 AEDAGEI-----AAELQGT-----PDEIIGNSDGNIVASILSYRMGITQCNIAALB 439
DB 289 VDGALAHILNMSKALGEQVGNRPLVPIYHGYADAGVAAALSGALVPMVLTGHSIG 348
QY 440 KTK---YPSDIFPMKNPDEKTHFSQCFADIIANNADFIITSYQELAGSNVGYE 495
DB 349 RMYLSQLKQGRMSKEIDSTYKIMRIRIGEBIALDASELVITSTQED-----EQM- 401
QY 496 SHTAFTLPGLYRVHGIDY-----PDKENIVSPGADMSIYPHTE 536
DB 402 -----GLY--DEEDYKLEKYLARARAGVSGHRVMPRVVPIPGKDFSNVVH-- 448
QY 537 KAKRLTSLHSGSIENLTYDEQNDHEIG-----HLDKSKPLPSMAR 578
DB 449 -----EDIDGSDVDYDIDVLEGASPKSPPIWAEVRFILNPHKPMIALSR 496
QY 579 LDRVKNITGLVEAFKACAKLRELYNLVVAGYDVNKSXDRBEIAIEKHEILKTHMLF 638
DB 497 PDKPKNITLTVKAFGECPRLRELANLTLIMGNRDDIDDMSAGNASVLTIVLKILDKYDLY 556
QY 639 GCFRWSAOTNRARNGELYRYIADTHGAFOVOPALYEAGLTVVEAMTGLPTFATLHGSP 698
DB 557 GSVAF-PKHNGQADVETIYRLAKKMGVFINPALVEPGLTLEAAHGLPIVATKNGSP 615
QY 699 AEIIEHVSGFHIDYHPHQAIVNLADFPDRCKODPDHWNISGAGLQRIYEKTYKIS 758
DB 616 VDTNALNGLVDPHDQ-----NAIADALIKLVADKNLMQBCRRGNLTH-LYSWPHC 670
QY 759 ERLMT-LAGVYGFWMKYVSKLELETRRYLE 787
DB 671 RYTLTRVAGC-----RLRNPRLK 689

RESULT 12
US-09-051-341-7
; Sequence 7, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17351
; FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
 FILING DATE: 27-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/372,200
 FILING DATE: 12-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara Rae-Venter, Ph.D.,
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CANE.110.0205
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)328-4400
 TELEFAX: (415)328-4477
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1068 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-051-341-7

Query Match 10.5%; Score 444; DB 3; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 4.7e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGHVLMTLHLDITQADPSTLEKELRIEMI-----FNVVVSPHGYF- 288
 DB 141 GDTIGEL-----APVETTKKGFQNNFSDLTWSDNKKKLYIVLSVHGLVR 188
 QY 289 GQANVLGL-PTGGQIVYILDQVRLNEMVRLKKGGLVSP--KLIYTRLI--PD- 341
 DB 189 GNNELGSDSDTGGQVKKVVELARA-----MSMWPGVYRDLFTROVSSPDV 235
 QY 342 -----AKGSCNQRLERISGTQHTYILRVFPFNNENILKKWISRFVWPYLETFF 390
 DB 236 DMSYGEPTMLCAGNDGEMGESSG--AYIVRLPC--GPRDKYLKEALNPYLQEF 288
 QY 391 AEDAGEI-----AAELQGT-----PFIIGNYSDGNLVAISLSTYKMGITOCNLAHALE 439
 DB 289 VDGLAHLNLSKALGEQVGNRPVLPYIHHYADAGVAAALSGALNVPVWLGHSLG 348
 QY 440 KTK-----YPSDIEFNKDEKTHFSCQFTADIIANNADFIITSTYQELTAGSKNTVGYE 495
 DB 349 RNKLQLKQGMSEKDEIDSTYKIMRIEGEIALDASLVTSTQCEID-----EQW- 401
 QY 496 SHTATLRLGLRVNHGIDV-----FDPKFNIVSPGADMSIYEPHTE 536
 DB 402 -----GLY--DGFVQLKELRLPARARRGVSCGRIMPRVAVLPQMDPSNVVH-- 448
 QY 537 KAKRLTSLHSGIENLIYDPENDEHIG-----HLDORSXPILFSMAR 578
 DB 449 -----EDIDGDGDVMDIYGLEGASPKSMPTMAEVMRLTPHKKMILALSR 496
 QY 579 LDRVKNITGLVFAFAKCAKRLRELVNLVVAGYNDVNSKDRBEIAIEKMHLEIKTHNLF 638
 DB 497 PDPKNIITLVAFGECREPLRELANLTLLMGNRDDIDMSAGNASVLTTLVKLIDKIDY 556
 QY 639 GQFRTSAGTNRARNGELRYIADTGAIVOPALVEAFGLTVVEAMTCGLPTFATLHGSP 698
 DB 557 GSAVF-PKHNDQDVDEIYRLAAKMGVFINPLVPPFGTLLEAAHGLPIYATKNGP 615
 QY 699 AEIIEHGVSGFHIDPYPHPOAVNLADFPDRCKQDPDHWVNISGAGIQRIYKTYTKIYS 758
 DB 616 VDIITNLANGLVDPHDQ-----NADIALKLVAQDKLMOECRRNGRLNTH-LYSWPEHC 670
 QY 759 ERLMT-LAGYVGFVKVSKLERLETRYLE 787
 DB 671 RYILTRVAGC-----RLRNPRWLK 689

RESULT 13
 US-09-394-272-8
 Sequence 8, Application US/09394272
 Patent No. 6472588

GENERAL INFORMATION:
 APPLICANT: Haigler, Candace H.
 APPLICANT: Holaday, A. Scott
 TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
 TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
 FILE REFERENCE: 201304/1000
 CURRENT APPLICATION NUMBER: US/09/394,272
 CURRENT FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 1068
 TYPE: PRT
 ORGANISM: Zea mays
 US-09-394-272-8

Query Match 10.5%; Score 444; DB 4; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 4.7e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGHVLMTLHLDITQADPSTLEKELRIEMI-----FNVVVSPHGYF- 288
 DB 141 GDTIGEL-----APVETTKKGFQNNFSDLTWSDNKKKLYIVLSVHGLVR 188
 QY 289 GQANVLGL-PTGGQIVYILDQVRLNEMVRLKKGGLVSP--KLIYTRLI--PD- 341
 DB 189 GNNELGSDSDTGGQVKKVVELARA-----MSMWPGVYRDLFTROVSSPDV 235
 QY 342 -----AKGSCNQRLERISGTQHTYILRVFPFNNENILKKWISRFVWPYLETFF 390
 DB 236 DMSYGEPTMLCAGNDGEMGESSG--AYIVRLPC--GPRDKYLKEALNPYLQEF 288
 QY 391 AEDAGEI-----AAELQGT-----PFIIGNYSDGNLVAISLSTYKMGITOCNLAHALE 439
 DB 289 VDGLAHLNLSKALGEQVGNRPVLPYIHHYADAGVAAALSGALNVPVWLGHSLG 348
 QY 440 KTK-----YPSDIEFNKDEKTHFSCQFTADIIANNADFIITSTYQELTAGSKNTVGYE 495
 DB 349 RNKLQLKQGMSEKDEIDSTYKIMRIEGEIALDASLVTSTQCEID-----EQW- 401
 QY 496 SHTATLRLGLRVNHGIDV-----FDPKFNIVSPGADMSIYEPHTE 536
 DB 402 -----GLY--DGFVQLKELRLPARARRGVSCGRIMPRVAVLPQMDPSNVVH-- 448
 QY 537 KAKRLTSLHSGIENLIYDPENDEHIG-----HLDORSXPILFSMAR 578
 DB 449 -----EDIDGDGDVMDIYGLEGASPKSMPTMAEVMRLTPHKKMILALSR 496
 QY 579 LDRVKNITGLVFAFAKCAKRLRELVNLVVAGYNDVNSKDRBEIAIEKMHLEIKTHNLF 638
 DB 497 PDPKNIITLVAFGECREPLRELANLTLLMGNRDDIDMSAGNASVLTTLVKLIDKIDY 556
 QY 639 GQFRTSAGTNRARNGELRYIADTGAIVOPALVEAFGLTVVEAMTCGLPTFATLHGSP 698
 DB 557 GSAVF-PKHNDQDVDEIYRLAAKMGVFINPLVPPFGTLLEAAHGLPIYATKNGP 615
 QY 699 AEIIEHGVSGFHIDPYPHPOAVNLADFPDRCKQDPDHWVNISGAGIQRIYKTYTKIYS 758
 DB 616 VDIITNLANGLVDPHDQ-----NADIALKLVAQDKLMOECRRNGRLNTH-LYSWPEHC 670
 QY 759 ERLMT-LAGYVGFVKVSKLERLETRYLE 787
 DB 671 RYILTRVAGC-----RLRNPRWLK 689

RESULT 14
 US-08-553-436A-6
 Sequence 6, Application US/08553436A
 Patent No. 586790
 GENERAL INFORMATION:
 APPLICANT: HESSE, Holger
 APPLICANT: MULLER-ROBER, Bernd
 TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

QY 759 ERLMT 763
: : :
Db 656 KTYLS 660

Search completed: May 24, 2004, 11:28:53
Job time : 21.5847 sec8

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:32:41 ; Search time 4575.6 Seconds

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Title: US-10-080-114a-11

Perfect score: 2757

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IDENTITY_NUC

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Searched: 27513283 segs, 14931090276 residues 55026578

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: em_escbm:*
- 3: em_escbu:*
- 4: em_escbv:*
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- 8: em_escbs:*
- 9: gb_esc1:*
- 10: gb_esc2:*
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- 14: gb_esc6:*
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- 25: em_escbfn:*
- 26: em_escbfn:*
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- 28: gb_esc1:*
- 29: gb_esc2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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4	794.6	28.8	1005	13	BO619258 RNOSB05F0

5	793	28.8	938	13	BO619406	BO619406 RNOSB07D0
6	722	26.2	835	14	CA280212	CA280212 SCVPEB2C0
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11	676.2	24.5	745	14	CD426853	CD426853 SA1_25_F0
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15	655.6	23.8	808	14	CB651486	CB651486 OSJNEB16H
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23	636.8	23.1	824	14	CB668706	CB668706 OSJNEB16L
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25	636	23.1	833	14	CB631361	CB631361 OSJTB08Y
26	635.6	23.1	802	14	CB633383	CB633383 OSJTB12D
27	635.2	22.7	836	14	CB631302	CB631302 OSJTB08M
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29	623.6	22.6	807	14	CB683304	CB683304 OSJNEB10H
30	622	22.6	767	14	CB682789	CB682789 OSJNEB10H
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35	602.2	21.8	651	14	CF632182	CF632182 ZMTW848_0
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38	594	21.5	700	14	CA195492	CA195492 SCEZSR109
39	593.2	21.5	787	14	CB629315	CB629315 OSJTB05H
40	592.8	21.5	756	14	CB628904	CB628904 OSJTB04L
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42	560.6	20.3	727	14	CB632976	CB632976 OSJTB11T
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RESULT 1	AY104856	2705 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY104856	PC0079420	mrna	sequence.	
DEFINITION	Zea mays				
ACCESSION	AY104856				
VERSION	AY104856.1	GI:21207934			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 2705)				
TITLE	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Korgante, M., and Tingey, S.V.				
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes				
REFERENCE	Unpublished (2002)				
AUTHORS	2 (bases 1 to 2705)				
TITLE	Direct Submission				
JOURNAL	Coe, B.H.				
COMMENT	Submitted (25-APR-2002) Maize Mapping Project. University of Missouri, Columbia, MO 65211, USA				

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at ksl.zmmap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schable, Iowa State, their clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

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..2705
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/mol_type="mRNA"
/db_xref="MaizeDB:634420"
/db_xref="taxon:4577"
/clone_id="Maize Mapping Project/Dupont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 95.7% Score 2637.8; DB 11; Length 2705;
Best Local Similarity 99.0%; Pred. No. 6.7e-304; Indels 1; Gaps 1;
Matches 2665; Conservative 0; Mismatches 27;

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QY 38 GGGACGCGCTCGAGACACCTCCACGCGACGCAAGAGCTCTGACCTCTCTCA 97
Db 1 GCGACGCGCTCGAGACACCTCCACGCGACGCAAGAGCTCTGACCTCTCTCA 60
QY 98 AGTACGTGAACAAAGGGAAGGCAATCTGACGCGCAACATCTCTGAGCGCTGACG 157
Db 61 AGTACGTGAACAAAGGGAAGGCAATCTCTGACGCGCAACATCTCTGAGCGCTGACG 120
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 ORGANISM Sacccharum officinarum
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 1 (bases 1 to 3056)
 AUTHORS Nogueira, F.T.S., de Rosa, V.E. Jr., Menossi, M., Ulian, E.C. and

TITLE RNA expression profiles and data mining of sugarcane response to
 JOURNAL low temperature
 MEDLINE Plant Physiol. 132 (4), 1811-1824 (2003)
 PUBMED 22795309
 COMMENT Contact: Nogueira FTS
 Bioinformatics Lab
 Organization for Nucleotide Sequencing and Analysis
 C.P. 6176, Campinas, SP 13083-970, Brazil
 Tel: 55 19 37881101
 Fax: 55 19 37881089
 Email: tebaldi@unicamp.br

FEATURES
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 Zea mays
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 1 (bases 1 to 3140)
 Hairey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
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 Maize Mapping Project/DuPont Consensus Sequences for Design of
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 Unpublished (2002)
 2 (bases 1 to 3140)
 Coe, R.H.
 REFERENCE
 JOURNAL
 TITLE
 AUTHORS
 SUBMITTED (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at NSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
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FEATURES
Source

www.zmsh.iasate.edu.

Location/Qualifiers
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ORIGIN

Query Match 42.2%; Score 1162.4; DB 11; Length 3140;
Best Local Similarity 68.3%; Pred. No. 5.4e-129;
Matches 1656; Conservative 0; Mismatches 761; Indels 7; Gaps 3;

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D8 2217 TTGAGCCCATGACCTGTGAGGCTTCTTACTTTCGCAACGCTTCGATGAGGCTTCAGTGA 2276
QY 2102 TCAATGACATGCGCTCTCGGCTTCCGATTTGACATTCGATCCGATCCGACGAGGCTGTTA 2161
D8 2277 TCAATGACATGCGCTCTCGGCTTCCGATTTGACATTCGATCCGATCCGACGAGGCTGCG 2336
QY 2162 ATCTGATGCGGAGCTCTTTCGACGCGTGCAGCAAGCCGATGATCTGCGTGAATATAT 2221
D8 2337 CCTCTCTGTGATCTTCTTCGACAGCTGCGAGCGGACCCGACGATCTGAGCAAGATCT 2396
QY 2222 CTGAGCAGCGGCTGACGCGCTATTAAGAACTACATGAAATATATCTCAGAGGCT 2281
D8 2397 CCGAGGCGGCGCTCAGCGATTCGAGGAGAACTACACCTGAAAGCTCTACTGAGAGGCG 2456
QY 2282 TGATGACATGCGCGGCTCTCAAGCTTCTGGAATATCTGTCGAAAGCTCGAGAGGCTGCG 2341
D8 2457 TGATGACATCTCAGCGGCTCTCAAGCTTCTGGAATATCTGTCGAAAGCTCGAGAGGCTGCG 2516
QY 2342 AGAGAGCGGCTGACGCGCTATTAAGAACTACATGAAAGCTTCGAGAGCTGCGAGAGCG 2401
D8 2517 AGAGCGGCGGCTGACGCGCTATTAAGAACTACATGAAAGCTTCGAGAGCTGCGAGAGCG 2576
QY 2402 TCCGCGCTTGCATTTGACCAACCGC 2425
D8 2577 TCCGCGCTGCGCTGAGAGGAGAGC 2600

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```

RESULT 4
BQ619258 1005 bp mRNA linear EST 06-SEP-2002
LOCUS BQ619258
DEFINITION RNOSE05F01.SK.ab1 Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSE05F01.SK.ab1 similar to sucrose synthase [Zea
mays], mRNA sequence.

```

```

ACCESSION BQ619258
VERSION BQ619258.1 GI:21622252
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
1 (bases 1 to 1005)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)

```

```

REFERENCE
AUTHORS Contact: Mark Fredrickson
TITLE Department of Plant Biology
JOURNAL University of Illinois
COMMENT 1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.

```

```

FEATURES
source Location/Qualifiers
1..1005
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="RNOSE05F01.SK.ab1"
/tissue_type="Roots"
/dev_stage="2 weeks old"

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/clone_lib="Salt stressed Zea mays roots cDNA library"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
mM NaCl"

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ORIGIN

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Query Match 28.8%; Score 794.6; DB 13; Length 1005;
Best Local Similarity 93.1%; Fred. No. 3.5e-85;
Matches 885; Conservative 0; Mismatches 56; Indels 10; Gaps 6;

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QY 1812 TGTGCTGTCGCGGCTTCAATGATGATCAACAGTCCAAAGAGCAGGAGAGATCGCGA 1871
D8 13 TGTGCTGTCGCGGCTTCAATGATGATCAACAGTCCAAAGAGCAGGAGAGATCGCGA 72
QY 1872 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1931
D8 73 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
QY 1932 CTCTGCGGAGCAAAACAGGCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGAT 1991
D8 133 CTCTGCGGAGCAAAACAGGCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGAT 191
QY 1992 TGTGCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
D8 192 TGTGCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
QY 2052 GACCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
D8 252 GACCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
QY 2112 TGTGCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2171
D8 312 TGTGCTGTCGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
QY 2172 GCACTTCTTCAACGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2231
D8 372 GCACTTCTTCAACGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 431
QY 2232 GCTGACGCGCATATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2291
D8 432 GCTGACGCGCATATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
QY 2292 GCGCGGCGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2351
D8 492 GCGCGGCGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
QY 2352 CTACCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2411
D8 552 CTACCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611
QY 2412 AATTGACCAACGCGAGTTCGCGCACTGCGATGCGTGAATGATGATGATGATGATGAT 2471
D8 612 AATTGACCAACGCGAGTTCGCGCACTGCGATGCGTGAATGATGATGATGATGATGAT 671
QY 2472 AACCTGAAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2531
D8 672 AACCTGAAGAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731
QY 2532 GCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2591
D8 732 GCTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 791
QY 2592 GGGTT---GCACTTGTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 2645
D8 792 GGGTTTGAAGTGTGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 851
QY 2646 GCAATTTCTTCTGCGGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 2703
D8 852 GCAATTTCTTCTGCGGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 911
QY 2704 TCT-GTTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2753
D8 912 TCTGTTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962

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```

RESULT 5
BO619406      938 bp      mRNA      linear      EST 06-SEP-2002
LOCUS          RNOSEQ7D02.SK.ab1 Salt stressed Zea mays roots cDNA library Zea
DEFINITION    mays cDNA clone RNOSEQ7D02.SK.ab1 similar to sucrose synthase [Zea
               mays], mRNA sequence.
BO619406
ACCESSION     BO619406.1 GI:21621400
VERSION
KEYWORDS
SOURCE
ORGANISM      Zea mays
               Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
               1 (bases 1 to 938)
               Wang, H. and Bohnert, H.J.
               Genomics of plant stress tolerance
               Unpublished (2002)
REFERENCE
AUTHORS       Contact: Mark Fredrickson
               Department of Plant Biology
               University of Illinois
               -201 W. Gregory Dr., Urbana, IL 61801, USA
               Tel: 2172655473
               Email: bohnertlab@life.uiuc.edu.
COMMENT
JOURNAL
FEATURES
source
               1..938
               Location/Qualifiers
               /organism="Zea mays"
               /mol_type="mRNA"
               /cui_xref="873"
               /db_xref="taxon:4577"
               /clone="RNOSEQ7D02.SK.ab1"
               /tissue_type="Roots"
               /dev_stage="2 weeks old"
               /clone_lib="Salt stressed Zea mays roots cDNA library"
               /note="Vector: Bluescript SK+; Stressed 24 hours at 150
               mM NaCl"
ORIGIN
Query Match      28.8%; Score 793; DB 13; Length 938;
Best Local Similarity 95.0%; Pred. No. 5.5e-85;
Matches 881; Conservative 0; Mismatches 36; Indels 10; Gaps 6;
QY      1812 TGTGCTGCTGCGCGGAGACATGATGCAACAAGTCCCAAGGACAGAGATGCGGGA 1811
DB      13 TGTGCTGCTGCGCGGAGACATGATGCAACAAGTCCCAAGGACAGAGATGCGGGA 72
QY      1872 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1931
DB      73 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
QY      1932 CTCTGCCAGACAAACAGGCGCGGTAAAGCGGAGCTTATGCTACATCGCTGATCCCA 1991
DB      133 CTCTGCCAGACAAACAGGCGCGGTAAAGCGGAGCTTATGCTACATCGCTGATCCCA 191
QY      1992 TGTGCTGCTGCGCGGAGACATGATGCAACAAGTCCCAAGGACAGAGATGCGGGA 2051
DB      192 TGTGCTGCTGCGCGGAGACATGATGCAACAAGTCCCAAGGACAGAGATGCGGGA 251
QY      2052 GACCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2111
DB      252 GACCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 311
QY      2112 TGGCGCTCTGCGGCTTCCACATGACCCGTACCAACCCGAAAGGCTGTATCTGATGGC 2171
DB      312 TGGCGCTCTGCGGCTTCCACATGACCCGTACCAACCCGAAAGGCTGTATCTGATGGC 371
QY      2172 CGACTCTTCTGACCGGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2231
DB      372 CGACTCTTCTGACCGGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 431
QY      2232 GCTGACGCGATATACGAGAGTACACATGAGAGATGATGATGATGATGATGATGATGATGAT 2291

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DB      432 SCTGACGCGATATACGAGAGTACACATGAGAGATGATGATGATGATGATGATGAT 491
QY      2292 GGCCTGGGCTCTACCGCTTCTGGAAGTACGCTGCAAGCTGCAAGGCTGCAAGGCTGCAAGGCTG 2351
DB      492 GGCCTGGGCTCTACCGCTTCTGGAAGTACGCTGCAAGCTGCAAGGCTGCAAGGCTGCAAGGCTG 551
QY      2352 CTACCTTGAGATGTTCTACATCTGAAAGTCCGCGAGCTGCGGAGACCGTCCGCTTGC 2411
DB      552 CTACCTTGAGATGTTCTACATCTGAAAGTCCGCGAGCTGCGGAGACCGTCCGCTTGC 611
QY      2412 AATTGACCAACGCGAGTACGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 2471
DB      612 AATTGACCAACGCGAGTACGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTG 671
QY      2472 AACCTGAGGACCTTACGATATTTAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 2531
DB      672 AACCTGAGGACCTTACGATATTTAGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 731
QY      2532 GCTGACGCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2591
DB      732 GCTGACGCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 791
QY      2592 GGGTT---GCACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2645
DB      792 GGGTTGCAAGTGTG33GTCGATTAAGTCTTAAATATGTCGCAAGCTGCGCT 851
QY      2646 GCAATTTG---TTTGCTGCGCAAGCGCGAGCGGAGCTGAGTGAAGTGTGATTAATATCAATAT 2703
DB      852 GCAATTTCTTTTCTGCGACCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 911
QY      2704 TCT-GTTGACCTGTGAAAAA 2729
DB      912 TCTGTTGACCTGTGAAAAA 938
RESULT 6
SCVPLB2C05C09.g LB2 Saccharum officinarum cDNA clone SCVPLB2C05C09
LOCUS          CA280212      835 bp      mRNA      linear      EST 26-SEP-2003
DEFINITION    5', mRNA sequence.
CA280212
ACCESSION     CA280212.1 GI:36007504
VERSION
KEYWORDS
SOURCE
ORGANISM      Saccharum officinarum
               Saccharum officinarum
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Saccharum.
               1 (bases 1 to 835)
               Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
               The libraries that made SUCEST
               Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
               Contact: Arruda P
               Centro de Biologia Molecular e Engenharia Genetica
               Universidade Estadual de Campinas
               Caixa Postal 6010, 13083-970, Campinas SP, Brazil
               Tel: 55 19 3788 1137
               Fax: 55 19 3788 1089
               Email: parruda@unicamp.br
               Clone distribution information can be found
               through the Brazilian Clone Collection Center (BCCC) at
               http://www.bcccenter.fcav.unesp.br
               Plate: C05 ROW: C column: 09
               Seq primer: T7 Promoter Primer.
FEATURES
source
               1..835
               Location/Qualifiers
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               /mol_type="mRNA"
               /db_xref="taxon:4547"
               /clone="SCVPLB2C05C09"
               /lab_host="DH10B"
               /clone_lib="LB2"
               /note="Organ: Lateral buds from plants adult plants

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growing in greenhouse; Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from po-3a+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucess1.lad.ic.unlcamp.br/public>

ORIGIN

Query Match 26.2%; Score 722; DB 14; Length 835;
Best Local Similarity 92.5%; Pred. No. 1.5e-76;
Matches 769; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

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OY 751 CCAGACCCATCTACCTGAGAAATTTCTTGGAGAGATCCCATGATTTTAACTGTT 840
DB 1 CCAGACCCATCAACCTGAGAAATTTCTTGGAGAGATCCCATGATTTTAACTGTT 60
OY 841 GTGGATCCCTCTATGATATCTTGTGCAAGTATATTTAGGCTTCCAGACAGAGA 900
DB 61 GTGGATCCCTCTATGATATCTTGTGCAAGTATATTTAGGCTTCCAGACAGAGA 120
OY 901 GGAACATGCTCTATATCTGAGACCAAGTCCGTGCATAGAAATGAGATGCTCCGT 960
DB 121 GGAACATGCTCTATATCTGAGACCAAGTCCGTGCATAGAAATGAGATGCTCCGT 180
OY 961 TTAAGGAAACAAGGCTTGAATTTTCCCAAGATTTCTCATGTTTACTGCGCTAGCA 1020
DB 181 TTAAGGAAACAAGGCTTGAATTTTCCCAAGATTTCTCATGTTTACTGCGCTAGCA 240
OY 1021 GATGCAAAAAGGAACTCATGCAATGCAAGGCTTGAAGATTTGAGAAACAAGATCT 1080
DB 241 GATGCAAAAAGGAACTCATGCAATGCAAGGCTTGAAGATTTGAGAAACAAGATCT 300
OY 1081 TACATATTACAGAGTCCCTTGAAGATGAAATGCGATCTTAAGAAATGATATCAGA 1140
DB 301 TACATATTACAGAGTCCCTTGAAGATGAAATGCGATCTTAAGAAATGATATCAGA 360
OY 1141 TTTGATGTGGCCATATCTGGAACATTTGCTGAGATGCTGCTGAGAAATGCTGCT 1200
DB 361 TTTGATGTGGCCATATCTGGAACATTTGCTGAGATGCTGCTGAGAAATGCTGCT 420
OY 1201 GATTTACAGAGTCTCCAGATCTCATTAATTTGAAATCTAGGATGGAATCTTGAGC 1260
DB 421 GATTTACAGAGTCTCCAGATCTCATTAATTTGAAATCTAGGATGGAATCTTGAGC 480
OY 1261 TCATTCCTATCTTACAGAGTGGAAATTAACAGTGCATGCTCATGCTGAGAAAG 1320
DB 481 TCATTCCTATCTTACAGAGTGGAAATTAACAGTGCATGCTCATGCTGAGAAAG 540
OY 1321 ACTAAGTATCCAGATTCAGACATTTTGGAGAAATTTGAGAGAAATTCATTTCTCC 1380
DB 541 ACTAAGTATCCAGATTCAGACATTTTGGAGAAATTTGAGAGAAATTCATTTCTCC 600
OY 1381 TCCAGTTCATCTGAGATTAATTTGCTATGAAACAATGATTTTATCATCAACAGACA 1440
DB 601 TCCAGTTCATCTGAGATTAATTTGCTATGAAACAATGATTTTATCATCAACAGACA 660
OY 1441 TACCAAGAAATTTGC-TGGAAGCAAAATCTGTTGAGACAGTATGAGAGTCACTGCTT 1499
DB 661 TACCAAGAAATTTGCTGGAAGCAAAATCTGTTGAGACAGTATGAGAGTCACTGCTT 720
OY 1500 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
DB 721 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
OY 1560 TATAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
DB 781 TATAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831

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RESULT 7

CB662799 888 bp mRNA linear EST 09-APR-2003
LOCUS
DEFINITION
OSUNED07C12 f OSUNED Oryza sativa (japonica cultivar-group) cDNA
clone OSUNED07C12 5', mRNA sequence.
ACCESSION
CB662799
VERSION
CB662799.1 GI:29666524
KEYWORDS
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukarjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 888)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Ming,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe oryzae
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel.: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR primers
FORWARD: gta aac cga cga cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: C column: 12
Seq primer: gta aac cga cga cca gtc.
Location/Qualifiers
1..888
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
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/clone="OSUNED07C12"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNED"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES

source
1..888
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="OSUNED"
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XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Query Match 25.6%; Score 704.8; DB 14; Length 888;
Best Local Similarity 87.8%; Pred. No. 1.6e-74;
Matches 780; Conservative 0; Mismatches 107; Indels 1; Gaps 1;

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OY 711 GAAAGTTGGGCTGATACAGACGACATGTTTGGAAATGATCCATCTCTTACAGAT 770
DB 1 GAAAGTTGGGCTGATACAGACGACATGTTTGGAAATGATCCATCTCTTACAGAT 60
OY 771 CATTCAGGCGCAGACCCATCTACCTTGAAGAAATTTGGGAGAGATCCCATGATTT 830
DB 61 GCTTCAGGCGCAGACCCATCTACCTTGAAGAAATTTGGGAGAGATCCCATGATTT 120
OY 831 TTAAGTTGTTGGTATCCCTCATGAGATTTGGTCAAGTATATGATTTAGCTTACC 890
DB 121 TTAAGTTGTTGGTATCCCTCATGAGATTTGGTCAAGTATATGATTTAGCTTACC 180
OY 891 AGACACAGAGGACAGATGCTATATCTGACCAAGTCCGTGACTAGAAAAATGAGAT 950
DB 181 AGATATCGAGAGGACAGATGCTATATCTGACCAAGTCCGTGACTAGAAAAATGAGAT 240
OY 951 GGTTCCTGTTTAAAGAAACAAGGCTTGAATTTTCCCAAAAGATCTCATGTTACTCG 1010
DB 241 GGTTCCTGTTTAAAGAAACAAGGCTTGAATTTTCCCAAAAGATCTCATGTTACTCG 300
OY 1011 GCTGATTCAGAGATGCAAAAGAAACATGATGATGAGGCTTGAAGAAATTTAGTGAAC 1070

```

Db	301	GCTGATATCCAGAAACCAAAAGGAGCATCATGCAATACAGGCTTTGAGAGAAATTAATGGGAC	360
QY	1071	ACAGCATACTACATATTACAGAGTTCCTCCAGAAATGAAATATGGAAATCTTAAGAAATG	1130
Db	361	ACACATATCTTACATATTACAGAGGCCATTCAGAAATGAAATGGGAATCTCAGAAATG	420
QY	1131	GATATCAAGATTTGATATGTGGCCATTTCTGGAACATTTGCTGAGATATGCTGCTGGTGA	1190
Db	421	GATATCAAGATTTGATATGTGGCCCTTACTGGAGAAATTTGCAGAGATGCTGCTGGTGA	480
QY	1191	AATTGCTGCTGAATTAAGAGTATCTCCAGACTTCATTAATGGAACTACAGTGAATGAAA	1250
Db	481	GATGTCGCGAATCTAAGAGTATCTCCAGACTTCATTAATGGAACTACAGTGAATGAAA	540
QY	1251	TCATTGGCGCTCATGCTGCTATTCTTAACAGATGGGAATTAACCAATGCAACATTTGCTCATC	1310
Db	541	TCATTGGCATCATGCTGCTATTCTTAACAGATGGGAATTAACCAATGCAACATTTGCTCATGC	600
QY	1311	TCCTGGAATTAAGCTAAGATCCAGATTCAGACATATTTTGGAAAGATTTGATGATGGAAGTA	1370
Db	601	TTTGGAAATTAAGCTAAGATTCAGACTCAGACATATATCTGAGAGATGAGAAATGA	660
QY	1371	CCATTTCCTCCGCCAGTCACTGCTGATATTAATGCTATGAAACATGCTGATTTTATGCT	1430
Db	661	CCATTTCCTCCGCTAGTTCACAGCTGATATTAATGCGATGAACATGCTGATTTTATGCT	720
QY	1431	CACCGACATATCCAGAAATGTCTGAAAGCAAAATATCTTTGGACAGTATGAGTCA	1490
Db	721	CACCGACATATCCAGAAATGTCTGCGAGCAAAACACAGTTGGACAGTATGAGAGCA	780
QY	1491	TATGCGCTTATCTGCGCTGGTCTGTAACCAAGTTGCCATGGAGATGATGCTTCGATC	1550
Db	781	TATGCGATTTATCTTCTCTGCTGTATGATGCAATGTCATGGGCAATATGTTTGTGACC	840
QY	1550	CAAGGTCATATATGTCCTCTCGAGAGTGAATGCAATGATATCTTC	1597
Db	841	CAAGGTCATATATGTCCTCTCGAGAGAGAGACATGCTTAATATCTTC	888

RESULT 8	CS629313	LOCUS	DEFINITION
CS629313	909 bp	mRNA	linear EST 08-APR-2003
OS1EB05H07.f	OS1EB	Oryza sativa	(indica cultivar-group) cDNA
clone OS1EB05H07.5,		mRNA sequence.	

ORIGIN

Query Match	25.5%	Score 702.8	DB 14	Length 909
Best Local Similarity	86.9%	Pred. No. 2,8e-74		
Matches 773; Conservative	0	Mismatches 117	Indels 0	Gaps 0

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/mol_type="RNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIIEB05H07"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIEB"
/notes="vector: pBluescript II KS +; Site 1: EcoRI; Site 2
XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

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/db_xref="taxon:39946"

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/L188ue_cype=Weak
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/dev_stgenc=0 mcken
/lab_host="DH10B"
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/clone lib="OSIIEb
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/note="Vector: pBl
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XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)

QY	422	ATGTCATAGTCCCAAGCCCAATGGATCATATATTTGAAACGGATGAGTTCCTCA	481
Db	19	ATGCTCGGTTCAGCGCCCAATGGATCATCAATTTGAAATGGCGTGAATTCTCA	78
QY	482	ACCGACACTTGTCTCTAATCATGTTCCGCAACAGGATGCTTGGAGGCCCTGTTGATT	541
Db	79	ACAGGCACTTGTCTTCATCATGTTCGAAACAAAGATGCTGAGGCCCTACTTGATT	138
QY	542	TCCCTCCGTGGCAACCGGCAACAGGGGAGATGTTAGATGCTTAATGATGATACAAACT	601
Db	139	TCTCTTGTCGATTCGGCATTAAGGTCAATGTCATGATGCTTAATGACAGATACAGATC	198
QY	602	TGGGAGAGCTTCAGTCTGTGCTGAACAAAGCTGAGAGACCTTGTCAAAAGCTCCTGCTG	661
Db	199	TGGAGAGCTTCAGTCTGTGCTGAACAAAGCTGAGAGACCTTGTCAAAAGCTCCCAAGCTG	258
QY	662	ACACACCACTCTCAATTTGCTATTATAATTTCAAGATGGGGGCTGGAGAAAGTTGAG	721
Db	259	ACACACCACTCTCAAGTTGCGCATATAAGTTCAAGATGGGAGATGAGAAAGGTTGAG	318
QY	722	GTCATCAGCAGGACATGTTTGGAAATGATCCATCTCTTCAGACATCATTCAGGCGC	781
Db	319	GCGACACAGCTGGATATATCTTTGAGATGATACATCTCTCTTGGATGTGCTCGCAAGGC	378
QY	782	CAGACCCATCTACCTTAGAGAAATTTCTGGGAGAGATCCCATGATTTTTAAAGTTGTT	841
Db	379	CTGATCCATCTACTCTTGAGAGCTTCTTGGAGAGATCCCATGATCTTTAAATGTGCTG	438
QY	842	TGATATCCCTCATAGTACTTGTGTCAGCTATATGATTAAGGCTTGCAGACACAGGAG	901
Db	439	TAGGTCTCCCTCAGATATATTTGGCCAAAGCCAAATGTGTGGCTTACCAATGACTGGAG	498
QY	902	GACAGATCGTCTATATACTGGACCAAGTCCGTGCACTAGAAATAGATGTTCTCCGTT	961
Db	499	GCGATTTGTCTATATTACTGGACCAAGTCCGTGCACTGGAGATAGATGTTCTTAGGT	558
QY	962	TAAAGAAACAAGGCGTGTATGTTTTCCCAAGATTTCTCATTTTACTGTGGCTGATACAG	1022
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QY	1022	ATGCAAAAGAAACATATGATGATCAGCGGCTTGGAGAAATAGTGGACACAGCATACTT	1081
Db	619	AAGCAAAAGGACATCATGCAATCAGCGCTTGGAGAAATAGTGGACACACATACTT	678
QY	1082	ACATTTACAGAGTCCCTTCAGAAATGAAATGGATACTTAAGAAATGATATCAAGT	1144
Db	679	ACATTTACAGAGTGCATTCAGAAATGAAATGGATATCAGGAAATGGATATCAAGT	738
QY	1142	TTGATGTGGCCATATCTGGAAACATTTGCTGAGATGTGCTGTGTAATTTGCTGCTG	1201
Db	739	TTGATGTATGGCCCTTACCTGGAGAAATTTGCTGAGAGATGTGCTGTGTAATTTGCTGCG	798
QY	1202	AATTTCAGATCTCCAGACTCATATTTGAAATCAACGATGAGAAATCTGTGCGCT	1261
Db	799	AATTCAGAGTACTCCAGACTTCATATTTGAAATCAACGATGAGAAATCTGTGCTGAT	858

QY 1262 CATTGCTATCTTACAGATGGGAATTACCCAGTCGCAACATTGCTCATGCT 1311
DB 859 CATTGCTATCTTACAGATGGGAATTACCCAGTCGCAACATTGCTCATGCT 908

RESULT 9
LOCUS CB648550
DEFINITION OSJNEB11P18.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEB11P18 5', mRNA sequence.
ACCESSION CB648550
VERSION CB648550.1 GI:29643543
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 841)
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: P column: 18
Seq primer: gta aaa cga cgg cca gtcg.
Location/Qualifiers
1..841
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/clone="OSJNEB11P18"
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XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

ORIGIN
Query Match 25.0%; Score 688.6; DB 14; Length 841;
Best Local Similarity 88.8%; Pred. No. 1.4e-72;
Matches 745; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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QY 1003 GTTACTCGGCTATACAGATGCAAGAAAGACATCATGCAATCAGCGCTTGAGAGATT 1062
DB 62 GTTACTCGGCTATACAGATGCAAGAAAGAGACATCATGCAATCAGCGCTTGAGAGAAATA 121

QY 1063 AGTGAACACAGATCTTACATATTACAGATTCCCTTGAGAAATGGAATGGAATCTT 1122
DB 122 AGTGGGACACAACTACTTACATATTACAGATGCAAGTCCCATTCAGAAATGGAATGGAATCTT 181

QY 1123 AAGGAATGATTCAGATTGATGATGTCGCCATATCTGGAACATTTGCTGAGATGCT 1182
DB 182 AAGGAATGATTCAGATTGATGATGTCGCCATATCTGGAACATTTGCTGAGATGCT 241

QY 1183 GCTGTGAATTTGCTGCTGAAATTACAAAGTACTCCAGATCTTCAATATTGGAACATACAGT 1242
DB 242 GCTGTGAATTTGCTGCTGAAATCTCAAGTACTCCAGATCTTCAATATTGGAACATACAGT 301

QY 1243 GATGGAATCTTTGGGGCTCATTTGCTATCTTACAAAGATGGAATTAACCAAGTCAACATT 1302
DB 302 GATGGAATCTTTGGGGCTCATTTGCTATCTTACAAAGATGGAATTAACCAAGTCAACATT 361

QY 1303 GCTCATGCTGTGAAAAGAACTAAGTATCCAGATTCAGACATATTTTGGAGAATTTGAT 1362
DB 362 GCTCATGCTGTGAAAAGAACTAAGTATCCAGATTCAGACATATTTGAGAATTTGAT 421

QY 1363 GAGAATGACATTTCTCTCCGCAAGTTCATCTCGATATTAATTGTAACATGCTGAT 1422
DB 422 GAGAATGACATTTCTCTCTCCGCAAGTTCATCTCGATATTAATTGTAACATGCTGAT 481

QY 1423 TTTATCATACAGACATACCAAGAAATTTGCTGGAACCAAAAATAGTGTGAGAGAT 1482
DB 482 TTTATCATACAGACATACCAAGAAATTTGCTGGAACCAAAAATAGTGTGAGAGAT 541

QY 1483 GAGAGTCTACTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542
DB 542 GAGAGTCTACTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

QY 1543 TTGATCCAAAGTTCAATATATGCTCTCTCTGAGCTGACATGCTCATATATCTTCCACAT 1602
DB 602 TTGATCCAAAGTTCAATATATGCTCTCTCTGAGCTGACATGCTCATATATCTTCCACAT 661

QY 1603 ACCGAGAAAGGCAAGCACTACCTCTCTTCAAGTCAATGAAATTTGATTAAGC 1662
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QY 1663 CCGAGCAAAACGATGAAACATTTGAGCATCTGATGACCGGCTCAAGGCTCATCTTCTTC 1722
DB 722 CCGAGCAAAACGATGAAACATTTGAGCATCTGATGACCGGCTCAAGGCTCATCTTCTTC 781

QY 1723 TCCATGCAAGCTCTGACAGGCTGAAAGACATTAACAGGCTGCTGCAACCTTTGCTAA 1781
DB 782 TCCATGCAAGCTCTGACAGGCTGAAAGACATTAACAGGCTGCTGCAACCTTTGCTAA 840

RESULT 10
LOCUS CB628458 886 bp mRNA linear EST 08-APR-2003
DEFINITION OSIEB04A18.f OSIEB Oryza sativa (indica cultivar-group) cDNA
clone OSIEB04A18 5', mRNA sequence.
ACCESSION CB628458
VERSION CB628458.1 GI:29623447
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 886)
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: A column: 18
Seq primer: gta aaa cga cgg cca gtcg.

QY 730 GCAGAGCATGTTGGAAATGATCATCTCTCTTAGACATCATTCAGGCGCCAGACCA 789
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 DB 121 TCAACCTAGAAATCTTGGGAGATCCCAATTTTAACTGTTGTGTATCC 180
 QY 850 CCGCATGATATCTTGGTCAAGCTAATGTAATTAGCTTGCAGACAGAGACATC 909
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 QY 910 GCTATATATCTGACCAAGTCCGTGCACTAGAAAATGATGTTCTCCGTTTAAAGAA 969
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 QY 970 CAAGGCTTGAATGTTTCCCAAGATCTCATGTTACTCGGCTGATACGATGCAAA 1029
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 QY 1030 GGAACATCAAGCAATCGGCGCTGAGAGATGAGAACACAGACATCTACATTA 1089
 DB 361 GGAACATCAAGCAATCGGCGCTGAGAGATGAGAACACAGACATCTACATTA 420
 QY 1090 CGAGTCCCTCAGAGATGAAAATGGGATCTTAAGAAATGGAATCAAGATTGATGTG 1149
 DB 421 CGAGTCCCTCAGAGATGAAAATGGGATCTTAAGAAATGGAATCAAGATTGATGTG 480
 QY 1150 TGGCCATATCTGAAACATTTGCTGAGATGCTGCTGTAATGCTGCTGAATTA 1209
 DB 481 TGGCCATATCTGAAACATTTGCTGAGATGCTGCTGTAATGCTGCTGAATTA 540
 QY 1210 GGTCTCCAGACTTATATGGAATACAGTGAATGGAATCTGCTGCTGCTGCTA 1269
 DB 541 GGTCTCCAGACTTATATGGAATACAGTGAATGGAATCTGCTGCTGCTGCTA 600
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 QY 1330 CCAAGTATGACATAT-TTGGAGAAATTTGATGAGAAATGCTGCTGCTGCT 1387
 DB 661 CCAAGTATGACATAT-TTGGAGAAATTTGATGAGAAATGCTGCTGCTGCT 720
 QY 1388 TCACGTGATATATGCTATGAA 1412
 DB 721 TCACGTGATATATGCTATGAA 745

RESULT 12 836 bp mRNA linear EST 08-APR-2003
 C9631982
 LOCUS OSIIIB09015.f OSIIIB Oryza sativa (indica cultivar-group) cDNA
 DEFINITION
 OSIIIB09015.5, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 836)
 Jantschiyarak, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
 Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe grisea
 Unpublished (2003)
 Contact: Rod Wang
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA

Tel: 520 626 3967
 Fax: 520 621 9288
 Email: <http://genome.arizona.edu>
 PCR Primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 09 row: 0 column: 15
 Seq primer: gta aac cga cgg cca gtc.
 Location/Qualifiers
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 XhoI; 24 hrs after inoculation with Rice Blast (P06-6-3)"

ORIGIN

Query Match 24.5%; Score 676; DB 14; Length 836;
 Best Local Similarity 88.0%; Pred. No. 4,3e-71;
 Matches 736; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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 QY 721 GATGATACAGAGACATGTTTGGAAATGATCCATCTCTCTCTAGACATCATTCAGGCG 780
 DB 61 GCGCAGACAGCTGATGCTTGGAGATGATACATCTCTCTCTGATGTGCTGCAAGG 120
 QY 781 CCAAGCCATCTACCTTGAAGAAATCTTGGGAGAGATCCCATGATTTTAACTGTT 840
 DB 121 CCGTATCAATCTACTTGGAGCGTTCTTGGAGAGATCCCATGATTTTAACTGTT 880
 QY 841 GGTGATCCCTCATGATGATCTTGGTCAAGCTAATGATGATGCTTGGTCAAGACAGA 900
 DB 181 GGTGATCCCTCATGATGATCTTGGTCAAGCTAATGATGATGCTTGGTCAAGACAGA 240
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 DB 241 GGGCAGATGCTTATATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCCG 300
 QY 961 TTAAGAAACAGAGGCTGATGTTTCCCAAGATCTCATGTTACTGCTGCTGATACCA 1020
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 QY 1021 GATGCAAAAGAACATCATGCAATCGGCGCTTGAAGAAATTAAGTGAACACAGCATCT 1080
 DB 361 GATGCAAAAGAACATCATGCAATCGGCGCTTGAAGAAATTAAGTGAACACAGCATCT 420
 QY 1081 TACATATACAGTTCCTTCAAGAAATGAAATGGAATCTTAAGAAATGATATCAAGA 1140
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 QY 1321 ACTAAGATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAAATGCAATTTCTCC 1380

Db 661 ACTAATATCCAGACTCAGACATATATGAGCAAGTACGATGAGAGTACCATTTCTCC 720

Qy 1381 TCCGCTTCTACTGCTGATATATGCTATGAAACAATGCTGATTTATCATCCAGCA 1440

Db 721 TGTCAAGTTCACAGCTGATATATCCGCAAGAACAAAGCTGATTTATTAATCCAGCA 780

Qy 1441 TCCGAGAAATGCTGGAGCAAGCAAAATATCCTGTGACAGATGAGTCACTG 1496

Db 781 TACCGAGAAATGCTGCGCAGCAAAACAGAGTTGACAGTATGAGGCCATCTGC 836

RESULT 13

CD442316 690 bp mRNA linear EST 03-JUN-2003

LOCUS ELUTIN0407HE37.b Endosperm_4 Zea mays cDNA, mRNA sequence.

CD442316

ACCESSION CD442316

VERSION CD442316.1 GI:31357959

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.

AUTHORS Sequencing of the maize endosperm ESTs

TITLE Unpublished (2002)

JOURNAL Contact: Lai, Jinsheung

COMMENT Dr. Joachim Messing's lab

Wakeman Institute, Rutgers University

193 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-3801

Fax: 732-445-5735

Email: jlai@wakeman.rutgers.edu

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..690

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/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 24.1%; Score 664; DB 14; Length 690;

Best Local Similarity 97.8%; Pred. No. 1.2e-69;

Matches 673; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 918 ACTGAGCAAAATGCTGCTGCTAGTAAATGAGATGCTTCTCGTTTAAAGAAACAAGGCT 977

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Qy 978 TGAATTTTCCCAAAAGTCTTCAATGTTTCTCGGCTGATACAGATGCAAAAGGAATC 1037

Db 63 TGAATTTTCCCAAAAGTCTTCAATGTTTCTCGGCTGATACAGATGCAAAAGGAATC 122

Qy 1038 ATGCAATCAGGCGCTTGAAGAAATTAAGTGAACAACAGATCACTTACATTTACAGATTC 1097

Db 123 ATGCAATCAGGCGCTTGAAGAAATTAAGTGAACAACAGATCACTTACATTTACAGATTC 182

Qy 1098 CTTTCAGAAATGAAATGAGATCTTAAAGAAATGATATCAAGATTTGATGTGTGCGCAT 1157

Db 183 CTTTCAGAAATGAAATGAGATCTTAAAGAAATGATATCAAGATTTGATGTGTGCGCAT 242

Qy 1158 TCTGGAATCATTTCTGCTGAGATGCTGTGCTGGAATTTGCTGCTGATTAACAAGTACCC 1217

Db 243 TCTGGAATCATTTCTGCTGAGATGCTGTGCTGGAATTTGCTGCTGATTAACAAGTACCC 302

Qy 1218 AGACTTCATATATGAAATCACTACAGTATGAAATCTTGTGCGTCAATGCTATCTTACAA 1277

Db 303 AGACTTCATATATGAAATCACTACAGTATGAAATCTTGTGCGTCAATGCTATCTTACAA 362

Qy 1278 GATGGGAATTACCGATGCAACATTTCTCATGCTCTGAAAAAGACTAATGATTC 1337

Db 363 GATGGGAATTACCGATGCAACATTTCTCATGCTCTGAAAAAGACTAATGATTC 422

Qy 1338 AGACATATTTTGGAAAGATTTGATGAGAGTACCAATTTCTCTGCGATTCAGTCTGA 1387

Db 423 AGACATATTTTGGAAAGATTTGATGAGAGTACCAATTTCTCTGCGATTCAGTCTGA 482

Qy 1398 TATATGCTATGAAACAATGCTGATTTTATCATCAGACAGACATACCAAAATTTGCTG 1457

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Qy 1458 AAGCAAAATATCTGTTGACAGATGAGATCACTGCTTACTGCTGCTGCTGTA 1517

Db 543 AAGCAAAATATCTGTTGACAGATGAGATCACTGCTTACTGCTGCTGCTGTA 602

Qy 1518 CCGAGTTGTCATGAGATGAGATGCTCTTGATCCAAAGTTCAATATGCTCTCTGAGC 1577

Db 603 CCGAGTTGTCATGAGATGAGATGCTCTTGATCCAAAGTTCAATATGCTCTCTGAGC 662

Qy 1578 TGAATGCTCATATCTTCTTCCACATACC 1605

Db 663 TGAATGCTCATATCTTCTTCCACATACC 690

RESULT 14

CB627276 860 bp mRNA linear EST 08-APR-2003

LOCUS OS1IB02C04.f OS1IEB Oryza sativa (indica cultivar-group) cDNA

DEFINITION clone OS1IEB02C04 5', mRNA sequence.

ACCESSION CB627276

VERSION CB627276.1 GI:29622265

KEYWORDS EST.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 860)

Jant-surilarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.

TITLE Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

JOURNAL Unpublished (2003)

COMMENT Contact: Rod Wang

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 02 row: C column: 04

Seq primer: gta aac cga cgg cca gtc.

FEATURES

source

1..860

/organism="Oryza sativa (indica cultivar-group)"

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/tissue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_idb="OS1IEB"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (Poc-6-3)"


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QY 1171 GGTGAGATGCTGCTGGTGAATTCGCTGATTAAGAAGTACTCCAGACTTCATTAAT 1230
Db 482 GAGAGAGTCTGCTGCTGATGATTCGCAAGACTACAGTACTCCAGACTTCATTAAT 541
QY 1231 GGAATCTACAGTATGGAATCTTGTGGGTCATTCCTATCTTACAGATGGGAATTACC 1290
Db 542 GGAATCTACAGTATGGAATCTTGTGGGTCATTCCTATCTTACAGATGGGAATTACC 601
QY 1291 CAGTGCAATGCTGCTGCTGCAAGAAAGACTAAGTATCCAGATTCAGACATTAATTGG 1350
Db 602 CAGTGCAATGCTGCTGCTGCAAGAAAGACTAAGTATCCAGATTCAGACATTAATTGG 661
QY 1351 AAGAAATTCGATGAGAAAGTACCATTTCTCTGCCAGTTCAGTCTGATTAATTGCTATG 1410
Db 662 ACGAAGTACGATGAGAAAGTACCATTTCTCTGCCAGTTCAGTCTGATTAATTGCTATG 721
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Db 722 AACAAATGCTGATTTTATCATCAACGACACATACCAAGAAATTCCTGAAAACAAAATACT 781
QY 1471 GTTGACAGTATGAGAGTCACTGC 1496
Db 782 GTTGACAGTATGAGAGTCACTGC 807
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 19:59:12 ; Search time 787.858 Seconds
(without alignments)

15903.652 Million cell updates/sec

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Perfect score: 2757

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Gapop 10.0 , Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2189.2	79.4	2275	13	US-10-425-114-6036 Sequence 6036, Ap
4	1837.4	66.6	1874	13	US-10-425-114-6561 Sequence 6561, Ap
5	1352.4	49.1	2832	13	US-10-425-114-15113 Sequence 15113, A
6	1325.6	48.1	3131	13	US-10-424-599-98889 Sequence 98889, A
7	1309.8	47.5	1340	13	US-10-425-114-5285 Sequence 5285, Ap
8	1249.8	45.3	2430	9	US-09-938-842A-2415 Sequence 2415, Ap
9	1181.2	42.8	2334	11	US-10-217-939-29 Sequence 29, Appl
10	1173.4	42.6	2388	15	US-10-080-114a-6 Sequence 6, Appl
11	1173.4	42.6	2386	13	US-10-425-114-2283 Sequence 2283, Ap
12	1173.4	42.6	2386	13	US-10-425-114-26430 Sequence 26430, A
13	1173.4	42.6	2386	13	US-10-425-114-26430 Sequence 26430, A
14	1173.4	42.6	2386	13	US-10-425-114-5310 Sequence 5310, Ap

15	1173.4	42.6	3419	13	US-10-425-114-17596	Sequence 17596, A
16	1172	42.5	2418	15	US-10-217-939-27	Sequence 27, Appl
17	1153.8	41.8	2601	13	US-10-425-114-9604	Sequence 9604, Ap
18	1152.2	41.8	3101	13	US-10-424-599-12144	Sequence 12144, A
19	1142.6	41.4	5069	13	US-10-424-599-115562	Sequence 115562, A
20	1138.2	41.3	2722	13	US-10-425-114-9534	Sequence 9534, Ap
21	1136.6	41.2	3438	13	US-10-424-599-11459	Sequence 11459, A
22	1135.6	41.2	2754	15	US-10-289-757-13	Sequence 13, Appl
23	1134.6	41.2	2671	13	US-10-425-114-31764	Sequence 31764, A
24	1134.6	41.2	2817	13	US-10-425-114-33573	Sequence 33573, A
25	1133	41.1	2714	15	US-10-289-757-133	Sequence 133, Appl
26	1133	41.1	2716	15	US-10-289-757-12	Sequence 12, Appl
27	1133	41.1	2746	15	US-10-080-114a-4	Sequence 4, Appl
28	1132.6	41.1	2906	16	US-10-393-840-139	Sequence 139, Appl
29	1132.4	41.1	2957	15	US-10-289-757-134	Sequence 134, Appl
30	1131	41.0	2913	16	US-10-393-840-15	Sequence 15, Appl
31	1131	41.0	3103	15	US-10-137-036-57	Sequence 57, Appl
32	1128.2	40.9	2825	15	US-10-289-757-15	Sequence 15, Appl
33	1124.4	40.8	2950	15	US-10-289-757-14	Sequence 14, Appl
34	1123.8	40.8	2722	13	US-10-425-114-6460	Sequence 6460, Ap
35	1123.8	40.8	3360	13	US-10-424-599-11458	Sequence 11458, A
36	1116	40.5	2638	14	US-10-425-114-2574	Sequence 2574, Ap
37	1104.6	40.1	2625	14	US-10-003-405-1	Sequence 1, Appl
38	1083.2	39.3	5877	16	US-10-260-238-25	Sequence 25, Appl
39	1062.6	38.5	2427	9	US-09-938-842A-1620	Sequence 1620, Ap
40	1062.6	38.5	2427	11	US-09-938-842A-1620	Sequence 1620, Ap
41	1053.4	38.2	2505	13	US-10-425-114-35609	Sequence 35609, A
42	1024.4	37.2	2279	13	US-10-425-114-9355	Sequence 9355, Ap
43	961.2	34.9	2307	13	US-10-425-114-35558	Sequence 35558, A
44	955.6	34.7	2210	13	US-10-425-114-8902	Sequence 8902, Ap
45	947.4	34.4	2127	13	US-10-425-114-10123	Sequence 10123, A

ALIGNMENTS

RESULT 1
US-10-080-114a-11
Sequence 11, Application US/10080114A
Publication No. US2003005482A1
GENERAL INFORMATION:
APPLICANT: Dnagga, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080,114A
PRIOR APPLICATION NUMBER: 2002-04-30
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2757
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CD6
LOCATION: (1)...(2430)
FEATURE:
NAME/KEY: source
LOCATION: (1)...(39)
OTHER INFORMATION: Sorghum pronominum
FEATURE:
NAME/KEY: source
LOCATION: (40)...(2757)
OTHER INFORMATION: Zea mays
US-10-080-114a-11

Query Match 100.0%; Score 2757; DB 15; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCTGCCCGAAGCTGAACCGGACGAGCATCCGGAGACCGCGTGAAGACCCCTC 60

1 ATGCTGCCCCGAGGCTGTAACCGCAACGCGAGCATCCGGGACCGGTGAGGACACCCCTC 60
QY 61 CAGCGGACCCGCAACAGACTGTGCGCTCTCTTCCAAAGTACGTGAACAAAGGAGC 120
Db 61 CACGCGACCCGCAACAGACTGTGCGCTCTCTTCCAAAGTACGTGAACAAAGGAGC 120
QY 121 ATCCGCAAGCCGCAACAGACTGTGCGCTCTTCCAAAGTACGTGAACAAAGGAGC 180
Db 121 ATCCGCAAGCCGCAACAGACTGTGCGCTCTTCCAAAGTACGTGAACAAAGGAGC 180
QY 181 GCGCTGCGCAAGGAGACCTTCTTGAAGTCTCCGCTCCGCGAGAGAGAGAGAGAGAG 240
Db 181 GCGCTGCGCAAGGAGACCTTCTTGAAGTCTCCGCTCCGCGAGAGAGAGAGAGAGAG 240
QY 241 CCGCGCTTCTGCGCAAGGAGACCTTCTTGAAGTCTCCGCTCCGCGAGAGAGAGAGAG 300
Db 241 CCGCGCTTCTGCGCAAGGAGACCTTCTTGAAGTCTCCGCTCCGCGAGAGAGAGAGAG 300
QY 301 AACGTTACAG 360
Db 301 AACGTTACAG 360
QY 361 GAGCTTGTCAAGGAG 420
Db 361 GAGCTTGTCAAGGAG 420
QY 421 AATGTCAG 480
Db 421 AATGTCAG 480
QY 481 AACGCAACATTCCTGCAAG 540
Db 481 AACGCAACATTCCTGCAAG 540
QY 541 TTCTCTCGTGGCGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 TTCTCTCGTGGCGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TTGGGAGAGGCTTCAAGTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 TTGGGAGAGGCTTCAAGTGTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 GACAACACATCTCAATCTTCTTAAATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 GACAACACATCTCAATCTTCTTAAATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GGTATACAG 780
Db 721 GGTATACAG 780
QY 781 CCAGACCATCTACCCCTAG 840
Db 781 CCAGACCATCTACCCCTAG 840
QY 841 GTGGATACCCCTCTGATGATCTTGTCAAGTATGATGATGATGATGATGATGATGATG 900
Db 841 GTGGATACCCCTCTGATGATCTTGTCAAGTATGATGATGATGATGATGATGATGATG 900
QY 901 GGAAGAGATCTCTATATCTGAAAGTCTGCGTCACTAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 GGAAGAGATCTCTATATCTGAAAGTCTGCGTCACTAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TTAAAG 1020
Db 961 TTAAAG 1020
QY 1021 GATGCAAAAG 1080
Db 1021 GATGCAAAAG 1080
QY 1081 TACATATTACAGAGTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 TACATATTACAGAGTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

1081 TACATATTACAGAGTCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 TTGATGTGCGCCATATCTGAAACATTTGCTGAGAGTGCCTGCTGAGAGAGAGAGAGAG 1200
Db 1141 TTGATGTGCGCCATATCTGAAACATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 GAATTAAGAGTCTCCAG 1260
Db 1201 GAATTAAGAGTCTCCAG 1260
QY 1261 TCATTTGATCTTCAAG 1320
Db 1261 TCATTTGATCTTCAAG 1320
QY 1321 ACTAGATTCAGAGTCTGAG 1380
Db 1321 ACTAGATTCAGAGTCTGAG 1380
QY 1381 TGCCAGTTCAGAGTCTGAG 1440
Db 1381 TGCCAGTTCAGAGTCTGAG 1440
QY 1441 TACCAAGAGAGTCTGAG 1500
Db 1441 TACCAAGAGAGTCTGAG 1500
QY 1501 ACTGCGCTGCTGTAAG 1560
Db 1501 ACTGCGCTGCTGTAAG 1560
QY 1561 AATGTCCTCTGAG 1620
Db 1561 AATGTCCTCTGAG 1620
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Db 1621 CTGACCTCTCTTCAAGTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 CACATGAG 1740
Db 1681 CACATGAG 1740
QY 1741 AGGATGAAG 1800
Db 1741 AGGATGAAG 1800
QY 1801 CTGGTAAACCTTGTGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 CTGGTAAACCTTGTGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 GAGATGCGAG 1920
Db 1861 GAGATGCGAG 1920
QY 1921 TTCCGCTGAGATCTTCCGCAAG 1980
Db 1921 TTCCGCTGAGATCTTCCGCAAG 1980
QY 1981 GCTGATACCATGAG 2040
Db 1981 GCTGATACCATGAG 2040
QY 2041 GTTGAAGCAG 2100
Db 2041 GTTGAAGCAG 2100
QY 2101 ATCATAG 2160
Db 2101 ATCATAG 2160
QY 2161 AATCTGATGCGAG 2220
Db 2161 AATCTGATGCGAG 2220

[illegible]

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RESULT 2
US-10-080-114A-1
; Sequence 1, Application US/10080114A
; Publication No. US20030305482A1
; GENERAL INFORMATION:
; APPLICANT: Dhara, Karwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; TITLE OF INVENTION: To Improve Stalk and Grain Quality
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080.114A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Zea mays
US-10-080-114A-1

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	Query Match	Similarity	Score	DB	Length
Best Local	98.4%	99.8%	2714	15	2737
Matches	2117	Conservative	0	Mismatches	5
				Indels	0
				Gaps	0

Db	136	CGAGGTCCAGGGCTCCGGGGGCGCGCGCTAGGCGAAGGAGACCTTCTCCGACGTCCTCG	195
QY	216	CTCCGCGCAGAGGCGCATCGTGTCTCCGCCGTTCTGTGGCCATCGCGGTGGCGCGCGCC	275
Db	196	CTCCGCGCAGAGGCGCATCGTGTCTCCGCCGTTCTGTGGCCATCGCGGTGGCGCGCGCC	255
QY	276	GGAGTTTGGGAGTAACTCCGGCGTCAAGTTCAGACTCAGACTCGAGAGCTCAAGAT	335
Db	256	GGAGTTTGGGAGTAACTCCGGCGTCAAGTTCAGACTCAGACTCGAGAGCTCAAGAT	315
QY	336	CTCGAGTACTCCGCTTCAAGAGGAGCTGTCTGACGGCGCAGACATGATCCCTACGT	395
Db	316	CTCGAGTACTCCGCTTCAAGAGGAGCTGTCTGACGGCGCAGACATGATCCCTACGT	375
QY	396	TCTGAGCTTGACTTCGAGCGCGTTCAATGTCTAGTCCACGCCCAATCGATCATC	455
Db	376	TCTGAGCTTGACTTCGAGCGCGTTCAATGTCTAGTCCACGCCCAATCGATCATC	435
QY	456	TATTGGAACGGGTGCGATTCCTCAACCGACATGTCTCCATCATGTCGCCCAAG	515
Db	436	TATTGGAACGGGTGCGATTCCTCAACCGACATGTCTCCATCATGTCGCCCAAG	495
QY	516	GGATTGCTGGAGCCCCGTGTGATTCCTCCGGGCGCACCGGCGCAAGGGCATGTAT	575
Db	496	GGATTGCTGGAGCCCCGTGTGATTCCTCCGGGCGCACCGGCGCAAGGGCATGTAT	555
QY	576	GATGCTTAATGATGAATACAAAGCTTGGGAGGCTTCAGTGTGTCTGACCAAGCTGA	635
Db	556	GATGCTTAATGATGAATACAAAGCTTGGGAGGCTTCAGTGTGTCTGACCAAGCTGA	615
QY	636	GGAGACCTTGCAAAAGCTCCTCGCTGACACGCCATCATCAATTTGCTTAAATTTCA	695
Db	616	GGAGACCTTGCAAAAGCTCCTCGCTGACACGCCATCATCAATTTGCTTAAATTTCA	675
QY	696	AGAGTGGGGCTGGAGAAAGTTGGGGGTATACAGCAGAGCATGTTTGGAAATGATCA	755
Db	676	AGAGTGGGGCTGGAGAAAGTTGGGGGTATACAGCAGAGCATGTTTGGAAATGATCA	735
QY	756	TCTCCTTCAACATCATTCAGGGCGCCAGCCCATACCTTAGAATAATCTTGGGAG	815
Db	736	TCTCCTTCAACATCATTCAGGGCGCCAGCCCATACCTTAGAATAATCTTGGGAG	795
QY	816	GATCCCATGATTTTAAAGTTGTGTGTGTATCCCTCATGATGATCTTTGGCAAGCTTA	875
Db	796	GATCCCATGATTTTAAAGTTGTGTGTGTATCCCTCATGATGATCTTTGGCAAGCTTA	855
QY	876	TGTATTAGGCTTGCAGACAGAGGAGCAGATCGTCTATATACGACCAAGTCGTC	935
Db	856	TGTATTAGGCTTGCAGACAGAGGAGCAGATCGTCTATATACGACCAAGTCGTC	915
QY	936	ACTAGAAAATGATGTTCTCCGTTTAAAGAAACAAGGCGTTGATGTTTCCCAAAGT	995
Db	916	ACTAGAAAATGATGTTCTCCGTTTAAAGAAACAAGGCGTTGATGTTTCCCAAAGT	975
QY	996	TCTCATTTGTACTCGGCTGATACCAAGATGCAAAAGGAATCATGATGCATACGCGCTGA	1055
Db	976	TCTCATTTGTACTCGGCTGATACCAAGATGCAAAAGGAATCATGATGCATACGCGCTGA	1035
QY	1056	GAGATTAGTGAACAAGCATACTTACATTAAGATTTCCCTCAGAAATGAAATGG	1115
Db	1036	GAGATTAGTGAACAAGCATACTTACATTAAGATTTCCCTCAGAAATGAAATGG	1095
QY	1116	GATACCTTAAGAAATGATATACAGATTGATGTGGCCATATCTGGAACATTTGCTGA	1177
Db	1096	GATACCTTAAGAAATGATATACAGATTGATGTGGCCATATCTGGAACATTTGCTGA	1155
QY	1176	GGATGCTGCTGTGAATTCGCTGATTAACAAGTATCCAGACTTCATTAATGGAAA	1233
Db	1156	GGATGCTGCTGTGAATTCGCTGATTAACAAGTATCCAGACTTCATTAATGGAAA	1211
QY	1236	CTACAGTATGGAATCTTGTGGGCTCATGCTATCTTACAAGATGGGAATTAACCAAGT	1293
Db	1216	CTACAGTATGGAATCTTGTGGGCTCATGCTATCTTACAAGATGGGAATTAACCAAGT	1271

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1792 ATGGTTATGTAAGCAAGATCAAGCCCAATATTTCTCCATGCGAAGGCTGACACGA 1851
QY 1744 GTGAGAAACATAGAGGCGTGTGAGAGCTTTGCTAATGCGGTAAGCTGAGGAGGCTG 1803
DB 1852 GTAAAAACATACACTGATGATGTAAGAAAGCTTTGTAAGAACAGCAATTAAGGGAACCTG 1911
QY 1804 GTAAACCTTGTCTGCTGCTCCGAGTACAAATGATGTCACAAAGTCCAAAGACAGGAGAG 1863
DB 1912 GTCAACCTTGTCAATAGTAGTGTGATATATGATGTAAGAAAGTCCAGTACAGAGAGAA 1971
QY 1864 ATGCGGAGATAGAGAAATGATCATGATCATCAAGACCCCAAACTTGTTCGGGAGTTC 1923
DB 1972 ATTCAGAAATTTGAAAGATCATGAGCTCATGAAAAAGTATTAATTAGTGGGATTTT 2031
QY 1924 CGCTGATCTCTGCGCCAGACAAACAGGCGCGTAAAGCGGAGCTCTATGCTACATGCT 1983
DB 2032 CGTTGATGCTGCGCCAAACAAATGAGGACGTAAATGAGGAGCTGATGCTACATGACGA 2091
QY 1984 GATACCATGCTGCTTCTGTAACAGCCGCGCTTGTATGAGAGCGTTGCTGACCGCTGCT 2043
DB 2092 GACACAGAAAGTGTCTTCTGTAAGCTGCTTCTATGAGAGCTTTGACATTAAGTTGTG 2151
QY 2044 GAGGCGATGACCTGTGCGCTTCTTCTTCTGAGCGCTCCATGAGAGTTCAGCTGAGATC 2103
DB 2152 GAGGCGCATGAAATGTGAGACTCCCACTTTGCTGCTGCTGCTGCTGCTGAGATC 2211
QY 2104 ATAGAGATGAGCGCTGCTGCGGCTTCCATGATGAGCCGCTGACACCCGAGACAGGCTGTAT 2163
DB 2212 ATTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2271
QY 2164 CTGATGCGCGAATTCTTCTGACCGGCTGCAAGACCCAGATCATCTGAGTGAATATATCT 2223
DB 2272 CTATATGATGATTTTCTCAAAAAGGCAAGGAGGAGCCAGGCAATGGAAGAAATATCT 2331
QY 2224 GAGAGCGGCTGCGACCGCATATGAGAAATGATGATGATGATGATGATGATGATGATG 2283
DB 2332 GATGATGCTTCTCAAAAGATTTATGAAAGTACAGTGAAGATTTATTCGAAAGGCTT 2391
QY 2284 ATGACACTGCGCGGGCTCTAGCGTTCTGGAAGTACGTGCAAGCTGAGAGGCTGAG 2343
DB 2392 ATGATTTGCGGAGATTTATGATTTCTGGAATACGTTTCCAAATTGAGAGGCTGAA 2451
QY 2344 ACAGAGCGCTACCTTGAATGTTCTACATCTGAAGTTCGCGAGCTGCGAGAACCGTG 2403
DB 2452 ACTGACGATATCTGAGATGTTCTATATCTCAAGTTCGCGATTTGCAAAATCTGTT 2511
QY 2404 CGGCTTGCATTTGACCAACCGCATGCTTC 2435
DB 2512 CGGCTAGCTAAGATGATGCAAGTATCTAGC 2543

RESULT 6
US-10-424-599-98889
Sequence 98889, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 98889
LENGTH: 3191
TYPE: DNA
ORGANISM: glycine max
FEATURE:
NAME/KEY: unsure

LOCATION: (1)..(3191)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1
US-10-424-599-98889
Query Match 48.14; Score 1325.6; DB 13; Length 3191;
Best Local Similarity 72.44; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 664; Indels 8; Gaps 3;
QY 10 CGGAGCTGAAACCGCAACGAGAGATCCGGAGCCGCGACAGACCCCTCCAGCGCAC 69
DB 204 CCAAGCTTGTGATGATCCAGATGATGAGAGCGAGTTGAAAGACCTCTCTGCTCAC 263
QY 70 CGCAACGATCTGTGCGCTCTCTCTCCAAAGTACGTAACAAAGGAGAGGAGATCTGAG 129
DB 264 CGTAAACGATCTATCTCTCTCTCTCCAGATATGATGCTGAGGAGAGGAGATTTGCA 323
QY 130 CGGACCAATCTGAGCGCTGAGCAGAGCTCCAGGCGC-----TCGGGGTCCGGCG 183
DB 324 CCCATATTTGATGATGAACTTGACAAATCCCTGCGATGATCAAGCAATAGAT 383
QY 184 CTCGCCAGAGACCTTCTCTGAGAGTCTCTGCGCTCCGCGAGAGAGGAGATGCTGCGC 243
DB 384 CTAAATATGATCTCTTGTGTAATGCTTAAGTCTGAAAGAGACCAATGTTTGGCT 443
QY 244 CGTTGCGGATCTGCGGCTGCGCGCGCGCGCGCGGAGTTTGGAGTACGCTGCTGAC 303
DB 444 CTTTGTGAGCAATGAGAGTCTGTCAGAGCCTGCTGTTGGAAATATGCTGTTAT 503
QY 304 GTTACAGCTCAGGCTGAGCAGCTCAGCTCTGAGAGTACTCTGCTTCAAGAGGAG 363
DB 504 GTCTGTGCTGAGGCTGAGGAGCAATTAAGTGTGTAATATCTGAGCTTCAAGAGAG 563
QY 364 CTGTGCGAGCGGACGAC-AATGATCCCTACGTTCTGAGCTTGAAGCTTCAAGCTTCA 422
DB 564 CTGTGAGTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 623
QY 423 TGTCTGAGTCCGAGCGCAATGCTGATCATCTATGTAATGGAACGCT-GTCAAGTCTCA 481
DB 624 TGCCATTTCTGCTGCAATCTGCTGAGCAATGCAATGCAATGCAATGCAATGCAAT 683
QY 482 ACCGACATCTGCTGATCATGATGCTTCCGCAAGGAGTTGCTGAGACCCCTGTTGAT 541
DB 684 ATCTCACCTTCTCATCTATTAATGTTTCCGCAAGGAGTTGCTGAGACCCCTGTTGAT 743
QY 542 TCTCTGAGCGCAACGCGCAAGGAGGAGTGTATGATGCTTATGATGATGATGATGATG 601
DB 744 TCTCTGAGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 803
QY 602 TGGGAGGCTGAGTGTGCTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661
DB 804 TTTCAAATCTGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 863
QY 662 ACAGACCATCTCAATTTGCTTATTAATTTCAAGAGTGGGAGGAGGAGGAGGAGGAGG 721
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QY 722 GTGATACAGAGGAGATGTTGGAATGATTCATCTCTCTGATGATGATGATGATGATG 781
DB 924 GTGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 983
QY 782 CAGACCATCTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 841
DB 984 CTGATCTCTTCAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1043
QY 842 TGTATCCCTCATGATGATCTTGTGCAAGGATGATGATGATGATGATGATGATGATG 901
DB 1044 TATATCTCTATGATGATCTTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1103
QY 902 GACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 961
DB 1104 GCGAGGTTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1163

QY 962 TAAAGAAACAAGGCTTGAATGTTTCCCAAGATTCCTATTGTACTGGCTGATACAG 1021
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DB 1224 ATGCAAAAGGGAACAATGCAACAGCGGCTTGAAAGATGAGTGTACTGACCAATAC 1283
QY 1382 ACATATTAAGAGTTCCTTCAAGAAATGAATGGCACTCTTAAGAAATGATATCAAGT 1141
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QY 1142 TTGATGTGGGCAATCTGGAACAACTTGGAGAGTGGTGTGTAATTTGCTGTG 1201
DB 1344 TTGATGTGGGCTTATCTGAGACTTATGCAAGAGATTTGGCAATGAAATTTGCTGTG 1403
QY 1202 AATTACAAAGTATCTCCAGACTTCAATATTTGAAACTACAGTATGGAATCTTTGGGCT 1261
DB 1404 ACTTACAAAGGATATCTGATTTCAATTTGAAACTACAGTATGGAATCTTTGGGCT 1463
QY 1262 CATTCGTATCTTAAAGATGGGAATTTCCAGTGCACATTTGCTCATGCTTGGAAATA 1321
DB 1464 CTATTGCTTATTAATAATGGGAGTTACAGTGCACATTCGCGCATGCACTTGAAGAA 1523
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DB 1524 CAATATATCAGATTCAGATTTATATTTGAGAAATTTGAGATTAATTTGCTCT 1583
QY 1382 GCCAGTTCAGTCTGATATATTTGCTATGAAACAATGCTGATTTATCATCAGACAT 1441
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DB 1544 ACCAGAGATTTGCAAGAAAGAAATATCTGTGGCAATATGAGAACCAAGCTGTTTA 1703
QY 1502 CTCTGCTGCTGCTGATCCAGTTGTCATGAGTGCATGCTGATGCTGATGCTGAT 1561
DB 1704 CTCTTCTGCTGCTGATGAGGTTGTCATGAGTGCATGCTGATGCTGATGCTGAT 1763
QY 1562 TAGTCTCTCTGAGCTGATCATGTCATATTTCTTCAATACACAGAAAGCAAGGAC 1621
DB 1764 TTGTCTCTCTGAGCTGATGATGTCATATTTCCCTTCACTGAAAGCAAGACAGAC 1823
QY 1622 TCACTCTCTTCAATGCTTCAATGAAATTTGATTTATGACCCGAGCAAAAGATGAC 1681
DB 1824 TTACAGCCCTGATGCTTCAATGAAAGCTATTTGCTCTGAGCAAGCTGATGAT 1883
QY 1582 ACATTTGGGATCTGAGATGACCGGTCAGAGCCATCCCTCTCTCATGAGCAAGCTGACA 1741
DB 1884 ACATTTGGTATTTGAAAGATGATGAGCTTCAAGCCCTTATTTCTCATGAGCAAGCTGACA 1943
QY 1742 GAGTGAAGAAATTAACAAGGCTGTCAGAACTTTTGTAAAGTCCGCTAAGCTGAGGAGC 1801
DB 1944 GAGTAAAGAAATTAACAAGGCTGTCAGAACTTTTGTAAAGTCCGCTAAGCTGAGGAGC 2003
QY 1802 TGGTAAACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1861
DB 2004 TGGTCAACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2063
QY 1862 AGATTCGAGATTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1921
DB 2064 AATTTGAGAAATTTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2123
QY 1922 TCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
DB 2124 TTGCTTGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2183
QY 1982 CTATATCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2041
DB 2184 CAGACACAAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2243

QY 2042 TTGAGCCATGACCTGTGGCTTCTTACTTTTGGCGAGCTCCATGAGAGTTCAGCTGAGA 2101
DB 2244 TGAAGCCATGATATGTGAGTCCCACTTTTGTCTACTTTCCTGCAATGTGTGCTGAG 2303
QY 2102 TCATAGAGATGAGCTGTGGGCTTCCATATGAGCCGATACCAAGCCGAGAGCTGTA 2161
DB 2304 TCATAGAGATGAGTATGAGATTTCCATATGATCTTATCACTGATCAAGCTTAC 2363
QY 2162 ATCTGATGCTGCTTCTTCAACCGCTGCAAGCAAGCCAGATCACTGGGTATATAT 2221
DB 2364 AGCTATTTAGTGAATTTTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2423
QY 2222 CTGAGCAGGCTGAGCCGATATACAGAGATGACATGAGATATATCTGAGAGCT 2281
DB 2424 CTGATGTGTGCTTCAAGAAATTTAAGAAAGTACAGTGAAGATTTATTTGAGAGG 2483
QY 2282 TGATGACATGCGCGGCTTCAAGCTTCTGAGAGTACGATGAGAGCTGAGAGGCTG 2341
DB 2484 TTATGACTTTGGGAGGATTAATGTTCTGGAATTAAGTTTCAATTAAGAGGCTG 2543
QY 2342 AGACAGAGGCTACCTTGAATGTTCTATACATGAAATTCGCGAGCTGCGAGAGAG 2401
DB 2544 AATCTGAGATATCTTGAATGTTCTATATCTCAAGTTCGATTTGAGAGAGCTG 2603
QY 2402 TGGCGCTTGCATTTGACCAACCGAGTACCTGC 2435
DB 2604 TTCCGCTAGCTAGATGATGACAGTTAATGAC 2637

RESULT 7
US-10-425-114-5285
; Sequence 5285, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yinda
; APPLICANT: Kovalic, David K.
; APPLICANT: Screet, Steven B.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5285
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454567_FLI
US-10-425-114-5285

Query Match 47.5%; Score 1309.8; DB 13; Length 1340;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1328; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1377 CTCTGCAAGTTCAGCTGATATATTTGCTATGAAACAATGCTATTTATCATCACAG 1436
DB 1 CTCTGCAAGTTCAGCTGATATATTTGCTATGAAACAATGCTATTTATCATCACAG 60
QY 1437 CACATACCAAGAAATTTGCTGAGCAAAATTTCTGTTGACAGTATGAGAGTCAATGCTC 1496
DB 61 CACATACCAAGAAATTTGCTGAGCAAAATTTCTGTTGACAGTATGAGAGTCAATGCTC 120
QY 1497 CTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1556
DB 121 CTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 1557 CAATATGCTCTCTCTGAGCTGACATGTCATATTAATTTTCAATACCAAGAGAGCCAA 1616
DB 181 CAATATGCTCTCTCTGAGCTGACATGTCATATTAATTTTCAATACCAAGAGAGCCAA 240

Db 541 CTGATGTTCCCTTAAGGTCATAGTACAAAGGTATCCGTTGATGTTGAATGATGAT 600
Qy 595 CAAAGCTTGGGAGGCTTCACTCTGTCTGACCAAGCTGAGAGCACTTGTCAAGCTC 654
Db 601 CAAAGCATATCTAGGCTTCAATCCAGCTTAGTAAAGCAAGATCAATCTCTAAGCTT 660
Qy 655 CTTGTGTACACACCTACTACAAATTTGCTTAAATTTCAAGATGAGGGCTGAGAAA 714
Db 661 TCACAAAGAACTCCGTTCTCGGAATTCGAATACGGGTTGCAAGGAATGGGTTTGA 720
Qy 715 GATTGGGCTGATACAGACGACATGTTTGAATATGATCTCTCTTGAACATCAT 774
Db 721 GGAATGGGAGATACCGCAGGAGAGTTCTTGAATGATGATCTCTCTCTGATTTCTT 780
Qy 775 CAGGCGCAGACCCATCTACCTAGAGAAATTTCTTGGGAGGATCCCATGATTTTAA 834
Db 781 CAAAGTCTGATCTCTGCTTGGAGAAATTTCTTGGAGATGATCAATGGTTTCAAC 840
Qy 835 GTTGTGTGTGATCCCTCTCATGATATCTTGTCAAGCTAATGATATGAGCTTGCAC 894
Db 841 GTTGTGATCTTATCTCCATGATGATATTTGCGGCAAGCCAAATGTTTAAAGCTTAC 900
Qy 895 ACAGAGGACAGATGCTATATCTGACCAAGTCCGTCACCTAGAAAATGAGATGAT 954
Db 901 ACTGTGTGACAGATGCTATATCTTGAACAAAGTCCGCTTGAAGCTGAAATGCTG 960
Qy 955 CTGCTTTAAAGAAACAAAGGCTTAAATGTTTCCCAAGATTTCAATGTTTACTG 1014
Db 961 TTGAGAAATTAAGAGACAGGGGTTGATATATCACTAGATTTCTTAACTAGGTTG 1020
Qy 1015 ATACCGATGCAAAAGAAATCATGACATGACGGCTTGAAGAAATTAAGAGAAACAG 1074
Db 1021 ATACCGATGCTAAAGAAATCATGATGACAGGGTTGAAGAGATGACGGAAACAG 1080
Qy 1075 CATACTCATATTTAGATTCCTCTCAGAAATGAAATGAGATCTTAAAGAAATGATA 1134
Db 1081 CATACTCATATTTCTCGGGTTCTTTAGATCTGAAAGAAATCTCTCGTAAATGAT 1140
Qy 1135 TCAAGATTTGATGTGTGCTATCTGAAACATTTGCTGAGATGCTGCTGTAAT 1194
Db 1141 TCAAGATTTGATGTGTGCTATCTGAAACATTTGCTGAGATGCTGCTGTAAT 1200
Qy 1195 GCTGTGATTTAACAAGTATCTGACATTTGATTTGAAATGAAATGAAATGAAAT 1254
Db 1201 GTGCGTGAATTCAGAGGCTGACGATTTATCATGATGATGATGATGATGAT 1260
Qy 1255 GTGCGTGAATTTCTTAAAGATGAGATTTACCGATGCAACATGCTGATGCTG 1314
Db 1261 GTTGTGATTTAACAAGTATCTGACATTTGATTTGAAATGAAATGAAATGAAAT 1320
Qy 1315 GAAAAGCTAAGTATCAGATTCAGATATTTTGAAGATTTGATGAGATGATGAT 1374
Db 1321 GAAAAGCTAAGTATCAGATTCAGATATTTTGAAGATTTGATGAGATGATGAT 1380
Qy 1375 TTCTCTGCAAGTCTGATGATATTTATGATGATGATGATGATGATGATGAT 1434
Db 1381 TTCTCTGCAAGTCTGATGATATTTATGATGATGATGATGATGATGATGAT 1440
Qy 1435 ACACATATCAAGAAATTTCTGAGACAAATATCTGTTGACATGATGAGTCACT 1494
Db 1441 ACACATATCAAGAAATTTCTGAGACAAATATCTGTTGACATGATGAGTCACT 1500
Qy 1495 GCTTTAATCTGCTGCTGCTGATCCAGATTTCCAGGATGATGATGATGATGAT 1554
Db 1501 GCTTTAATCTGCTGCTGCTGATCCAGATTTCCAGGATGATGATGATGATGAT 1560
Qy 1555 TTCAATATGCTCTCTGAGATGATGATGATGATGATGATGATGATGATGAT 1614
Db 1561 TTCAATATGCTCTCTGAGATGATGATGATGATGATGATGATGATGATGAT 1620
Qy 1615 AAGGCACTACCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 1674

Db 1621 AGGAGCTTACAGCTTTATCATGATTCATATAGAGAAATGCTCTATAGCCCTGACAGACT 1680
Qy 1675 GATGAACATATGGGCACTCTGATGATGATGATGATGATGATGATGATGATGAT 1734
Db 1681 GATGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Qy 1735 CTGACAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
Db 1741 CTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Qy 1795 AGGAGCTGATTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
Db 1801 AGGAGCTGATTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Qy 1855 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1914
Db 1861 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy 1915 GGGCAGTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1974
Db 1921 GGAAGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Qy 1975 TACATGCTGATTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2034
Db 1981 TACATGCTGATTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Qy 2035 ACCGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2094
Db 2041 ACCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
Qy 2095 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2154
Db 2101 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Qy 2155 GCTGTTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2214
Db 2161 GCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Qy 2215 AATATATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2274
Db 2221 AATATATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Qy 2275 GAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2334
Db 2281 GAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
Qy 2335 AGCTGAGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2394
Db 2341 CGTGTGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2400
Qy 2395 AAGACCGTGC 2405
Db 2401 AAAAGCTTCC 2411

RESULT 9
US-09-938-842A-2415
; Sequence 2415, Application US/09938842A
; Publication No. US2004009476A3
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCD1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2415
LENGTH: 2430
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-935-842A-2415

Query Match 45.3%; Score 1249.8; DB 11; Length 2430;
Best Local Similarity 70.2%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 712; Indels 6; Gaps 1;

QY 1 ATGTCGCCCGAGAGCTGAACCGCAAGCGGATCCGGACCGGTGAGAGACACCTTC 60
DB 1 ATGGCAACCCCTAGAGCTCACTAGAGGTTCTTAGCAACAAAGGATCGGTCAAGACACGCTT 60
QY 61 CAGGCGACCGGCAAGAGCTGTGGCCCTCTCTCCAGAGTACGTGAACAAGAGGAGG 120
DB 61 TCAGCTACCGGAGAGAGCTGTGTCTCTCTCCAGAGTACGTGAACAAGAGGAGG 120
QY 121 ATCCGAGCGGCAACCATCTCTGACGCTCGAGAGTCCAGAGGCTCCGGGCTCCGC 180
DB 121 ATCTTGAACCACTAATTAATGACGACTCGAATCTGTATCGAGAGACGATGAACA 180
QY 181 GCG-----CTGCGGAGGAGACCTCTCGACGCTCCGCTCGGCGGAGAGGAGATC 234
DB 181 AAGAGAGCTCTCTGATGAGTCTTTGAGAGATCTTAAATGAGCAATGAGACTATA 240
QY 235 GTGCGCCGCGGTGTGTGAGGCTATCGGAGTCCGCGCCCGGAGATTGGAGTACGTC 294
DB 241 GTTGACACCTTTTGTGTGAGGCTGTAGACGATGACCAAGACCTGAGTTGGAGATATGT 300
QY 295 CGCGTCAAGCTTCAAGAGCTCAGCGTCAAGAGCTCAAGTCTGAGAGTACCTCCGCTTC 354
DB 301 CGGTGTAATGTCTTGAAGTAAAGTGTGAACAATTAAGCTCTGAGATCTTGTGTTTC 360
QY 355 AAGAGAGCTTGTGAGCGGCGAGCAATGATCCCTACGTTCTGAGGTTGACTTCGAG 414
DB 361 AAGAGAGAGCTGTGATGAGTACCTAATATGACCTTTTGTGAGGTTGATATTCGAG 420
QY 415 CGGTCAAGTCTCAGTCCGCGGCAAGGCAATCGGTCACTATGAGAAACGATGTCAG 474
DB 421 CCTTTAAGCAAGCTGCTGCTCTCTCTCTCTGATGATGATGATGATGATGATG 480
QY 475 TTCTCAACCGACATCTGTCTCAATGATGTTCCGCAAGAGATGCTTGAACCCCTG 534
DB 481 TTCTCAACCGACATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 535 TTGAGTTCTCTCGTGGCGACCGGCAAGAGGCAATGATGATGATGATGATGATG 594
DB 541 CTGTGATTTCTTAGAGTTCAAGTAAAGGATCAAGGCTGATGATGATGATGATG 600
QY 595 CAAGCTTGGAGAGCTCTCAGTCTGTGCTGACCAAGAGTGAAGAGCACTTGCMAAGCTC 654
DB 601 CAAGCAATCTAGGCTTCAATCCAGCTTAGAAGAGAGAGATCAATCTCTAAGCTT 660
QY 655 CCTGTGACACCACTACTCAATTTGCTTAATTTTCAGAGTGGGGCTCGAGAAA 714
DB 661 TCACAGAGAACTCCGTTCTCGAATTCGAATACGCTTCGAGAGAAAGGATTTGAGAAA 720
QY 715 GTTGGGGGTGATACAGAGAGACATGTTTGAAGATGATCATCTCTCTAGACATCAT 774
DB 721 GATGGGGAGATACAGAGAGAGATGTTTGAAGATGATCATCTCTCTAGATTTCTT 780
QY 775 CAGGCGCAGACCATCTAACCCTAGAGAAATCTTGGGGAGATCCCATGATTTTAAAC 834
DB 781 CAGGCTCTGATCTCTGCTGTCTTGAAGAGTTCTTGGAGTGTACCAATGATTTCAAC 840
QY 835 GTTGTGTGATATCCCTTCAAGTACTTGTGAGAGTAACTATTAAGCTTGCAGAC 894
DB 841 GTTGTATCTTATCTCAGATGATATTTGAGGAGGCAAGGATGTTTAAAGCTTACCTGAC 900

QY 895 ACAGAGAGACAGATGCTATATATCTGACCAAGTCCGTGACATAGAGAAATGAGTGT 954
DB 901 ACTGTGAGCAAGTGTCTATATCTTACCAAGTCCGTGACATAGAGAAATGCTG 960
QY 955 CTCCGTTTAAAGAAACAAGGCTTGAATGTTTCCCAAGATTTCTCATTTGTTACTGCTG 1014
DB 961 TTGAGAAATAAGAGACAGGGGTTGATATATCACTAGATTTCTTATTTGATCTAGGTTG 1020
QY 1015 ATACAGATGCAAAAGAGACATGCAATGAGGCTTGAAGAAATGATGAGACAG 1074
DB 1021 ATACCGGATGCTAAAGAGACTAGTGAACAGGCTTGAAGAGTCAAGGAGAG 1080
QY 1075 CATACTTATATATGAGAGTCTCTTGAAGAAATGAGAAATGAGATCTTAAGAAATGAT 1134
DB 1081 CATACTTATATCTCCGGGTTCTTTTATGAGTGAAGAAATCTCCGTAAGTGTAT 1140
QY 1135 TCAAGATTTGATGTGTGACATATGGAACATTTGCTGAGAGTCTGCTGTAAT 1194
DB 1141 TCAAGATTTGAGTATGAGCTTATGAGAACTATGCTCAGAGATGAGAGAGAGAT 1200
QY 1195 GGTGCTGAATTAAGAGTACTCAGACTTCAATTAATGAGAACTAGAGATGAAATCTT 1254
DB 1201 GTGCTGATTTGCAAGGCTGACGACTTATATCATGATAGTATAGTAAAGGAACTT 1260
QY 1255 GTGCGTCAATGCTATCTTAAGAGTGAATTAACCGTGAACATTTGCTGCTG 1314
DB 1261 GTTGCATGTTAATGACATAGATGAGGTTTACCAATATGATATGACATGCTTTG 1320
QY 1315 GAAAGACTAAGTATCCGATTCAGACATTTTGAAGAAATTTGATGAGAGTACAT 1374
DB 1321 GAGAAACCAAGTATCCGATTCAGACATTTTGAAGAAATTTGATGAGAGTACAT 1380
QY 1375 TTCTCTGCGAGTCACTGCTGATATATATGCTAAGAACTGATTTTATCATACC 1434
DB 1381 TTCTCTGCTGATTAAGACTGATCTTATGCAATGAAAGAGGAACTTATCATCAACA 1440
QY 1435 AGCATAACCAAGAAATGCTGAGAAACAAATTAATCTGTAAGAGTGAATCT 1494
DB 1441 AGCATAACCAAGAAATGCTGAGAAACAAATTAATCTGTAAGAGTGAATCT 1500
QY 1495 GCTTTTACCTGCTGCTGCTGATGACGAGTGTCAAGGATGAGATGCTTGTGATCAAG 1554
DB 1501 GCTTTTACCTGCTGCTGCTGATGACGAGTGTCAAGGATGAGATGCTTGTGATCAAG 1560
QY 1555 TTCAATATAGTCTCTCTGAGAGCTGACATGCTCATATATCTTCAATACAGAGAGGCT 1614
DB 1561 TTCAATATAGTCTCTCTGAGAGCTGACATGCTCATATATCTTCAATACAGAGAGGCT 1620
QY 1615 AAGGACTCACTCTCTGATGATGATGAAATTTGATTTATGACCCGAGCAAAAC 1674
DB 1621 AAGGACTCACTCTCTGATGATGATGAAATTTGATTTATGACCCGAGCAAAAC 1680
QY 1675 GATGAAACAATTTGGAGATCTGATGACGAGTCAAGGCTCATCTCTCATGAGCAAG 1734
DB 1681 GATGAAACAATTTGGAGATCTGATGACGAGTCAAGGCTCATCTCTCATGAGCAAG 1740
QY 1735 CTGACAGGCTGAGAGAACTAACAAGGCTGTGAGAACTTTGCTAAGTGTGAGAGCTG 1794
DB 1741 CTGACAGGCTGAGAGAACTAACAAGGCTGTGAGAACTTTGCTAAGTGTGAGAGCTG 1800
QY 1795 AAGGAGCTGTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
DB 1801 AAGGAGCTGTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1855 AAGGAGAGATGCGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 1914
DB 1861 AAGGAGAGATGCGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 1920
QY 1915 GAGGAGTTCGCTGAGATCTTCTGCGCAGAGCAAGAGGCTGTAACGCTCTATGCT 1974
DB 1921 GAGGAGTTCGCTGAGATCTTCTGCGCAGAGCAAGAGGCTGTAACGCTCTATGCT 1980
QY 1975 TACATGCTGATACCAATGAGTGTCTTGTGATGACGCGGCTTGTATGAGAGGTTGCTC 2034

Db 1981 TACATCGCGATACAGAGGTCCTTTGCTCAGCTCGGTTCTACAGAGCTTTTGACTT 2040
Qy ACCGTCGTTAGGCGATGACCTGTTGGCTTCTACTTTTGGCAAGCTTCCATGAGAGTCCA 2094
Db 2035 ACCGTCGTTAGGCGATGACCTGTTGGCTTCTACTTTTGGCAAGCTTCCATGAGAGTCCA 2094
Qy 2041 ACGTGTGAGAGCGATGACCTTGGCGGCTCCGACCTTTTGGCATGTTGTCACGTTGCTCA 2100
Db 2095 GGTGAGATCATAGAGCATGGCGCTTCGAGGCTTCGACATTCAGCCCTTACCAAGCCGCAAG 2154
Qy 2101 GCGAGATCATAGAGCATGGCGCTTCGAGGCTTCGACATTCAGCCCTTACCAAGCCGCAAG 2160
Db 2155 GCTGTAACTGATGAGCGGACTTCTTTCGACCGGTCGAAAGCAAGCCAGATCATGAGGTTG 2214
Qy 2161 GCGGTTAATATATGATGAGCGGACTTCTTTCGACCGGTCGAAAGCAAGCCAGATCATGAGG 2220
Db 2215 AATATATCTGAGAGCGGCTTCGAGGCGATTCAGAGAGTACATGAGAGTATATCTCA 2274
Qy 2221 AAGGATCATAGAGCGGCTTCGAGGCGATTCAGAGAGTACATGAGAGTATATCTCA 2280
Db 2275 GAGAGGTTGAGAGCGGCTTCGAGGCGATTCAGAGAGTACATGAGAGTATATCTCA 2334
Qy 2281 GAGAGATGATGAGAGCGGCTTCGAGGCGATTCAGAGAGTACATGAGAGTATATCTCA 2340
Db 2335 AGGCTGAGAGCGGCTTCGAGGCGATTCAGAGAGTACATGAGAGTATATCTCA 2394
Qy 2341 GGTGTGAGAGCTCGGCGATTCATGAAATGTTCTACATTCGAAATTCGCGAGCTTGATG 2400
Db 2395 AAGACCTGCTCC 2405
Qy 2401 AAAACTGTTCC 2411

RESULT 10
US-10-217-939-29
/ Sequence 29, Application US/10217939
/ Publication No. US200301545-2A1
/ GENERAL INFORMATION:
/ APPLICANT: MITTENDORE, VOLKER
/ APPLICANT: HARBET, HEIKO A.
/ APPLICANT: CIRPOS, PETRA
/ TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
/ FILE REFERENCE: 16313-0157
/ CURRENT APPLICATION NUMBER: US/10/217,939
/ CURRENT FILING DATE: 2002-08-12
/ PRIOR APPLICATION NUMBER: 60/311,414
/ PRIOR FILING DATE: 2001-08-18
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 29
/ LENGTH: 2394
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-217-939-29

Query Match 42.84; Score 1181.2; DB 15; Length 2394;
Best Local Similarity 70.54; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 424 GTCTCAGTCCACGCCCAATGCTCATCATCTATTGAAACGCTGTGCACTTCTCAAC 483
Db 391 GCAACATTTGCTCGCCCAACTGTTCAATCATTCATGAGGAAATGAGGTTGATCTCCCAAT 450
Qy 484 CGACACTTGTCTCAATCATGTTTCCGCAACAGGATTTGTTGAGGCCCTTGTGATTTT 543
Db 451 GGTCACTCTCTCAATCATGTTTCCGCAACAGGATTTGTTGAGGCCCTTGTGATTTT 510
Qy 544 CTCGGGCGACCGGCAACAGGAGATGTTATGATGATGATGATGATGATGATGATGATGATG 603
Db 511 CTCGGGCGACCGGCAACAGGAGATGTTATGATGATGATGATGATGATGATGATGATGATG 570
Qy 604 GGAAGGCTTCAGTCTGTGCTGACCAAGAGTGAAGACACTTGTCAAGCTCCCTGCTGAC 663
Db 571 CCCATATCTTCAAGGAGCTTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
Qy 664 AGACCACTTCAATTTGCTTATTAATTTCAAGAGTGGGCTTGAGAGAAAGTGGGCT 723
Db 631 ACACCACTTCAATTTGCTTATTAATTTCAAGAGTGGGCTTGAGAGAAAGTGGGCT 690
Qy 724 GATACAG 783
Db 691 GACACAG 750
Qy 784 GACCCATCTACCTAGAGAAATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
Db 751 GATCTCTGCTTGTGAG 810
Qy 844 GATCTCTGCTTGTGAG 870
Db 811 TTGCTCTGCTTGTGAG 870
Qy 904 CAGATGCTATATATCTGAGCAAGTCCGTGCACTAGAGAGAGAGAGAGAGAGAGAGAGAG 963
Db 871 CAGATGCTATATATCTGAGCAAGTCCGTGCACTAGAGAGAGAGAGAGAGAGAGAGAGAG 930
Qy 964 AAGAAACAG 1023
Db 931 CAG 990
Qy 1024 GCAAG 1083
Db 991 GCAAG 1050
Qy 1084 ATATACAGAGTCCCTCAG 1143
Db 1051 ATTCTGAGATACATTTAG 1110
Qy 1144 GATGTGAG 1203
Db 1111 GATGTGAG 1170
Qy 1204 TTACAGAGTACTCCAGCTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1263
Db 1171 TTGAGAGAGTATCCCAATTCATTCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Qy 1264 TTGCTATCTTACAGAGTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
Db 1231 TTGCTATCTTACAGAGTGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
Qy 1324 AAGTATCAGATTCAGATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
Db 1291 AAGTATCAGATTCAGATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
Qy 1384 CAGTTCAGTGTGATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
Db 1351 CAGTTCAGTGTGATTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
Qy 1444 CAGAGAGTGTGAG 1503
Db 1411 CAGAGAGTGTGAG 1470

DB 825 AGATCCGTCACCCCTGGAGAGTTCTTGGAAAGATCCCATGGTGTTCATATCTGTAT 884
QY 843 GGTATCCCTCATGATGATCTTGTGTCAAGTATGATTTAGSTTGGCAGACACAGAG 902
DB 885 CCTCTCCCTCATGATGATCTTGTGTCAAGTATGATTTAGSTTGGCAGACACAGAG 944
QY 903 ACAGATGCTATATATCTGGACCAAGTCCGTGACATAGAAATAGATGTTCTCGT 962
DB 945 CAGAGTGTCTATCTTGTATGATGATGAGGCGCTATAGAGAAAGAAATGCTGTAGAT 1004
QY 963 AAGAAACAGAGGCTTGTATGTTCCCAAGATTCATTTTACTCGCTGATACAG 1022
DB 1005 CAGAGTGTGTCTTGTATGATGATGAGGCGCTATAGAGAAAGAAATGCTGTAGAT 1064
QY 1023 TGGAAAGAGACATCTGCAATATAGGCGCTTGGAGAAATAGTGAACACAGATCTTA 1082
DB 1065 TCGAATGCAACCACTGTGGCCAGGCGCTTGGAGAGTCTTGGAGACCAAGACCTGCCA 1124
QY 1083 CATATAGAGATTCCTCTGAGAAATAGAAATGGATTAAGAAATGATATCAAGATT 1142
DB 1125 TATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1184
QY 1143 TGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
DB 1185 TGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1244
QY 1203 ATTACAGATCTCTGCAATCTTCAATTTGGAAATCTGAGATGAGAAATCTTGTGCTG 1262
DB 1245 GCTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1304
QY 1263 ATGTGCTATCTGCAATGCTGCAATTTACCAAGTCAATCTGCTGCTGCTGCTGCTGCTG 1322
DB 1305 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1364
QY 1323 TAGATTCAGATCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1382
DB 1365 TAGATTCAGATCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1424
QY 1383 CAGATTCAGATCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1442
DB 1425 CAGATTCAGATCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1484
QY 1443 CCAAGAAATGCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1502
DB 1485 CCAAGAAATGCTGCAATTTTGGAAATTTGAGAAATGAGTGAAGTACATTTCTCTG 1544
QY 1503 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1562
DB 1545 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1604
QY 1563 AGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1622
DB 1605 CAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1664
QY 1623 CAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1682
DB 1665 GAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1724
QY 1683 CATGGGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1742
DB 1725 CATGGGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1784
QY 1743 GGTGAAGACATTAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1802
DB 1785 TGGAGAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1844
QY 1803 GGTGAAGACATTAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1862
DB 1845 GGTGAAGACATTAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1901
QY 1863 GATGCGGAGATTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1922

DB 1902 GCAGCCGAGTTCAGAAAGATGTTTGAACCTCATGAGCAGTACAACTGAAACGGGCAT 1961
QY 1923 CCGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1982
DB 1962 CCGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2021
QY 1983 TGAATCCATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2042
DB 2022 CAGACCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2081
QY 2043 TGAAGCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2102
DB 2082 TGAAGCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2142
QY 2103 CATAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2162
DB 2142 CATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2201
QY 2163 TCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2222
DB 2202 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2261
QY 2223 TGAAGCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2282
DB 2262 CAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2321
QY 2283 GATGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2342
DB 2322 GATGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2381
QY 2343 GACGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2402
DB 2382 GACGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2441
QY 2403 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2464
DB 2442 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2501

RESULT 12
US-10-425-114-2283
; Sequence 2283, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-215313B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2283
; LENGTH: 2986
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700221147_FLI
US-10-425-114-2283

Query Match 42.6%; Score 1173.4; DB 13; Length 2986;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 761; Indels 6; Gaps 2;

QY 6 TGGCCGAGAGCTGAACGCAAGCGAGCATCCGAGCGCTGCAAGACACCTTCACG 65
DB 167 TGAACGCTGCTGAGCGGCTTCACAGCGTCAAGGAGCGCATTTGGCGCATCTCTCGC 226
QY 66 GACCCGACAGAGCTGTGCGCTCTCTCCAAAGTACGTGAACAAAGGAGAAAGCGATCTCT 125

Db 227 CACCCCAATGATGCTTGTGCGCTTTTACCAAGGCTGAAAAACCTTGAAAAAGGATGCT 286
Qy 126 GCAAGCCGACCAATCTCTGAGCGCTGAC---GAGGTCCAAGGCTTCGGGGTCCGGCC 182
Db 287 GCAAGCCCAACCAATCATTTGCGAGTACAAACAAATGCAATCCCTGAGGCTGAGCGGAGAA 346
Qy 183 GCTGCGGAGGAGCCCTTCTCTGAGCTCTCGCTCCGCGCAGAGAGGAGTGTGCTGCC 242
Db 347 GCTCAAGGATGATGCTTTGAGAGATGCTTGAAGGCACTCAAGAGGAGATTTGATCCC 406
Qy 243 GCGGTGTGTGCAATCGAGGTGCGCGCGCGCGCGGAGTTTGGAGTACGTCCGCGTCAA 302
Db 407 CCAATGGGTGACTTGGCAATCGCCCTTAAAGGCTGATGCTTGGAGTATGAGAGGTCAA 466
Qy 303 CGTTACAGAGCTCAAGCGTCAAGCACTCACTCTGAGTACCTCGCTTCAAGAGAGA 362
Db 467 GGTGATGATGCTGCTTGTGAGAGCTGAGATTCCTGAGTACCTGCAATTCAGAGAA 526
Qy 363 GCTTGTGAGCGGCGCAGCAATGATCCCTAGCTTCTTCAAGCTTGAATTCGAGCCCTTGA 422
Db 527 GCTTGTGAGAGAGCGCCCAACCAACTTGTCTTGAAGCTGAGCTTGAAGCACTTCAA 586
Qy 423 TGTCTCAGTCCAGCGCCCAATCGGTCAATCTATTTGGAAGCGGTGCACTTCTCA 482
Db 587 TGTCTCTTCTCCCGCTCTTCTCTGATGAGTCACTTGGCAATGAGCTGATCTCTGA 646
Qy 483 CCGACACTTGTCTCAATGATGCTTCCGCAAGGATGCTTGAAGCCCTGTGATTT 542
Db 647 CAGGACCTGTGATCAAGCTCTTCCATGACAAAGAGAGATGATCCCTGTCTCACTT 706
Qy 543 CCTCGTGGCCACCGGCAAGAGGAGTATGATGCTTATGATGATGATGATGATGAT 602
Db 707 CTTTGGCGCCCAACTACAAAGGAGATGACATGATGATGATGATGATGATGATGAT 766
Qy 603 GGGAGAGCTCAGTCTGTGCTGACCAAGAGCTGAGAGCACTTGTCAAGAGCTCCCTGCTGA 662
Db 767 CAGTGTCTGCAAGGTGCGCTGAGAGAGCTGAGAGCACTGCTCAAGCTTCAAGCTGA 826
Qy 663 CACACATCTCAATTTGCTTATTAATTTCAAGATGAGGCTGAGAGAGGTTGGGG 722
Db 827 TACCCCAATCTGATTTTCAACAGGTTCAGAGAACTTGTGTGAGAGAGGTTGGGG 886
Qy 723 TGAATACAGAGACATGTTTGGAGATGATGATCTCTTGAAGATCAATTCAGGCGGC 782
Db 887 TGAATGCGTAAAGCGGCAAGAGATGATGATCTCTTGAAGATCCCATGAGTTCAT 946
Qy 783 AAGACCATCTACCTAGAGAAATTTCTGGGAGGATCCCATGATTTTGAAGTGTGT 842
Db 947 AATTCGCTCAACCTTGAAGATGCTTGTGAAGATCCCATGAGTTCATGATGAT 1006
Qy 843 GGTATCCCTCATGATCTTGTGTCAAGCTTATGATGATGATGATGATGATGATGAT 902
Db 1007 CCTCTCCCTCATGATCTTGTGTCAAGCTTATGATGATGATGATGATGATGATGAT 1066
Qy 903 AAGATGCTTATTAATCTGAGCAAGTCCGTGACAGAAATGAGATGATGATGAT 962
Db 1067 CCAAGTGTCTAATCTGATCAAGTGGCTTGAAGATGATGATGATGATGATGATGAT 1126
Qy 963 AAGAGAACAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1022
Db 1127 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186
Qy 1023 TGGCAAGAGACATCATGCAATGAGGCTTGAAGATGATGATGATGATGATGATGAT 1082
Db 1187 TGGCAATGAGACATCATGAGGCTTGAAGATGATGATGATGATGATGATGATGAT 1246
Qy 1083 CAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1142
Db 1247 TATCTTGTGAGCTTCAAGACAGAAATGATGATGATGATGATGATGATGATGAT 1306
Qy 1143 TGAATGTGAGCTTATCTGAGAAATTTGCTGAGATGCTGCTGATGATGATGATGAT 1202

Db 1307 TGAATGTGAGCTTATCTGAGAACTTACATGATGATGATGATGATGATGATGAT 1366
Qy 1203 ATTACAGATCTCAGACTTCAATATGGAATACAGTATGATGATGATGATGATGATGAT 1262
Db 1367 GCTTCAAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1426
Qy 1263 ATTGCTATCTTCAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322
Db 1427 TTTGTGTCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1486
Qy 1323 TAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
Db 1487 TAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1546
Qy 1383 CAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
Db 1547 CAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
Qy 1443 CAAAGAAATTTGAGAGCAAAATACTGTTGAGAGATGATGATGATGATGATGATGAT 1502
Db 1607 CCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1666
Qy 1503 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
Db 1667 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
Qy 1563 AGTCTCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
Db 1727 CAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
Qy 1623 CACTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
Db 1787 GACTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
Qy 1683 CATTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
Db 1847 CAGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
Qy 1743 GGTGAGAAATTAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1802
Db 1907 TGTGAGAAATTAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1966
Qy 1803 GGTGAGAAATTAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1862
Db 1967 GGTGAGAAATTAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2026
Qy 1863 GATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
Db 2024 GAGAGCGGAGTCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
Qy 1923 CCGTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
Db 2084 CCGTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
Qy 1983 TGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
Db 2144 CAGACCAAGAGGCGCTTGTGAGAGCTGATGATGATGATGATGATGATGATGATGAT 2206
Qy 2043 TGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
Db 2204 TGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2266
Qy 2103 CATAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
Db 2264 CATTGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
Qy 2163 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
Db 2324 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2386
Qy 2223 TGAAGCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2282
Db 2384 CAGAGGCGGCTCAAGCTATGAGAGAGATGATGATGATGATGATGATGATGATGAT 2446


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Qy 1563 AGTCTCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1622
Db 1727 CGTCTCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1786
Qy 1623 CACCTCTCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1682
Db 1787 GACCTCTCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1846
Qy 1683 CATGGGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1742
Db 1847 CAGCTCTCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1906
Qy 1743 GGTGAAGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1802
Db 1907 TGTGAAGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1966
Qy 1803 GGTGAAGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1862
Db 1967 GGTGAAGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2023
Qy 1863 GATCGGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1922
Db 2024 GATCGGCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2083
Qy 1923 CGGCTGAGCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 1982
Db 2084 CGGCTGAGCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2143
Qy 1983 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2042
Db 2144 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2203
Qy 2043 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2102
Db 2204 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2263
Qy 2103 CATATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2162
Db 2264 CATATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2323
Qy 2163 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2222
Db 2324 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2383
Qy 2223 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2282
Db 2384 TGTATACCACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2443
Qy 2283 GATGACACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2342
Db 2444 GATGACACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2503
Qy 2343 GATGACACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2402
Db 2504 GATGACACTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2563
Qy 2403 GCGGCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2425
Db 2564 GCGGCTGTGAGCTGACATGTCATATACCTTCCACATACCGAGAGGCCAGACCT 2586
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RESULT 14
US-10-425-114-5310

Sequence 5310, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jinsong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5310
LENGTH: 2992
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: clone ID: 700451030_FLI
US-10-425-114-5310

Query Match 42.6%; Score 1173.4; DB 13; Length 2992;

Best Local Similarity 68.3%; Pred. No. 0; Mismatches 761; Indels 6; Gaps 2;

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Db 173 TGACCGTGTCTGAGCCGCTTCCACAGCTCAGGAGGCGCATTTGGCGACTCATCTTTC 232
Qy 6 TGCCCGAAGCTGAACCGCAACGAGCATCCGAGCCGCTGAGACACCTTCCAGC 65
Db 66 GACCGCAAGAGCTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 125
Qy 223 CCACCCATAGAGCTTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 292
Db 126 GACCGCAAGAGCTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 182
Qy 293 GACCGCAAGAGCTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 352
Db 183 GCTGCGAGAGAGCTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 242
Qy 353 GCTGCGAGAGAGCTTCGCGCTTCCAGAGTGAACAGAGGAGGAGATCT 412
Db 243 GCGCTTGTGAGCATGCGGAGTGGCGCGCGCGCGAGTGGAGTACGTCGCGTCA 302
Qy 413 CCATGAGTGAATGCGCATGCGGAGTGGCGCGCGCGAGTGGAGTACGTCGCGTCA 472
Db 303 GCTTCCAGAGCTCAGCGTTCAGAGTGAACAGAGTGAACAGAGTGAACAGAGTGA 362
Qy 473 GCTTCCAGAGCTCAGCGTTCAGAGTGAACAGAGTGAACAGAGTGAACAGAGTGA 532
Db 363 GCTTCCAGAGCTCAGCGTTCAGAGTGAACAGAGTGAACAGAGTGAACAGAGTGA 422
Qy 533 GCTTCCAGAGCTCAGCGTTCAGAGTGAACAGAGTGAACAGAGTGAACAGAGTGA 592
Db 423 TGTCTCAGTCCAGCGCGCAATGCGCATCATCATATGGAACAGAGTGAACAGAGTGA 482
Qy 593 TGTCTCAGTCCAGCGCGCAATGCGCATCATCATATGGAACAGAGTGAACAGAGTGA 652
Db 483 CCGACACTGTCTCATCATATGCGCAACAGAGTGAACAGAGTGAACAGAGTGA 542
Qy 653 CCGACACTGTCTCATCATATGCGCAACAGAGTGAACAGAGTGAACAGAGTGA 712
Db 543 CCGACACTGTCTCATCATATGCGCAACAGAGTGAACAGAGTGAACAGAGTGA 602
Qy 713 CCGACACTGTCTCATCATATGCGCAACAGAGTGAACAGAGTGAACAGAGTGA 772
Db 603 CCGACACTGTCTCATCATATGCGCAACAGAGTGAACAGAGTGAACAGAGTGA 662
Qy 773 CAGTGTCTGAGAGTGTGCGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 832
Db 663 CAGTGTCTGAGAGTGTGCGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 722
Qy 833 TACCCATAGCTGATTTACACAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTC 892
Db 723 TGTATACGAGAGAGTGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 782
Qy 893 TGTATACGAGAGAGTGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 952
Db 783 AGACCATCTACCTTGAAGATTTCTTGGAGAGATCCCATGATTTTAACTGTTGT 842
Qy 953 AGATCGTCAACCTTGAAGATTTCTTGGAGAGATCCCATGATTTTAACTGTTGT 1012
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QY 843 GGTATCCCTCATGATCTTGTCAAGCTATGATAGGCTTGCAGACAGAGAG 902
DB 1013 CCTTCCCTCATGATCTTGTCAAGCTATGATAGGCTTGCAGACAGAGAG 1072
QY 903 ACAGATCGCTATATATAGTGAACCAAGTCCGTCAGTAAATGAAATGATTCCTCGTTT 962
DB 1073 CCGATGCTCATATCTTGGATTCAGAGTGGGCTATGAGAAAGAAATGCTCTGAGGAT 1132
QY 963 AAAGAAAGAGGCTTGTATGTTTCCCAAGATTCATCTTGTACTCGGCTATACAGAA 1022
DB 1133 CAGAGATGCTGTGATCATACAGCCGAAAGATCTTATTTGTCACAGATTCCTCGTGA 1192
QY 1023 TGCAGAGAAATATGATGATACAGAGGCTTGAAGATATAGTGAACACAGATATTA 1082
DB 1193 TGCAGAGTACAGCTTGTGAGGCTTGAAGATATAGTGAACACAGATATTA 1252
QY 1083 CATATTAAGATTCCTTCAAGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1142
DB 1253 TATCTTCCGCTGCTCATGAGAAAGAAATGAAATGAAATGAAATGAAATGAAAT 1312
QY 1143 TGATGTGAGGCAATCTTGAAGAAATGCTGAGATGCTGCTGAGAAATGCTGCTGA 1202
DB 1313 TGAAGTCCGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1372
QY 1203 ATTAAGATGATCTGAGATGATATATGAAATGAAATGAAATGAAATGAAATGAAAT 1262
DB 1373 GCTTACAGGCAATCTTGAAGAAATGCTGAGATGCTGAGTGAAGTGAAGTGAAG 1432
QY 1263 ATGCTATCTTCAAGATGAGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1322
DB 1433 TTTGCTCCGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1492
QY 1323 TAAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1382
DB 1493 TAAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1552
QY 1383 CAGATGCTGCTGATATATGCTATGAAATGAAATGAAATGAAATGAAATGAAAT 1442
DB 1553 CAGATGCTGCTGATATATGCTATGAAATGAAATGAAATGAAATGAAATGAAAT 1512
QY 1443 CCAAGAAATGCTGAGAAAGAAATGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1502
DB 1613 CCAAGAAATGCTGAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1672
QY 1503 TCTGCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1562
DB 1673 TAAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1732
QY 1563 AGTCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1622
DB 1733 CAGTCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1792
QY 1623 CAGCTCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1682
DB 1793 GAGCTCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1852
QY 1683 CATGAGGATCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1742
DB 1853 CAGTCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1912
QY 1743 GGTGAAGAAATATGAGGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1802
DB 1913 TGTGAAGAAATATGAGGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1972
QY 1803 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1862
DB 1973 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2029
QY 1863 GATGCGGAGATGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1922
DB 2030 GATGCGGAGATGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2089

QY 1923 CCGTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1982
DB 2090 CCGTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2149
QY 1983 TGAATCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2042
DB 2150 CCAACAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2209
QY 2043 TGAAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2102
DB 2210 TGAAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2269
QY 2103 CATGAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2162
DB 2270 CATGAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2329
QY 2163 TGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2222
DB 2330 CCGTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2389
QY 2223 TGAAGCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2282
DB 2390 CCAAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2449
QY 2283 GATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2342
DB 2450 GATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2509
QY 2343 GACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2402
DB 2510 GACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2569
QY 2403 GCGCTGTGCAATGACCAACCGC 2425
DB 2570 GCGCTGTGCAATGACCAACCGC 2592

RESULT 15
US-10-425-114-17596
Sequence 17596, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Sreen, Steven E.
APPLICANT: Tabaska, Jack E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 73128
SEQ. ID NO 17596
LENGTH: 3419
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3069-052-F8_FLI
US-10-425-114-17596

Query Match 42.6%; Score 1173.4; DB 13; Length 3419;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 761; Indels 6; Gaps 2;

QY 6 TGCCTGAGAGCTGAGACCGCAACGAGCATTCGAGACCGCTGAGAGCACTTCACGC 65
DB 567 TGAACCTGCTGAGACCGCTGAGACCGCTGAGACCGCTGAGACCGCTGAGACCGCT 626
QY 66 GACCGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 125
DB 627 CACCCCAATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686

QY 126 GCAGCCGACACACATCTCTGACGCGCTGAC---GAGGTCAGAGGCTCCGCGGTCCGAGC 182
DB 687 GCAGCCGACACACATCTCTGACGCGCTGAC---GAGGTCAGAGGCTCCGCGGTCCGAGC 746
QY 183 GCTGCGCAGAGGACCTTCTCTGACGCTCTCGCTCCGCGAGAGGCGCATCTGCTGCG 242
DB 747 GCTGAGAGAGTGTGCTTTGAGGATGTCTGAGGCGAGCTCAGAGGCGCATCTGCTGCG 806
QY 243 GCGGCTGCTGAGCATTCGCGGTGCGCGCGCGCGCGAGATTGGAGTACGTCGCTGCA 302
DB 807 CCGATGGGTGACATTCGCTGCTGAGGCTGAGGCTGCTGAGGCTGAGGCTGAGGCTGCA 866
QY 303 GCTTACAGAGCTCAGCGTCTGAGAGCTCAGCTCTGAGTACCTCCGCTTCAAGAGGA 362
DB 867 GCTTACAGAGCTCAGCGTCTGAGAGCTCAGCTCTGAGTACCTCCGCTTCAAGAGGA 926
QY 363 GCTTGTGAGCGGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 422
DB 927 GCTTGTGAGAGAGGCGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 986
QY 423 GCTTGTGAGAGGCGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 542
DB 987 GCTTGTGAGAGGCGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 1046
QY 483 CCGACACTTGTCTCAATCATGCTCCGACAGAGGCTTGAAGCTTGAAGCTTGAAGCTTGA 1106
DB 1047 CCGACACTTGTCTCAATCATGCTCCGACAGAGGCTTGAAGCTTGAAGCTTGAAGCTTGA 1166
QY 543 CCTTGTGAGCGGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 602
DB 1107 CCTTGTGAGCGGCGAGCAATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTGA 1166
QY 603 GCGGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 662
DB 1167 GCGGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 1226
QY 663 CACACACTTGTCTCAATCATGCTCCGACAGAGGCTTGAAGCTTGAAGCTTGAAGCTTGA 722
DB 1227 CACACACTTGTCTCAATCATGCTCCGACAGAGGCTTGAAGCTTGAAGCTTGAAGCTTGA 1286
QY 723 TGAATACAGAGAGCATGTTTGGAAATGATCCTCTCTTGAAGCTTGAAGCTTGAAGCTTGA 782
DB 1287 TGAATACAGAGAGCATGTTTGGAAATGATCCTCTCTTGAAGCTTGAAGCTTGAAGCTTGA 1346
QY 783 AACACCATCTACCTAGAGAAATCTTGGAGAGGATCCCATGATTTTAAAGTGTGT 842
DB 1347 AACACCATCTACCTAGAGAAATCTTGGAGAGGATCCCATGATTTTAAAGTGTGT 1406
QY 843 GGTATCCCTCATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
DB 1407 GGTATCCCTCATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1466
QY 903 ACGATGCTGTATATCTGAGACCAAGTCTGTGATGAGAAATGAGATGCTTCTCGTT 962
DB 1467 ACGATGCTGTATATCTGAGACCAAGTCTGTGATGAGAAATGAGATGCTTCTCGTT 1526
QY 963 AAGAGAAAGAGGCTTGAAGCTTCCCAAGAAATCTCATGTTTACCTGCTGATACCA 1022
DB 1527 AAGAGAAAGAGGCTTGAAGCTTCCCAAGAAATCTCATGTTTACCTGCTGATACCA 1586
QY 1023 TGCAGAGAGAGATCATGATCATGATCATGATCATGATCATGATCATGATCATGATCAT 1082
DB 1587 TGCAGAGAGAGATCATGATCATGATCATGATCATGATCATGATCATGATCATGATCAT 1646
QY 1083 CATATTTACAGATCTCTTCAAGAAATGAAATGAGATCTTAAAGATGATGATGATGAT 1142
DB 1647 CATATTTACAGATCTCTTCAAGAAATGAAATGAGATCTTAAAGATGATGATGATGAT 1706
QY 1143 TGAATGCTGAGCATCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
DB 1707 TGAATGCTGAGCATCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1766

QY 1203 ATTACAGAGTACTCCAGATCTTCAATATGGAATCAAGTATGGAATCTTGTGCGCTC 1262
DB 1767 GCTTCAAGGCAATCTCGACCTGATCATGAGAAATCAAGTATGAGAAATCTTGTGCGCTC 1826
QY 1263 ATTGCTATCTTCAAGATGAGAAATCCAGATGCAATTTGCTCATGCTCTGAGAAAGC 1322
DB 1827 TTGTGCTGCGCCCAAGATGAGGTTTACTCATGATGATGATGATGATGATGATGATGAT 1886
QY 1323 TGAATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
DB 1887 TGAATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1946
QY 1383 CAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
DB 1947 CAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2006
QY 1443 CCAAGAAATGCTGAGAGCAAAATCTGAGAGATGAGAGATGATGATGATGATGATGATGAT 1502
DB 2007 CCAAGAAATGCTGAGAGCAAAATCTGAGAGATGAGAGATGATGATGATGATGATGATGAT 2066
QY 1503 TCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
DB 2067 TCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2126
QY 1563 AGTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
DB 2127 AGTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2186
QY 1623 CACCTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
DB 2187 CACCTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2246
QY 1683 CATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
DB 2247 CATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2306
QY 1743 GGTGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1802
DB 2307 GGTGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2366
QY 1803 GGTGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
DB 2367 GGTGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2426
QY 1863 GATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
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DB 2484 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2546
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DB 2544 TGAATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2606
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DB 2604 TGAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2666
QY 2103 CATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
DB 2664 CATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2726
QY 2163 TGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
DB 2724 TGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2786
QY 2223 TGAAGAGAGGCTGAGAGCAATATGAGAGATGATGATGATGATGATGATGATGATGATGAT 2282
DB 2784 TGAAGAGAGGCTGAGAGCAATATGAGAGATGATGATGATGATGATGATGATGATGATGAT 2946
QY 2283 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2342

DB	2844	GATGAACCTTCACCGGCTGTACGGGTTCTGGAAGTACGTGTCCAACTGGAGAGGGCGCA	2903
QY	2343	GAAGAGGGCTTACCTTGAATGTTCTACATGAACTTCCGGAGCTGGCGAAGACCGT	2402
DB	2904	GACCCGGCGGTACCTGAGATGCTGTACGCGCTCAAGTACCGCACCATGGCGAGCACCGT	2963
QY	2403	GCCGCTTGCATTGACCAACCGC	2425
DB	2964	GCCGCTGGCCGTGAGGGAGAGC	2986

Search completed: May 26, 2004, 02:26:01
 Job time : 794.858 secs

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 14:40:36 ; Search time 694.519 Seconds

(without alignments)
16863.873 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgctgcgccgaagctgaa.....aaaaaaaaagggcgccgcg 2757

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2003cs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2757	100.0	2757	6	AAD45856 Corn sus3
2	2714	98.4	2737	6	AAD45849 Corn sus3
3	1809.6	65.6	2412	7	ADA69581 Rice gene
4	1249.8	45.3	2430	6	AB214610 Arabidops
5	1181.2	42.8	2394	7	AB276372 A. thalia
6	1173.8	42.7	2563	2	AAQ80005 Sucrose-s
7	1173.4	42.6	2308	6	AAD45852 Corn suc
8	1172	42.5	2418	7	AB276371 A. thalia
9	1162	42.1	2450	7	ADA71337 Rice gene
10	1162	42.1	2451	9	ADC08208 Rice DNA
11	1162	42.1	2451	9	ADC07855 Rice DNA
12	1135.6	41.2	2754	3	ADC68521 S. arundi
13	1134.6	41.2	2829	6	ABK98516 cDNA sequ
14	1133	41.1	2494	3	AAQ66090 Rice suc
15	1133	41.1	2714	9	ADC68423 Lolium pe
16	1133	41.1	2716	9	ADC68520 Lolium pe
17	1133	41.1	2746	6	ADA45851 Corn suc
18	1132.6	41.1	2906	3	AA67143 Eucalyptu
19	1132.4	41.1	2957	9	ADC68424 Lolium pe
20	1131	41.0	2913	3	AAA67087 Eucalyptu
21	1131	41.0	3103	3	AAC62807 Sucrose s
22	1131	41.0	3103	6	ABK17072 Eucalyptu
23	1128.2	40.9	2825	9	ADC68523 S. arundi

24	1124.4	40.8	2950	9	ADC68522 Lolium pe
25	1104.6	40.1	2625	6	ABK52880 Cotton su
26	1094.2	39.7	2260	3	AAC66096 PSS3 cDNA
27	1062.6	38.5	2427	6	AB213815 Arabidops
28	1062.6	38.5	2427	7	ADA68333 Arabidops
29	940.2	34.1	2334	7	ADA71106 Rice gene
30	940.2	34.1	2334	9	ADC07857 Rice DNA
31	940.2	34.1	2334	9	ADC08296 Rice DNA
32	899.6	32.6	2210	7	ADA69957 Rice gene
33	830.8	30.1	2397	7	ADA70504 Rice gene
34	830.8	30.1	2397	9	ADC07859 Rice DNA
35	789.6	28.6	1309	6	ABK98492 Consensus
36	775	28.1	1209	6	ABK98492 Consensus
37	574.6	20.8	1374	7	ADC08717 Wheat DNA
38	482.8	17.5	2700	2	AAV21641 Arabidops
39	482.4	17.5	1546	9	ADC07853 Rice DNA
40	459.2	16.7	2492	6	ADA42841 Maize suc
41	453.4	16.4	697	6	ABK98493 cDNA sequ
42	449.8	16.3	1169	3	AAA67120 Pinus rad
43	442.4	16.0	705	6	ABK98494 cDNA sequ
44	430.6	15.6	1145	6	AAA67119 Pinus rad
45	397.4	14.4	428	8	ADA58861 Maize suc

ALIGNMENTS

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RESULT 1
AAD45856
ID AAD45856 standard; DNA; 2757 BP.
XX
AC AAD45856;
XX
DT 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
XX
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; Sus3; chimeric; gene; ds.
XX
XX Zea mays.
XX Sorghum propinquum.
OS
OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..2430
XX FT /product= "Corn Sus3-Sorghum EST chimeric protein"
XX FT misc_feature 1..39 b
XX FT /tag= "Sorghum propinquum EST DNA"
XX FT misc_feature 40..2757 c
XX FT /tag= "Corn Sus3 DNA"
XX FT /note= "Corn Sus3 DNA"
XX
XX WO200257662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helentjaris TG, Nin X;
XX
XX MPI: 2002-691625/74.
XX P-PsDB: AA28502.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for

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modulating the level of sucrose synthase in transgenic plants (e.g. maize or soybean) to improve stalk length, reduce grain breakage, or improving plant or grain strength.

Claim 1: Page 116-119; 125pp; English.

The invention relates to two sucrose synthases, shrunken-1 (Sh1) and constitutive sucrose synthase (Ssu1) and their corresponding nucleic acids. The polynucleotide, or its encoded protein, is useful for modulating the level of sucrose synthase in a transgenic plant, increasing cellulose production in the stalk tissue of a transgenic plant, or increasing the concentration of cellulose in the tissues of a seed of a transgenic plant. This is particularly useful in plant (e.g. maize or soybean) breeding, especially for e.g. improving stalk length in maize, reducing grain breakage during combining, transport or movement into storage, or improving plant or grain strength. The present sequence is Corn Ssu3-809hum Bst chimeric DNA. (Updated on 29-Aug-2003 to standardise OS field)

Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 2757; DB 6; Length 2757;

Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTCGCCCGAAGCTGAACCGCAACGAGCATCCGAGCCGCTGAGAGACACCTTC 60
Db 1 ATGTCGCCCGAAGCTGAACCGCAACGAGCATCCGAGCCGCTGAGAGACACCTTC 60
QY 61 CAGCGCAACCGCAACGAGCTGTCGCTCTCTTCGAAAGTACGTAAGAGAGAGAGG 120
Db 61 CAGCGCAACCGCAACGAGCTGTCGCTCTCTTCGAAAGTACGTAAGAGAGAGAGG 120
QY 121 ATCCGAGACCGCAACGAGCTGTCGAGCTGTCGAGAGGTCAGAGGCTTCGAGG 180
Db 121 ATCCGAGACCGCAACGAGCTGTCGAGCTGTCGAGAGGTCAGAGGCTTCGAGG 180
QY 181 GCGCTGCGCAAGGAGACCTTCCTCGAGCTCTCGCTCCGCGAGAGAGAGAGAGG 240
Db 181 GCGCTGCGCAAGGAGACCTTCCTCGAGCTCTCGCTCCGCGAGAGAGAGAGAGG 240
QY 241 CCGCGCTTCGTCGAGCTGTCGAGCTGTCGAGCTGTCGAGCTGTCGAGCTGTC 300
Db 241 CCGCGCTTCGTCGAGCTGTCGAGCTGTCGAGCTGTCGAGCTGTCGAGCTGTC 300
QY 301 AAGCTTACGAGCTCAGGCTGAGAGAGTCAAGTCTCGAGTACCTCCGCTTCAAG 360
Db 301 AAGCTTACGAGCTCAGGCTGAGAGAGTCAAGTCTCGAGTACCTCCGCTTCAAG 360
QY 361 GAGCTTTCGAGCGAGCAAGATGATCCCTAGCTTCGAGCTTCAAGCTTCGAG 420
Db 361 GAGCTTTCGAGCGAGCAAGATGATCCCTAGCTTCGAGCTTCAAGCTTCGAG 420
QY 421 AATGCTTCAGTCCAGCGCCCAATCGGTCATCATCTATTTGAAACGGTGTCACT 480
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QY 481 AAGCGAAGCTTGTCTCATATGTCGCAAGAGATTCCTTGAAGCCCTGTGGAT 540
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QY 601 TTGGGAGGCTTCAGCTCTGTCTGACCAAGCTGAGAGCACTTGTCAAGCTCC 660
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QY 661 GAGCAGCAATCTACAAATTTGCTTAAATTTCAAGAGTGGGCTGAGAGAGGTT 720
Db 661 GAGCAGCAATCTACAAATTTGCTTAAATTTCAAGAGTGGGCTGAGAGAGGTT 720
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QY 721 GGTGATACAGAGACATGTTTGGAAATGATCCATCTCTTCTAGACATCATGAGG 780
Db 721 GGTGATACAGAGACATGTTTGGAAATGATCCATCTCTTCTAGACATCATGAGG 780
QY 781 CCGAGCCCATTCACCTTGAAGAAATTTGGAGAGATCCCATGATTTTAAAGTT 840
Db 781 CCGAGCCCATTCACCTTGAAGAAATTTGGAGAGATCCCATGATTTTAAAGTT 840
QY 841 GGGATATCCCTCATGATCTTGGTCAAGCTTAAATGATGAGCTTGGCAACAGA 900
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QY 1021 GATGAAAGAAACATCAATGCAATCAGGAGCTTGAAGATTAAGGAAACAGAT 1080
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Db 1081 TACATATTACGAGTTCCTTCAGAAATGAAATGGATTAATTAAGAAATGATACA 1140
QY 1141 TTTGATGTTGGCCATATCTGAAACATTTGCTGAGATGCTGCTGAGAAATGCT 1200
Db 1141 TTTGATGTTGGCCATATCTGAAACATTTGCTGAGATGCTGCTGAGAAATGCT 1200
QY 1201 GAATTAACAGGATCCGAGCTCATTAATGAGAACTACAGATGAGAAATCTGAG 1260
Db 1201 GAATTAACAGGATCCGAGCTCATTAATGAGAACTACAGATGAGAAATCTGAG 1260
QY 1261 TCATTCGATCTTCAAGATGAGAAATTAACAGATGAGAAATCTGAGAAAG 1320
Db 1261 TCATTCGATCTTCAAGATGAGAAATTAACAGATGAGAAATCTGAGAAAG 1320
QY 1321 ACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAGATGCT 1380
Db 1321 ACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAGATGCT 1380
QY 1381 TGGCAGTTCATGCTGATATATTTGCTATGAAATGCTGATTTATCATCCAGACA 1440
Db 1381 TGGCAGTTCATGCTGATATATTTGCTATGAAATGCTGATTTATCATCCAGACA 1440
QY 1441 TACCAAGAAATTTGCTGAGAGCAAAATATCTGAGACAGTATGAGATCATAC 1500
Db 1441 TACCAAGAAATTTGCTGAGAGCAAAATATCTGAGACAGTATGAGATCATAC 1500
QY 1501 ACTGCTGCTGATCTGATCCGAGTGTGCTATGAGATGATGCTTCAAGAGTTCA 1560
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Db 1621 CTGACCTCTCTTCAATGCTGATGAAATTTGATTTATGACCCGAGCAAAAGAT 1680
QY 1681 CAGATTTGGGATCTGATGATCCGATCAAGGCTTCTCTCTGATGAGAGCTGAC 1740
Db 1681 CAGATTTGGGATCTGATGATCCGATCAAGGCTTCTCTCTGATGAGAGCTGAC 1740
QY 1741 AGGATGAAGAAATTAACAGGCTGATGAGCTTTGCTAAGTGGCTAAGCTGAGAG 1800
Db 1741 AGGATGAAGAAATTAACAGGCTGATGAGCTTTGCTAAGTGGCTAAGCTGAGAG 1800
QY 1801 CTGGTAAACCTTGTCTGTGTCGCGGATCAATGATGCAACAGTCCAGAGAG 1860
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[illegible]

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RESULT 2
AADD5849
ID    AADD5849 standard; cDNA; 2737 BP.

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AC	AA045849;	
XX		
DT	27-DEC-2002	(first entry)
XX		
DE	Corn sucrose synthase (Sus3)	CDNA

XV	Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XVI	transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XVII	cellulose; corn; Sus3; gene; ss.
XX	
XXI	Zea mays.
XXII	
XXIII	Key Location/Qualifiers
XXIV	CDS 2..2410
XXV	FT /*tag= a
XXVI	FT /product= "Corn Sus3 protein"
XXVII	
XXVIII	MO20267662-A1.
XXIX	
XXX	06-SEP-2002.
XXXI	
XXXII	21-FEB-2002; 2002WO-US005137.
XXXIII	
XXXIV	22-FEB-2001; 2001US-0270777P.
XXXV	
XXXVI	(PION-) PIONEER HI-BRED INT INC.
XXXVII	
XXXVIII	Dhuga KS, Helentjaris TG, Niu X;
XXXIX	
XXXX	WPI: 2002-691625/74.
XXXXI	P-PsDB; AAE28493.
XXXXII	
XXXXIII	New polynucleotide and its encoded sucrose synthase, useful for
XXXXIV	modulating the level of sucrose synthase in transgenic plants (e.g. maize
XXXXV	or soybean) to improve stalk length, reduce grain breakage, or improving
XXXXVI	plant or grain strength.
XXXXVII	
XXXXVIII	Claim 1; Page 102-103; 125pp; English.
XXXXIX	
XXXXX	The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XXXXXI	constitutive sucrose synthase (Sus1) and their corresponding nucleic
XXXXXII	acids. The polynucleotide, or its encoded protein, is useful for
XXXXXIII	modulating the level of sucrose synthase in a transgenic plant,
XXXXXIV	increasing cellulose production in the stalk tissue of a transgenic
XXXXXV	plant, or increasing the concentration of cellulose in the tissues of a
XXXXXVI	seed of a transgenic plant. This is particularly useful in plant (e.g.
XXXXXVII	maize or soybean) breeding, especially for e.g. improving stalk length in
XXXXXVIII	maize, reducing grain breakage during combining, transport or movement
XXXXXIX	into storage, or improving plant or grain strength. The present sequence
XXXXXX	is corn Sus3 cDNA
XXXXXXI	
XXXXXXII	Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;
XXXXXXIII	
XXXXXXIV	Query Match 98.4%; Score 2714; DB 6; Length 2737;
XXXXXXV	Best Local Similarity 99.8% Pred. No. 0;
XXXXXXVI	Matches 2717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XXXXXXVII	
XXXXXXVIII	CCGGGACCGGCTCGAGGACAACCTTCACAGGCATCGTCCGCCCTCCTC 95
XXXXXXIX	
XXXXXXX	16 CGGGACCGGCTCGAGGACAACCTTCACAGGCATCGTCCGCCCTCCTC 75
QY	CAAGTAGTGTAACAAGGGAAGGGCATCTGTGACACCGCACCAACTCTGACGCGCTCGA 155
QB	76 CAAGTAGTGTAACAAGGGAAGGGCATCTGTGACACCGCACCAACTCTGACGCGCTCGA 135
QY	156 CGAGGTCCAGGCGCTCCGGGCTCCGGCGGCTGCCGAGGAGACCCTTCTCCACAGTCTCCG 215
DB	136 CGAGGTCCAGGCGCTCCGGGCGGCTGCCGAGGAGACCCTTCTCCACAGTCTCCG 195
QY	216 CTCGCGCAGGAGGCGATCGTGTGCTGCGCGCGCTTCGTGTGSCCATCGCGGTGCGCCGCGCCC 275
DB	196 CTCGCGCAGGAGGCGATCGTGTGCTGCGCGCGCTTCGTGTGSCCATCGCGGTGCGCCGCGCCC 255
QY	276 GGGAGTTGGAGTAGCTCCGCGCTCAAGCTTTCACAGCTCAGCGCTGACGACTCAAGT 335
DB	256 GGGAGTTGGAGTAGCTCCGCGCTCAAGCTTTCACAGCTCAGCGCTGACGACTCAAGT 315
QY	336 CTGCGAGTAGCTCCGCGCTTCAAGAAGAGCTTTGTCACGCGCAAGCAATGATCCCTACGT 395

Db 316 CTGGAGTACCTCCGCTTCAAGAGGAGAGCTGTGAGCGGCCAGACACATGATCCCTACGT 375
Qy 396 TCTGACCTTGAACCTTGCAGCGCTTCAATGCTCAGTCCCAAGCCCAATGCTATATC 455
Db 376 TCTGACCTTGAACCTTGCAGCGCTTCAATGCTCAGTCCCAAGCCCAATGCTATATC 435
Qy 456 TATGAGAAAGCTGTGAGATCTCAACCGACATTGCTCATCATCATGTTCCGCAAG 515
Db 436 TATGAGAAAGCTGTGAGATCTCAACCGACATTGCTCATCATCATGTTCCGCAAG 495
Qy 516 GGAATGCTTGAAGCCCTGTGATTTCTCCGTGGCCACCGGACAAAGGGGCAATGTTAT 575
Db 496 GGAATGCTTGAAGCCCTGTGATTTCTCCGTGGCCACCGGACAAAGGGGCAATGTTAT 555
Qy 576 GATGCTTAATGATGATTAACAAGCTTGGGAGGCTTCACTGCTGCTGACCAAGCTGA 635
Db 556 GATGCTTAATGATGATTAACAAGCTTGGGAGGCTTCACTGCTGCTGACCAAGCTGA 615
Qy 636 GAGACACTTGTCAAGCTCCCTGCTGACACACCATACTCAAAATTTGCTTAATTTCA 695
Db 616 GAGACACTTGTCAAGCTCCCTGCTGACACACCATACTCAAAATTTGCTTAATTTCA 675
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Db 1156 GATGCTGCTGGTGAATTTGCTGATTAACAAGTACTCCAGCTTCAATTAATGAAA 1215
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Qy 1296 CAACATGCTCATGCTGAGAAAGACTAAGTATCAGATCAGACATATTTTGAAGAA 1355
Db 1276 CAACATGCTCATGCTGAGAAAGACTAAGTATCAGATCAGACATATTTTGAAGAA 1335
Qy 1356 TTTGATGAGAGATGACATTTTCTCCGCAAGTTCACTGCTGATATATATGCTATGAA 1415
Db 1336 TTTGATGAGAGATGACATTTTCTCCGCAAGTTCACTGCTGATATATATGCTATGAA 1395
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Db 1396 TGTCTATTTATCATCAACAGCATATCAAGAAATGCTGGAAGCAAAATACCTTTG 1455
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Db 1636 TTATGACCCGAGCAAAACATGAAACATTTGGGCAATCTGATGACCCGTCAMAGCCAT 1695
Qy 1716 CCTCTTCTCAATGGCAAGCTCGACAGGCTGAAGACATTAACGGCTGTGCAAGCTTT 1775
Db 1696 CCTCTTCTCAATGGCAAGCTCGACAGGCTGAAGACATTAACGGCTGTGCAAGCTTT 1755
Qy 1776 TGTATAGTGGCTTAACTGAGAGGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTG 1835
Db 1756 TGTATAGTGGCTTAACTGAGAGGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTG 1815
Qy 1836 TGTCAACAAGCTCAAGACAGAGAGATGCGGAGATGAGAAAGATGATGATGATCTAT 1895
Db 1816 TGTCAACAAGCTCAAGACAGAGAGATGCGGAGATGAGAAAGATGATGATGATCTAT 1875
Qy 1896 CAAGACCAACATTTGTTGGGCGCTTCCGCTGATCTCTGCTCCAGACAAACAGGCCCCG 1955
Db 1876 CAAGACCAACATTTGTTGGGCGCTTCCGCTGATCTCTGCTCCAGACAAACAGGCCCCG 1935
Qy 1956 TAAAGGAGGCTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2015
Db 1936 TAAAGGAGGCTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1995
Qy 2016 GTATGAGGCTTGGCTTCAACCTGCTGAGGCGCATGACCTGTGGGCTTCTACTTTGCG 2075
Db 1996 GTATGAGGCTTGGCTTCAACCTGCTGAGGCGCATGACCTGTGGGCTTCTACTTTGCG 2055
Qy 2076 GACGCTCATGAGGCTCAAGCTGATGATATGAGATGAGATGAGATGAGATGAGATGAG 2135
Db 2056 GACGCTCATGAGGCTCAAGCTGATGATATGAGATGAGATGAGATGAGATGAGATGAG 2115
Qy 2136 CCGGTACCAACCCGGAACAGGCTGTTAATCTGATGAGGCGCATCTTCAACGCTGCAAGCA 2195
Db 2116 CCGGTACCAACCCGGAACAGGCTGTTAATCTGATGAGGCGCATCTTCAACGCTGCAAGCA 2175
Qy 2196 AGACCAATCATCTGGTGAATATATCTGAGCAAGGCTGCAAGGCGCATATACAGAAATG 2255
Db 2176 AGACCAATCATCTGGTGAATATATCTGAGCAAGGCTGCAAGGCGCATATACAGAAATG 2235
Qy 2256 CACATGAAAGATATCTCAAGAGGCTGATGACATCTGCGCGGGGCTTACCGTTCTGAAA 2315
Db 2236 CACATGAAAGATATCTCAAGAGGCTGATGACATCTGCGCGGGGCTTACCGTTCTGAAA 2295
Qy 2316 GTAAGTGTGAGAGCTGAGAGGCTGAGAGCGAGGCTCACTTGAATATTTTCAATACT 2375
Db 2296 GTAAGTGTGAGAGCTGAGAGGCTGAGAGCGAGGCTCACTTGAATATTTTCAATACT 2355
Qy 2376 GAAATTCGCGAGCTGGCGAAGACCTGTGCGCTTGCATTTGACCAACCGCAGTACCTTGC 2435
Db 2356 GAAATTCGCGAGCTGGCGAAGACCTGTGCGCTTGCATTTGACCAACCGCAGTACCTTGC 2415
Qy 2436 GAACTCTGAGCTGAGCTGAGACTTGTGATGAGAGCTGAAACCTGAAGGCTTCAATAT 2495
Db 2416 GAACTCTGAGCTGAGCTGAGACTTGTGATGAGAGCTGAAACCTGAAGGCTTCAATAT 2475
Qy 2496 AGGCGCGGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2555
Db 2476 AGGCGCGGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2535

Yy		2556	AAATTAAGGCGCATATAACAATAATTCTGAAGCAGGTGGTGTGCAGTGTTGGTTCTAC	261757
Dd		2536	CATATTGGCGCATATAACAATAATTCTGAAGCAGGTGGTGTGCAGTGTTGGTTCTAC	25998
Oy		2616	TGTTACTGTATTATATGTCAGACGTGCGCTCCAAATTTTGTGTCGCAAGCGCAGCAC	267157
Dd		2596	TGTTACTGTATTATATGTCAGACGTGCGCTCCAAATTTTGTGTCGCAAGCGCAGCAC	265157
Oy		2676	TGTTGAAGTGTGTAATAATACATCATATTCTGTTGACCTGTGAAAAA	27358
Dd		2656	TGGTAAGTGTGTAATAATACATCATATTCTGTTGACCTGTGAAAAA	27158
Oy		2736	AAAAAAAAAAGGCGCGCGCGC	2757
Dd		2716	AAAAAAAAAAGGCGCGCGCGC	2737
 RESULT 3 ADA69581				
ID	ADA69581	standard; DNA;	2412 BP.	
XX	ADA69581;			
DT	20-NOV-2003	(first entry)		
DE	Rice gene, SEQ ID 2904.			
XX				
KM	Plant; bacterial infection; fungal infection; viral infection; rice;			
XX	gene; ds.			
OS	Oryza sativa.			
PN	MO200300898-AI.			
XX				
PD	03-JAN-2003.			
PF	22-JUN-2001; 2001WO-IB001105.			
XX				
PA	22-JUN-2001; 2001WO-IB001105.			
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.			
PI	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;			
PI	Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;			
DR	WPI; 2003-175290/17.			
PT	Identifying at least one gene involved in plant resistance or response to			
PT	pathogenic infection for conferring resistance or tolerance to a plant to			
PT	bacterial, fungal or viral infection by determining or detecting plant			
PT	gene expression.			
XS				
XS	Claim 6; SEQ ID NO 2904; 899bp; English.			
XX				
CC	The present invention relates to a method (M1) for identifying genes			
CC	involved in plant resistance or response to pathogenic infection. M1			
CC	comprises identifying a gene whose expression is significantly altered in			
CC	the incompatible interaction of plant gene expression relative to			
CC	expression of the gene in an uninfected plant, in a mutant plant that			
CC	does not express a gene associated with response to pathogenic infection,			
CC	or in a corresponding incompatible or compatible interaction. (M1) is			
CC	useful for conferring resistance to resistance or tolerance to a plant to			
CC	bacterial, fungal or viral infection. The present sequence was used to			
CC	illustrate the invention.			
SQ	Sequence 2412 BP; 633 A; 573 C; 599 G; 600 T; 0 U; 7 Other;			
Query March	65.6%; Score 1809.6; DB 7; Length 2412;			
Best Local Similarity	84.9%; Pred. No. 0;			
Matches 2062; Conservative	6; Mismatches 340; Indels 22; Gaps 3			
Yy	1 ATGTCTGCCCGGAAGCTGAACCGAAGCGAGCATCCGAGACCGCGTAGACACCCTC	60		

Db	1	ATGTGGAGCCCGAAGCTTGAACCGGACCCCGAGATCCGGCAACCGCTTCAGAGACACCTTC	60
Qy	61	CACGCGACCGCAACGAAGCTCGTCGACCTCTCTCCAAATACGTGAACAAAGGGAAGGCG	120
Db	61	CAGCCCAACCGCAACGAGCTCGTCGCCCTCTCTCCAAATACGTGAACCAAGGGAAGGCG	120
Qy	121	ATCTGCAAGCTCGACCAATCTTGACGCGCTCGACGAGGTCCAGGGCTCCGGGCTCCG	180
Db	121	ATCTGCAAGCTCGACCAATCTTGAGAGCGCTCGACGAGGTCCAGAGCTCCGGGCGCGC	180
Qy	181	GGGCTGGCGAAGGAGCCCTTCTTGAGAGTCTCCGCTCCGCGGAGAGGAGATGGTGTG	240
Db	181	GGCTTCGTGCAAGGCGCCCTTCTTGAGAGTCTCCGCTCCGCGGAGAGGAGATGGTGTG	240
Qy	241	CCGCGCTTCGAGGCATTCGCGAGTCCGCGCGCGCCGAGAGTTTGGAGTACGTCGCGTC	300
Db	241	CCGCGCTTCGTGAGGATTCGCGAGTCCGCGCGCGCGGAGGGGTGGAGTACGTCGCGTC	300
Qy	301	AACGTTACAGAGCTCAAGCTTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAG	360
Db	301	AACGTGACAGAGCTCAAGCTTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAG	360
Qy	361	GAGTTGTGCAAGGCGCGACCAATGATTCCTAGGTTTCGAGCTTGACTTCGACCGCTC	420
Db	361	GAGTTCGTGCAAGGCGCGACCAAGATCCGATACCTTGAGCTTGATTTGAGCCATTC	420
Qy	421	AATGTTCAGTCCGACGCCAAATCGGTCAATCTATTGGAAGAGGTGTCAGATTCTC	480
Db	421	AATGCTCGGTGTCAGCGCCAAATCGGTCAATCTATTGGAAGATGGGTGTCAGATTCTC	480
Qy	481	AACCGACACTTGTCTCAATCATGTTCCGACAAGGATTTGCTTGAGCCCTGTGGAT	540
Db	481	AACGAGCACTTGTCTTGATCATGTTCCGGAACAGAGATTTGCTTGAGCCCTGTGGAT	540
Qy	541	TTCCTCCGTGGCCACCGGCAAGAGGGCAATGTTATGATGCTATGATGAAATCAAGC	600
Db	541	TTCCTGTGTGGGCAATCGGCAATAGGATCAGT-----ATACAGGT	580
Qy	601	TGGGAGAGGCTTC-AGTCTGTC-TGACCAAGCTGAGAGCACTTGCAAGCTCCCTG	658
Db	581	CTGGGAAGACTTCAGATCTGTGCTTGACCAAGCTGAGAGCACTTGTCGAAATCTCCAG	640
Qy	659	CTGACACACCATCTCAATTTGCTTAAATTTCAAGAGTGGGCTCTGAGAAAGTT	718
Db	641	CTGACACACCATCTCAAGTTGCTATTAAGATTTGAGAGTGGAGAAAGGTT	700
Qy	719	GGGGTGATACAGCAGGACATGTTTGGAAATGATTCATCTCTCTTGACACTCATTCAG	778
Db	701	GGGGCGACACAGCTGATATGTTTGAGATGATACATCTCTCTTGATGTGCTTCAAG	760
Qy	779	CGCAGAGCCCATTAACCTAGAGAAATTTCTTGGGAGAGATCCCATGATTTTAAAGTT	838
Db	761	CGCTGATCCATCTACTCTTGAGACGTTCTTGGAGAAAGATCCCATGATCTTTAATGTC	820
Qy	839	TTGTGTATCCCTCATAGATCTTGTGTAAGCTTTCAGAGCTTCGACAGCAG	898
Db	821	TCTGATGTCTCTCATAGATATTTTGGCAAGCCAAATGTTTGGGCTTACCAATCTG	880
Qy	899	GAGACAGATGTTTAACTGACCAAGTCCGTGCACTGAAATGAGATGGTTCTCC	958
Db	881	GAGGCGAGTGTCTTAATCTGACCAAGTCCGTGCACTGGAATGAGATGGTTCTTA	940
Qy	959	GTTTAAAGAAACAAGGCTTGATGTTTCCCAAGATTTCTCATGTTTCTCGGCTGATAC	1018
Db	941	GTTTAAAGAAACAAGGCTTGATTTTACCTTAAATTTCTTATGTTTACTGGCTGATAC	1000
Qy	1019	CAGATGCAAAAGAACATCATGCAATCAGCGGCTTGAGAGATTAAGTGAACACAGATA	1078
Db	1001	CAGAAACAAAAGGACATCATGCAATCAGCGCTTGAAGAGATTAAGTGGACACAACTTA	1060
Qy	1079	CTTACATTTACAGGTTCCCTTCAGAAATGAAATGGGATCTTAAGAAATGATATCA	1138

Db 1061 CTTACATATTACAGAGTGCATTCAGAAATGAAATGGATGACTCAGAAATGATATCA 1120
 QY 1139 GATTGAGCTGTGGCCATATCTGGAAACAATTGCTGAGAGATGCTGCTGGAATTCG 1138
 Db 1121 GATTGAGCTGTGGCCATATCTGGAAAAATTTGCAAGAGATGCTGCTGGAATTCG 1130
 QY 1199 CCGAATTAAGAAGTATCTCAGAGCTTCAATATGGAATGAACTAGTGAATGAAATCTTG 1258
 Db 1181 CAGAAATTAAGAAGTATCTCAGAGCTTCAATATGGAATGAACTAGTGAATGAAATCTTG 1240
 QY 1259 CCGTATGCTATCTTAAGAATGGAATTAACCAAGTCAATTCCTATGCTCTGAAA 1318
 Db 1241 CAGTATGCTATCTTAAGAATGGAATTAACCAAGTCAATTCCTATGCTCTGAAA 1300
 QY 1319 AAGCTAAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCAGATTCATTTCT 1378
 Db 1301 AAGCTAAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCAGATTCATTTCT 1360
 QY 1379 CCGTCCAGTTCAGTCTGATTAATGATTAAGATTCAGATTCAGATTCATTTCT 1438
 Db 1361 CCGTCCAGTTCAGTCTGATTAATGATTAAGATTCAGATTCAGATTCATTTCT 1420
 QY 1439 CATACCAAGAAATTCCTGGAAGCAAAATTAATCTGGAAGATTAAGATTCATTTCT 1498
 Db 1421 CATACCAAGAAATTCCTGGAAGCAAAATTAATCTGGAAGATTAAGATTCATTTCT 1480
 QY 1499 TTAATCTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1558
 Db 1481 TTAATCTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1540
 QY 1559 ATATAGTCTCTCTGAGAGTGCATTCATTAATGATTCAGATTCAGATTCATTTCT 1618
 Db 1541 ATATAGTCTCTCTGAGAGTGCATTCATTAATGATTCAGATTCAGATTCATTTCT 1600
 QY 1619 GACTCACTCTCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1678
 Db 1601 GACTCACTCTCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1660
 QY 1679 AACCAATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1738
 Db 1661 AACCAATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1720
 QY 1739 AACAGATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1798
 Db 1721 AACAGATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1780
 QY 1799 AGCTGTAACCTTGTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1858
 Db 1781 AGCTGTAACCTTGTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1840
 QY 1859 AAGAGATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1918
 Db 1841 AAGAGATTCGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1900
 QY 1919 AGTTCGCTGATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1978
 Db 1901 AGTTCGCTGATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 1960
 QY 1979 TCGTGTATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2038
 Db 1961 TCGTGTATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2020
 QY 2039 TCGTGTATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2098
 Db 2021 TCGTGTATTCATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2080
 QY 2099 AGATCATAGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2158
 Db 2081 AGATCATAGAGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2140
 QY 2159 TTAATCTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2218
 Db 2141 TTAATCTGCTGCTGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2200

QY 2219 TATCTGAGCAGGAGCTGACGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2278
 Db 2201 TATCTGAGCAGGAGCTGACGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2260
 QY 2279 GGTGATGACATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2338
 Db 2261 GGTGATGACATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2320
 QY 2339 TGGAGACAGGAGCTGACGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2398
 Db 2321 TGGAGACAGGAGCTGACGATTCAGATTCAGATTCATTTTGAAGATTCAGATTCATTTCT 2380
 QY 2399 CCGTCCAGTTCAGTCTGATTAATGATTAAGATTCAGATTCATTTCT 2458
 Db 2381 CCGTCCAGTTCAGTCTGATTAATGATTAAGATTCAGATTCATTTCT 2410

RESULT 4

ABZ14610
ID ABZ14610 standard; DNA; 2430 BP.

AC ABZ14610;

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2415.

KM Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

PN W0200216655-A2.

PD 28-FEB-2002.

PF 24-AUG-2001; 2001MO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

PR 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-0300111P.

PA (SCRT) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Harper JF, Kreps J, Wang X, Zhu T;

PT WPI; 2002-304127/34.

PS Claim 144: SEQ ID NO 2415; 577pp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office

XX Sequence 2430 BP; 680 A; 498 C; 574 G; 678 T; 0 U; 0 Other;

XX Query Match 45.3%; Score 1249.8; DB 6; Length 2430;

XX Best Local Similarity 70.2%; Pred. No. 3.7e-272;

XX Matches 1693; Conservative 0; Mismatches 712; Indels 6; Gaps 1;

QY 1 ATGCTGCCCCGAGCTGAACCGCAACGAGCATCCGAGCCGCTCGAGGACACCTTC 60
DB 1 ATGCGAAACCTTAGCTCACTAGGGTTCTAAGCAAGAGATGCGTGCAGACAGCTT 60
QY 61 CAGCGCACCGCAACGAGCTGTCGCGCTTCCTCCAAAGTACGTGAACAAGGAGAGGC 120
DB 61 TCGGCTCACCGCAACGAGCTGTCGCTTCCTCCAAAGTACGTGAACAAGGAGAGGC 120
QY 121 ATCTGAGCGGACCAATCTCGAGCGCTCGACGAGTCCAGGGCTCCGAGGCTCCG 180
DB 121 ATCTGAGCGGACCAATCTCGAGCGCTCGACGAGTCCAGGGCTCCGAGGCTCCG 180
QY 181 GCG-----CTCGCGAGGAGACCTTCCTCGAGCTCCGCTCCGCGAGGAGGAGATC 234
DB 181 AAGAAAGTCTCTCTGATGCTCTTTTGAAGAGATCTTAAATCAGCAATGGAAGCTATA 240
QY 235 GTCCTCGCGGCTTCGCGCATCGCGGTCGCGCGCGCGCGCGAGTTTGGAGTACGTC 294
DB 241 GTGTACACCTTTGTGTGCGTTAGCGGTAGACCAAGACCTGGTGTGTTGGAAATATGT 300
QY 295 CGGCTCAAGTACGAGCTCAGCGTGCAGAGCTCAAGTCTTCGAGTACCTCCGCTTC 354
DB 301 CGGTAAATGCTCTGAGCTAAGTGTGAACAATTAAAGTCTCTGAGTATCTTCGTTTC 360
QY 355 AAGGAGAGCTTGTGACGCGCAGCACAATGATCCCTACGTTCTCGAGCTTGACTTCGAG 414
DB 361 AAGAAAGATCTGTTGATGAGACCTTAATGAGACCTTTGTGCTGAGCTGATTTGAG 420
QY 415 CGGTAAATGCTCAGCTCCAGCGCCCAATGCTCATCATATTTGAAACGCTGTCAG 474
DB 421 CCTTTAAGCAACGTCAGCTCTCTCTGCTCTTCGATGTTGTAATGAGTTCAG 480
QY 475 TTGCTCAACGCAATCTGCTCTCAATGATCCGCAACGAGATGCTTCGAGCCCTG 534
DB 481 TTCTGATCTGCACTGCTCTCTGATGATGCTGTAACAAGATGCTTCGAGCTTCG 540
QY 535 TTGGAATCTCTCCGTGCGCAACGCGCAACAGGAGCTATGAGCTTAATGATAGATA 594
DB 541 CTGATCTCTTGAAGTCAATGATCAAGATGATGATGATGATGATGATGATGATGATG 600
QY 595 CAAGCTTGGAGAGCTTCAAGTCTGCTGCTGCAACAGCTGAGAGCACTTGTCAAGCTC 654
DB 601 CAAGCAATCTAGGCTTCAATCCAGCTTGAAGCAAGATCATCTCAAGCTT 660
QY 655 CTGCTGACACCATCTCAATGATGCTTAAATTTGAGAGTGGGCTCGAGAAA 714
DB 661 TCACAAAGAACTCGCTTCGGAATGGAATACGCGTTGCAAGGAATGGTTTGAAGAA 720
QY 715 GATTGGGCTGATACAGCAGAGCATGTTTGGAAATGATCCATCTCCTTAGACATCAT 774
DB 721 GGAATGGGAATACCGAGGAGAGTCTTGAATGATGATGATGATGATGATGATGATGAT 780
QY 775 CAGCGCGCAAGCCATCTACCTTAGAGAAATCTTGGAGAGATCCCATGATTTTAAAC 834
DB 781 CAGAGCTCTGATCTGCTCTTGAAGAGTCTTGGAGATGATCAATGATGATTTTAAAC 840
QY 835 GTTGTGTGATCTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 894
DB 841 GTTGTGTGATCTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 895 ACAGAGAGAGATCTCTATATCTGAGCAAGTCCGTCATAGAAATGATGATGAT 954
DB 901 ACTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 955 CTGCGTTTAAAGAAACAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1014
DB 961 TTGGAATTAAGAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1015 ATACCAATGCAAGAGAAATCATGCAATGAGGCTGAGAGAAATTAAGGAGAAACAG 1074
DB 1021 ATACCAATGCAAGAGAAATCATGCAATGAGGCTGAGAGAAATTAAGGAGAAACAG 1080
QY 1075 CATACTTAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134

DB 1081 CATACTTAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1135 TCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
DB 1141 TCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1195 GCTGTAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1254
DB 1201 GCTGTAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1255 GTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
DB 1261 GTTGCATCTGTTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1315 GAAAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1374
DB 1321 GAGAAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1375 TTCTCCGCGAGTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1434
DB 1381 TTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1435 AGCAATACCAAGAAATGCTGAGAGCAAAATTACTGTTGAGAGATGAGATGATGAT 1494
DB 1441 AGCACTTACCAAGAAATGCTGAGAGCAAAATGCTGTTGAGAGATGAGATGATGAT 1500
QY 1495 GCTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
DB 1501 GCTTTAAGCTCTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1555 TTCAATTAAGCTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1614
DB 1561 TTCAATTAAGCTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1615 AAGGAGCTCACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1674
DB 1621 AAGGAGCTCACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1675 GATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1734
DB 1681 GATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1735 CTGAGAGGCTGAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1794
DB 1741 CTGAGAGGCTGAGAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1795 AGGAGCTGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1854
DB 1801 AGGAGCTGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
QY 1855 AGGAGAGATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1914
DB 1861 AGGAGAGATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1915 GAGGAGTCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1974
DB 1921 GAGGAGTCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
QY 1975 TACATGCTGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2034
DB 1981 TACATGCTGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
QY 2035 ACCGCTGTTAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2094
DB 2041 ACCGCTGTTAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
QY 2095 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2154
DB 2101 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
QY 2155 GCTGTTAATCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2214

Db 2161 GCGGGTAACATATAGCTGATTTCTTTGAAAGCTTGAAGAGATCCAAACCATTTGAAAG 2220
 Qy 2215 AATATATCTGAGAGAGGCTGACACCGCATATACGAGAGATACATGGAAGATATACCA 2274
 Db 2221 AAGATATCAAGCGTGTCTCCAAAGATATACGAAAGATACATGGAAGATATACCTG 2280
 Qy 2275 GAGAGTGAATGACACTGCGCGGCTCAACGTTTCTGAAAGTACGTGTGCAAGCTCGAG 2334
 Db 2281 GAGAGATGATGACACTGCTGTGTGTATGTTCTCGAAATATGTAATTCGAAATTGAG 2340
 Qy 2335 AGGCTGAGAGAGCGCTACCTTGAAGATTTCTACATCTGAAGTTCCGAGCTGAGC 2394
 Db 2341 CGTGTGAGACTCGCGCATCTTGAAGATTTCTACATTCGAAATTCGCGACTGTGTG 2400
 Qy 2395 AAGACCGTGGC 2405
 Db 2401 AAAACTGTTC 2411

RESULT 5

ABZ76372
 ID ABZ76372 standard; cDNA; 2394 BP.

AC AEZ76372;

XX 12-JUN-2003 (first entry)

DE A. thaliana LMP encoding cDNA-clone ID PK118-1.

XX Lipid metabolism protein; LMP; seed storage; plant; transgenic; gene; ss.
 OS Arabidopsis thaliana.

XX Key Location/Qualifiers
 FT 1..2394
 FT /*tag= a
 FT /product= "LMP"
 FT /note= "Lipid metabolism protein"

XX W020C3014376-A2.

XX 20-FEB-2003.

XX 12-AUG-2002; 2002W0-US025586.

XX 10-AUG-2001; 2001US-0311414P.

XX (BAD1) BASF PLANT SCI GMBH.

XX Miltendorf V, Haertel H, Clirpus F;

XX WPI; 2003-256595/25.

XX P-PSDB; ABR39586.

XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 producing transgenic plants, for modulating seed storage compounds, e.g.
 lipid or fatty acid, in plants, and for evolutionary and protein
 structural studies.

XX Claim 1; Fig 12C; 108pp; English.

XX The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polymucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABZ76358-373 represent A. thaliana LMP encoding cDNA sequences
 XX Sequence 2394 BP; 671 A; 480 C; 564 G; 679 T; 0 U; 0 Other;

Query Match 42.8%; Score 1181.2; DB 7; Length 2394;
 Best Local Similarity 70.5%; Pred. No. 1.2e-256;
 Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 184 CTCGCCAGGAGACCTTCTCGAGCTCTCTCCGCTCCCGGAGAGAGCCATCGTGCAGC 243
 Db 151 CTAAACAAAGATCATATCAAAAGTTTGAGCTGTGAGAGAAACCAATGTTTGGCT 210
 Qy 244 CCGTTGCGGCATCGCGGTGCGCCCGCGCCGAGTTTGGAGTACGTCGCGCTCAAC 303
 Db 211 CCAATTTGCTGTGGCTATAGCTCCAGACCTGTGTAGGAATATGTCGTGTGAAT 270
 Qy 304 GTTCAAGAGCTAGAGTGAAGAGCTCAAGCTTCGAGATCTTCGCTTCAAGAGAG 363
 Db 271 GTGATAGCTGAGGATGATCATTTAAGTTTCTGAAATCTTCGGTTTAAAGAAAG 330
 Qy 364 CTGTGAGCGCCAGCAATGATATCCCTACGTTCTCGAGCTTGAAGCGGTCAAT 423
 Db 331 CTGCTTAATGACCAATGCAATGAGATTAATCTCTGAACTTGATTTGAACCTTCAAT 390
 Qy 424 GTCTAGTCCAGCGCCAAATCGCTCATCTATTTGAAACGATGTGCAATTCCTCAAC 483
 Db 391 GCAACATGCTCGGCCCAACTGTTCATCATTCATTTGGAATAGGGGTTCACTTCAAT 450
 Qy 484 CGACACTGTCTCATATATGTTCCGCAAGAGATGCTTGGAGCCCTGTGATTTTC 543
 Db 451 CGTCACTCTCTCAATTAATGTTCCGTAAACAAAGAAAGATGAGCTTGTGATTT 510
 Qy 544 CTCCGTGCGCACCGGCAAGAGGCAATTTATGATGCTTAATGATGATACAAAGCTTG 603
 Db 511 CTGCGCACTCAAAACATGATGAGCGCTCATGATGCTGATGATGATGATGATGATG 570
 Qy 604 GGGAGCTTCACTGTCTGTGACCAAGCTGAGAGACTTGTCAAAAGCTCTCTGTAC 663
 Db 571 CCCATCTCTGAGAGCTTGTGCAAGAGAGAGAGGTTCTTTCAATCTCTCTGTGCA 630
 Qy 664 ACACCATCTCAATTTGCTTAATAATTTCAAGAGTGGGCTTGAAGAAAGTTGGGCT 723
 Db 631 ACACCATCTCTCAATTTGCTTAATAATTTCAAGAGTGGGCTTGAAGAAAGTTGGGCT 690
 Qy 724 GATACAGAGAGCAATGTTTGAAGATGATCCATCTCTCTGAGACATTCAGGCGCA 783
 Db 691 GACAGAGAGAGAGGTTTCAAAATGATGATCTTCTCTGAGACATTCAGGCGCA 750
 Qy 784 GACCATCTACCTTGAAGATTTCTTGGAGAGATCCCATGATTTTAAAGTTGTG 843
 Db 751 GATCTCTGCTTGGAGAGCTTCTTGAAGAGATCTTATGTTCAATGTTGTGAT 810
 Qy 844 GTATCCCTCATGATATCTTGTGCAAGATATGATATGAGCTTGGCAAGACAGAGGA 903
 Db 811 TTGTCTCCCATGATATCTTGTGCAAGATATGATATGAGCTTGGCAAGACAGAGGA 870
 Qy 904 CAGATCGCTATATGCTGAGCAAGTCCGTCAGCTGAGAAATGAGATGTTCTCGTTTA 963
 Db 871 CAGGTTGCTATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 930
 Qy 964 AAGAAACAAGGCTGATGATTTTCCCAAGATTTCTATGTTACTGCTGATACAGAT 1023
 Db 931 CAGAACAGAGACTGAGATGATTTCAAGATTTCTATGTTAAAGATGCTGATACCGAA 990
 Qy 1024 GCAAAAGAGATCATGATATGAGCGCTTGGAGAAATGAGAAACAGACATCTTAC 1083
 Db 991 GCAAAAG 1050
 Qy 1084 ATATACAGATTTCTTCAAGAAATGAAATGAGATCTTAAGAAATGATATCAAGATTT 1143
 Db 1051 ATTTCTGGAATACATTTGAGATGAGAAAGGAATCTTGGCAAGAGATCTCAAGGTTT 1110
 Qy 1144 GATGTGTGCAATATCTGAAACATTTGAGAGATGCTGTTGAATTTGCTGCTGAA 1203
 Db 1111 GATGTGTGCAATATCTGAGAGATTTTGGCAAGAGATGATCAAAATTTTCTGCGAG 1170

D	b	141	GTCTCTGAATTGATGTGAGCGCTTAACTGTCTCTGAGTACTTCATTTCAAAAGAA	200
Q	y	364	CTTGTGACGCGCAGCAACAATGATCCCTACGTTCTCGAGCTTGACTTGAGCCGTTCAAT	423
D	b	201	CTTGTGATGGAAGGCTGATGACCACTATGTCTTGAGCTTATATTCAGAGCTTTTAAT	260
Q	y	424	GTCCTAGTCCAGGCCCAATTCGGTCACTACCTAATGGAAACGGTGTGAGTTCCCAAC	483
D	b	261	GAATCAAGTTCCAGCTCCACTCGCTCTTCACTAATGGTATATGATGTCTCAAT	320
Q	y	484	CGACACTGTTCCTCAATCATGTTCCCGCAACAGGAGATTGCTGGAGCCCTGTGTGAATTC	543
D	b	321	CGGACCTGTTCATTAAGCATGTGTTTGCAAGAAATTCCTGGAGCCGTTACTGAATTT	380
Q	y	544	CTCCGTGCGCACCGGACAAAGGGGCAATGTATGATGCTTAATGATAGAAATCAAACTTG	603
D	b	381	CTTAGAGTGCACAAACATAAGGAGTGTGATGATGTGAATGATCGATACAGATCAATC	440
Q	y	604	GGGAGGCTTACGTCTGTGTACCAAAAGCTGAGGAGCACTTTCAAAAGCTCCCTGTGAC	663
D	b	441	CAGGCTCTCAAGTCTGATTTGTCTAAAGCTGAGGATATCTTAATCAAACTTCCAGAGAT	500
Q	y	664	ACACCAATCTCACAATTGCTTAAATTTCAAGAGTGGGGCCCGGAGAAAGGTGGGGT	723
D	b	501	ACACCTTACTGTGATTGCAATTTGTATTCCAAGATATGGATTTGAAAGAGGCTGGGGT	560
Q	y	724	GATACAGAGACACATGTTTGGAAATATCATCTCCTTTCAGACATCATTCAGGGCCA	783
D	b	561	GATCTGTGAAAGGGTCTAGAAATATGATGATCTACTAGATATCTTCAGGCTCCC	620
Q	y	784	GACCCATCTACCTAGAGAAATCTTGGGGAGATCCCATGATTTTAACTGTGTGTG	843
D	b	621	GATCCGTTCAATTAGAGACATTTCTGGGAAAGCTTCCCATGGGTATTAATGTGCTAAT	680
Q	y	844	GTATCCCTCATGATTACTTTGGTCAAGCTTAACTATTAAGCTTGCAGACACAGAGGA	903
D	b	681	TTGTCTGTACATGATTAATTTTGGACAGGCAATGTGCTCGGCTGTGACACTGGTGG	740
Q	y	904	CAGATCGCTATTAATCTGAGCCAAAGTCGTCATAGAAATGAGATGGTCTCCGTTTA	963
D	b	741	CAGATAGTTTAAATCTTGACCAAGTGGGGTCTCTGAAACATGAATATGCTTCACAGATA	800
Q	y	964	AAGAAACAAGGGCTGATGTTTCCCAAGATTCCTCATGTTACTCGGCTGATACAGAT	1023
D	b	801	AAGAGCAGAGCACTGATGTGATCTCTTGAAATCTTATCTGAGTGGTGTATTCCTGAC	860
Q	y	1024	GCAAAAGGAATCATATGCAATCAGGGGCTTAGAGAAATTAATGGAACAACACTACTTAC	1083
D	b	861	GCATAAGGACACAGCTGCATCTCAATCAGTATGAGAAAGTCAAGTGAACAGAGCATGTAAT	920
Q	y	1084	ATAATACAGATCCCTCTCAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATT	1143
D	b	921	ATCTCGAAGATCTCTTCCGATCAGAGAAAGGAATCCCTCCCAATATGATATCTAAGATT	980
Q	y	1144	GATGTGTGGCCATATCTGAAAATTTTGCTGAGATGCTGTGCTGTAATTCGTGTGA	1203
D	b	981	GATGATAGGCTTATTTAGAGACTTCACTGAGATGAGCTGTGTGAATTAATTTGGCCAG	1040
Q	y	1204	TTACAGAGTATCTCCAGACTTCAATTTGGAACCTACAGTATGAGAAATCTTGTGGCGTCA	1263
D	b	1041	TTGCAAGGGTCGCCAGATCTGTAATTTGGCAACTACAGGATGGGAAATATATGTGCTTCT	1100
Q	y	1264	TTGCAATCTTACAGATGGAAATTAACCCAGTCAACATGTGCATGCTCTGAAAAAGAT	1323
D	b	1101	TTATGTCTCCCAAAAATGGGTGTCAACCCAGTCAATATATAGCCCATGCAATGGAGAAAC	1160
Q	y	1324	AAGTATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAAATCAATTTCTCTGCG	1383
D	b	1161	AAGTATCCAGATTCAGATTTTACTGGAAGAAATTTGAGACAAATATCACTCTCGGT	1220
Q	y	1384	CAGTTCACGTCTGATTAATTTGATAGCAATGGCAATTTTATCATACAGACATAC	1443

D	1221	CAATTTTCAAGTACCTTGATGGCAATGAAATCATGCTGATTTTCAACATTAACGAGTACTAC	1583
Q	1444	CAAGAAATTTGCTGAGACCAAAAAATCTGTGGACAGATATGAGACTCATACTAGCCCTTACT	1583
D	1281	CAATAGATAGCTGGAAAGAAATATCTGTGGTCAATATGATGAAGCAATAGAGCCCTTTACT	1544E
Q	1504	CTGGCTGTGTGTATCCAGATGTGTCCATGGATCGATGCTTCGATCCAAAGTCAATATA	1563
D	1341	TTTCCGGGGCTGTATCCGGGTGTTCAAGGATTTGATGTTTGATCCCAAGTTAATATTT	1400
Q	1564	GTCTCTCTCGAGCTGACATGTCCATATATCTTTCCACATACCGAAGAA--GCCAAGGA	1622
D	1401	GTCTCGCAAGGGGACAGATGCGCATCTACTCTCCATTTTCAAGAAAGATGCACCTGT	1467
Q	1621	CTCACTCTCTCTTAAATGTTCAAATGAAATTTGATTTTATGACCCGGACAAACGATGAA	1680
D	1461	CTCACTTCACTTCAATAGACTTATATAGACAGCTCTCTATTCAAACCTGAGACAAACGAA	1522
Q	1681	CACATGGGACATCGATGATGACCGGATCAAAAGCCATCTCTTCTCCATGCGAAGCTGCAC	174
D	1521	CACATGGTGTATATGATGATACCTCAAAAGCCATATATTTTCCATGGCGAGGCTTACAC	1580
Q	1741	AGGTTGAAGAACATACAGGGCTGTGTGCAAGCTTTTGCTAATGGTGGTAAAGTGAAGGG	1800
D	1581	CGTGGAAAGAAATATACAGGGCTGTGTAGTGTATGTGCAAGATGCAAACTCAGGGAA	164
Q	1801	CTGTGAACCTTTGTGTGTGCGGGTATCAATGATGTCAACAGTCCAAAGACAGGAA	1867
D	1641	CTGGCAAACTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1700
Q	1861	GAGATCGCGAGATAGAGAAAGTCAATGATCAATCTCAAGACCCACAACTTTGTCCGGGAC	192
D	1701	GAAATTCGCGAAATGAGAAAGATGACAGGCTTATATACAGAGATATATATTTAAGAGCAA	176
Q	1921	TTCCGCTGTGATCTCGCCCAAGCAAAAGGGCCCGTAAAGCGAGACTCTATGCTACATC	198
D	1761	TTTCGTGTGATGCTTCTCAAAATTAAGTACAAATGTGTGAATCTCATGTGCTACATTT	182
Q	1981	GCTGATACCAGTGTGTCTTCTGTACAGCCGAGCTTGTATGAAAGCTTCCGTCTACCGTC	204
D	1821	TGTGCAAAAGAGGATATTTTTCGAGAGCTGTGATTTAAGAACATTTGGGCTTACAGTT	188
Q	2041	GTTGAGGCGATACCTGTGTGGTCTTCATCTTGTGGAGCGTCATATGAGGTCAGCTGAG	210
D	1881	GTTGAAGCCATACCTGTGTGTCTTCCCAATTTGTACTCTGCAAGGTGTGTGACGTGAG	194
Q	2101	ATCATAGAGCATGGCGCTCGGGCTTCCACATTTGACCCGTCACACCCCGAACAAGCTGTT	216
D	1941	ATTATATGAAAGCGGTGTTCAAGATTTCAATATGATTCATATCATCTGATCAGGACGAA	200
Q	2161	AATCTGATGGCCGACTTCTTGCACCGGTGCAAGCAAGACCAGATACAGTGGGTGATATTA	222
D	2001	AA---AATGATCGAATTTCTTTGTCAAGTGCAGAGAGAGATCCAAATCTACGTGATTAATC	205
Q	2221	TCTGAGCGAGGGCTGAGAGGCAATATCGAAGATACACATGGAAGATATATCTCAGAGAG	228
D	2058	TCTGCGAGAGGGTACTTAAAGATCAAGAAAGATATACCTGCGAAGAAAGTATCTGAAAG	211
Q	2341	GAGACGAGGCGCTACTCTTGAAGTGTCTACATATGAAAGTTCCGACAGCTGGGAAAGAC	240
D	2178	GAAACACGAGGTTATCTTGAAGTGTCTACATTTTGAAGTTCCGTGATCTGGCAACTCT	223
Q	2401	GTCGCGCTTGCATATGACCAACCGC 2425	
D	2238	GTTCCGCTGCGCAACAGATGAAGGC 2262	

RESULT 7
PAD45852

ID AAD45852 standard; cDNA; 2908 BP.
 XX AC AAD45852;
 XX DT 27-DEC-2002 (first entry)
 XX DE Corn sucrose synthase (Sus1) cDNA.
 XX XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 XX cellulose; corn; chromosome 9; gene; ss.
 XX OS Zea mays.
 XX XX Key Location/Qualifiers
 XX FH 28..2478
 XX FT /*tag= a
 XX FT /product= "Corn Sus1 protein"
 XX PT WO200267662-A1.
 XX PN 06-SEP-2002.
 XX PD 21-FEB-2002; 2002WO-US005137.
 XX PE 22-FEB-2001; 2001US-0270777P.
 XX PR (PION-) PIONEER HI-BRED INT INC.
 XX PA Drugga KS, Helentjaris TG, Niu X;
 XX PI WPI; 2002-691625/74.
 XX DR P-PSDB; AAE28501.
 XX XX New polynucleotide and its encoded sucrose synthase, useful for
 XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
 XX or soybean) to improve stalk length, reduce grain breakage, or improving
 XX plant or grain strength.
 XX XX Example 10; Page 110-114; 125pp; English.
 XX CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
 XX acids. The polynucleotide, or its encoded protein, is useful for
 XX modulating the level of sucrose synthase in a transgenic plant,
 XX increasing cellulose production in the stalk tissue of a transgenic
 XX plant, or increasing the concentration of cellulose in the tissues of a
 XX seed of a transgenic plant. This is particularly useful in plant (e.g.
 XX maize or soybean) breeding, especially for e.g. improving stalk length in
 XX maize, reducing grain breakage during combining, transport or movement
 XX into storage, or improving plant or grain strength. The present sequence
 XX is corn Sus1 cDNA. Corn Sus1 gene is located at chromosome 9
 XX SQ Sequence 2908 BP; 623 A; 815 C; 808 G; 662 T; 0 U; 0 Other;
 XX
 XX Query Match 42.6%; Score 1173.4; DB 6; Length 2908;
 XX Best Local Similarity 68.3%; Pred. No. 7.2e-255;
 XX Matches 1656; Conservative 0; Mismatches 761; Indels 6; Gaps 2;
 XX
 XX 6 TCCTCCGAGCTGACCGCAACGCGAGCATCCGGGACCGGTCGAGACACACCTCCACGC 65
 XX 45 TGACCTGTCTGAGCGGCTCCAGAGCTCAGGAGCGCATGCGACTCATCTCTGC 104
 XX 66 GCACCGCAACGAGCTCGTCCCTCTCTCCAGTAGCTGAAACAGGGAGGGATCCCT 125
 XX 135 CCAGCCCAATGAGCTTGTGCGGCTTCCACAGGCTGMAAAACCTTGGAAAGGATGCT 164
 XX 126 GAGCGCGACCATCTCTGACGCGCTCGAC---GAGTCCAGGCTCCGGGTCGCGC 182
 XX 165 GCAGCCCAACCATCATTTGCCAGTAGTACAAATGCGATCCCTGAGGCTGAGCGCAGAA 224
 XX 183 GCTCGCGAGGAGACCTTCTCTGACGCTCCCTCGCTCCGCGCAGGAGCGGATCGTCTGCC 242
 XX
 XX DB 225 GCTCAAGGATGCTGCTTTTGGAGGATGTCTCTGAGGCGAGCTCAGAGGCGGATGTCTATCC 284
 XX QY 243 GCCGTTCGTGGCCATCGCGGTGCGCCGCGCGCGGAGTTTGGGAGTAGTCTCGCGTCGA 302
 XX DB 285 CCCATGGGTGCACTTGGCCATCCGGCCCTAGGGCTTGGTGTCTGGGAGTATGTGAGGGTCGA 344
 XX QY 303 CGTTCACGAGCTCAGCGTCGAGCAGCTCACAGTCTCTCGAGTACCTCCGCTTCAAGGAGGA 362
 XX DB 345 CGTCACTGAGCTCGCTGTGTGAGGAGCTGAGAGTCTCTGAGTACCTCGAGTTCAGGAACA 404
 XX QY 363 GCTTGTGCAAGCGCCAGCACAATGATCCCTACGTTCTCGAGCTTGAGTTCGAGCGGTCGA 422
 XX DB 405 GCTTGTGGAAGAGGCGCCCAACAACACTTGTCTCTGAGCTGAGTCTTGGAGCAATTCGA 464
 XX QY 423 TGTCTCAGTCCCAAGCGCCAAATCGGTTCATCATCTATTGGAAGGCTGCGAGTTCCTCA 482
 XX DB 465 TGCCTCTCTCCCGCGCTCTCTGTCAAAGTCCATTTGGCAATGGCGTGCAGTTCCTCA 524
 XX QY 483 CGGACACTTGTCTCAATCATGTTCGCAACAGGAGTTCCTTGGAGCCCTGTTCGATTT 542
 XX DB 525 CAGGACACTGTCTCATCAAGCTCTTCCATGCAAGGAGAGCATGTACCCCTTGTCTCACTT 584
 XX QY 543 CCTCCGTGGCCACCGGCAACAGGGGCAATGTTATGATGCTTTATGATAGATAGATACAAAGCTT 602
 XX DB 585 CCTTCGCGCCCAACTACAGGGGATGACCATGATGTTGAACGACAGAAATCCCGAGTCT 644
 XX QY 603 GGGGAGGCTTCAGTCTGTCTGACCAAGCTCAGGAGGACCTTGTCAAAGCTCCCTGCTGA 662
 XX DB 645 CAGTGTCTGCAAGGTCGCTGAGGAAGCTGAGGAGCACCTGTCCACCTCAAGCTGA 704
 XX QY 663 CACACCACTCACTCAATTTGCTTATAAATTCAGAGTGGGGCTGGAGAAAGGTTGGGG 722
 XX DB 705 TACCCCACTCTGAAATTTCAACACAGGTTCCAGGAATTTGGTCTGGAGAAAGGTTGGGG 764
 XX QY 723 TGATACAGCAGGACATGTTTTGGAATGATCTCTCTCTAGATCATCTTTCAGGGGCC 782
 XX DB 765 TGATGGCGTAAAGCGTGCACAGGAGACTATCCACCTCTCTTGGACCTCTCGAGGGCCCC 824
 XX QY 783 AGACCACTCTACCTTAGAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGTGTGTGT 842
 XX DB 825 AGATCGCTCACCTCGAGAGATTTCTTGAACGATCCCGCTGGTTCATGTCTGTAT 884
 XX QY 843 GGTTATCCCTCATGAGTACTTTGGTCAAGCTAATGATTTAGGCTTGCACACACAGGAG 902
 XX DB 885 CCTTCCTCTCAGTACTTCTCGCTCAGCTAATGCTTGGGTACCTGACACCGGAGG 944
 XX QY 903 ACAGATCGCTATATATCTGACCAAGTCCGTCAGCTAGAAATGAGATGTTTCCGTTT 962
 XX DB 945 CCAGGTTGTCTACATCTTGGATCAAGTGGCGGCTATGGAGAACGAAATGCTGCTGAGAT 1004
 XX QY 963 AAGAAACAGGCGCTTGTGTTTCCCAAGATTTCTCATTTTACTCGGCTGATACAGGA 1022
 XX DB 1005 CAAAGAGTGTGCTTGAACATACGCGGAGATTCCTTATTTGTCACAGGTTCTCCCTGA 1064
 XX QY 1023 TGCAAAAGGAACATCATGCAATCAGCGGCTTGGAGAAATTAGTGGAAACACAGCANACTTA 1082
 XX DB 1065 TGCACTGCGCACCACTGTGGCCAGCGCTTGAAGAGTCTCTTGGCACCGGACACTGCCA 1124
 XX QY 1083 CATATTACGAGTTCCTTCAGAAATGAAATGGGATCTTAAGAAATGGATATCAAGATT 1142
 XX DB 1125 TATCTCTCGGTGCCATTCAGAAACGGAATCGTTTCGCAAGTGGATCTCGCATT 1184
 XX QY 1143 TGATGTGCGCCATATCTGGAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGCTGA 1202
 XX DB 1185 TGAAGTCTGCGCGTACTCTGAGACTTACATGATGAGCTGGCGCATGAGATTTCTTGAGA 1244
 XX QY 1203 ATTACAGGTACTTCCAGACTTCTAATTTGGAATCTACAGTGTAGTGAATTTTGTGGGCTC 1262
 XX DB 1245 GCTTCAGGCCAATCTCTGACCTGATCATCGGAATCTACAGTACAGGAACCTTGTGGGTG 1304
 XX QY 1263 ATTGCTATCTTCAAGATGGGAATTCACCTAGTGGAACTTGTCTATCTCTGGAAGAC 1322
 XX DB 1305 TTTGCTCGCCCAAGATGGGTGTTACTCACTGTACCATTTGCCATTCGCTTGAAGAAC 1364

1323	QY	TAAGTATCCAGATTCAGACATA	TTTTGGAGAAGTTTCGATGAGAAGTACCAATTCCTCTG	1381
1365	DB	TAAGTATCCCTAACTCCGACCTCTACTCGAAGAAGTTTGAGATCACTTACCACCTTCCTCGTG	1424	
1383	QY	CCAGTTTCACCTGCTGATATAATTCGTATGACAAATGCTGATTTTATCATCACACGACACATA	1442	
1425	DB	CCAGTTTCACCACTGACTTGATTGCAATGAAACATGCGCACTTCTATCATCACCAGTACCTT	1484	
1443	QY	CCAAGAAATTCCTGGAGCAAAAATACTGTTGGACAGTATGAGAGTCACTACTCCCTTTTAC	1502	
1485	DB	CCAAGAGATCGCCGGAAACAAGGACACCGTCGGCCAGTACGAGTCAACATGCGCTTCAC	1544	
1503	QY	TCGCTCTGCTCTGACCGAGTTCCTCCATGCGATCGATGCTTCGTGATCCAAAGTTCAAATAT	1562	
1545	DB	ATGCTCTGGCCTGTACCGCGTGTGACCGGCAATGATGTTGCGACCCCAAGTTCACCAT	1604	
1563	QY	AGTCTCTCTGGAGCTGACATGTCATATACTTTCCACATACCGGAGAAGCCCAAGCGACT	1622	
1605	DB	CGTGTCTCTCGCGCGGACCTGTCCATCTACTTTCCCGTACACCGAGTCGCACAAAGGCT	1664	
1623	QY	CACCTCTCTTCATGCTTCATCGAAATTTGATTTATGACCCGGAGCGAAACGATGAACA	1682	
1665	DB	GACCTCCCTTCACCCCGAGATTGAGAGGCTCTGTGTACGCAAACTCGAGAAACGCGAGCA	1724	
1683	QY	CATTGGGCATCTGGATGACCGGTCAAAAGCCATCTCTTCTCCATGCGAAGACTCGACAG	1742	
1725	DB	CAAGTTCTGTTCTGAACGACAGGAAACAGCAATCATCTTCTCCATGGCTGCTCGACCG	1784	
1743	QY	GGTGAAGACATTAACAGGCTGTGTGAAAGCTTTTGTAACTGCTGAAGCTGAGGAGCT	1802	
1785	DB	TGTGAAGAACTTGACTTGGCTGTGTGGAGCTGTACGGCCGGAAACAAGCGGCTGCAGAGCT	1844	
1803	QY	GGTAAACCTCTGTGCTCGTTGCGGGTACATGATGTCAACAAGTCCAAAGGACAGGGAAGA	1862	
1845	DB	GGTGAACCTCTGTGGTCTGTGCGCGACCA---TGGCAACCTTCCAAAGACAAAGGAGGA	1901	
1863	QY	GATCGCGGAGATAGAAAGATGCATGAACCTCATCAAGACCCCAAACTTGTTCGGGCGAGTT	1922	
1902	DB	GCAGGCCGAGTTCAAAGAAGATGTTTGACTCATCTGAGCAGTACAACTGAACCGGCACAT	1961	
1923	QY	CCGCTGGATCTCTGCCGAGCAAAACAGGGCCCGTAAACGGGAGCTCTATTCGCTACATCGC	1982	
1962	DB	CCGCTGGATCTCCGCCACAGATGAACCCGCTCCGCAACGGCGAGCTGTACCGCTACATCTG	2021	
1983	QY	TGATACCCATGCTGTGCTTTTGTAACAGCGCGCTCTGATGAAGCGTTCGGCTCTCACCGTCTG	2042	
2022	DB	CGACACCAAGGGCGCTTCGTGCAGCGCTGTTTCTACGAGGCTTTCGGGCTGACGGTGT	2081	
2043	QY	TGAGGCCATGACCTGTGGCTTCCTACTTTCCGGACGCTCCATGAGAGTTCGACTGAGAT	2102	
2082	DB	TGAGGCCATGACCTGTGGGCTGCGCCAGTTTCGCAACCGCTACCGCTACGAGCGGCGAGAT	2141	
2103	QY	CATAGAGCATGGCGTCTCGGCTTCCACATGACCCGCTACCAACCCCGAACAGAGCTGTAA	2162	
2142	DB	CATCGTGCAACGGCTGTCTGCTACCACTGACCTTACAGGGCGCAAGGCGCTCGGC	2201	
2163	QY	TTTGATGGCGCACTTCTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATC	2222	
2202	DB	CCTGCTCGTGCACTTCTTCGACAAGTGCACAGCGGAGCCGAGCCACTGGAGCAAGATCTC	2261	
2223	QY	TGAGCAGCGGCTCAGGGCATATACGAGAGTACATGGAAGATATCTCTCAGAGAGTT	2282	
2262	DB	CCAGGGCGGCTCCAGCGTATCGAGGAGAAGTACACTGGAAGCTGTACTTCGAGAGGCT	2321	
2283	QY	GATGACACTGGCCGGGCTCTACCGTTTCTGGAAGTACGTTCTCGAAGCTCGAGAGGCTGGA	2342	
2322	DB	GATGACCTTCAACGGCGTGTACGGTTCTGGAAGTACGTTCTCCAACTTGAGAGGCGCGA	2381	
2343	QY	GACGAGCGCTACTGTGAGATGTTCTTACATATGGAAGTTCGCGAGCTGCGGGAAGACCGT	2402	
2382	DB	GACCCGCGGTACTCTGAGATGCTGTATCGGGCTCAAGTACCGCACCATGCGGACGCT	2441	

QY	2403	GC	CGCTTGC	AATG	CAAC	ACCGC	2425
Db	2442	GC	CGCTG	CGCGT	GAGG	GAGC	2464
RESULT 8							
ABZ76371	ABZ76371 standard; cDNA; 2418 BP.						
XX	AC	ABZ76371;					
XX	DT	12-JUN-2003 (first entry)					
XX	DE	A. thaliana LMP encoding cDNA-clone ID Pk118.					
XX	KW	Lipid metabolism protein; LMP; seed storage; plan					
XX	OS	Arabidopsis thaliana.					
FH	Key	Location/Qualifiers					
FT	CDS	1..2418					
FT	/*tag= a	/product= "LMP"					
FT	/note= "lipid metabolism protein"						
XX	WO2003014376-A2.						
XX	20-FEB-2003.						
XX	12-AUG-2002; 2002WO-US025586.						
XX	10-AUG-2001; 2001US-0311414P.						
XX	(BADI) BASF PLANT SCI GMBH.						
XX	Mittendorf V, Haertel H, Cirpus P;						
XX	WPI; 2003-256595/25.						
XX	P-FSDB; ABR39585.						
XX	New nucleic acid molecule encoding lipid metaboli						
XX	producing transgenic plants, for modulating seed						
XX	lipid or fatty acid, in plants, and for evolution						
XX	structural studies.						
XX	Claim 1; Fig 12A; 108pp; English.						
XX	The invention relates to isolated lipid metabolis						
XX	polynucleotides. The LMP functions as a modulator						
XX	compound in a plant. The LMP nucleic acid and pro						
XX	producing transgenic plants and in modulating the						
XX	compounds. These are used to modify or increase l						
XX	cofactors, and enzymes in microorganisms and plan						
XX	LMP nucleic acid and protein may be used in ident						
XX	being Arabidopsis thaliana, as markers for specifi						
XX	genome, and in evolutionary and protein structura						
XX	CC ABZ76358-373 in evolutionary A. thaliana LMP encoding c						
XX	Sequence 2418 BP; 676 A; 491 C; 562 G; 689 T; 0 U						
XX	Query Match	42.5%; Score 1172; DB 7;					
XX	Best Local Similarity	70.9%; Pred. No. 1.4e-254;					
XX	Matches 1556; Conservative	0; Mismatches 640;					
QY	222	GC	AGGAGC	GAATCG	TGCTCC	CCCGCTCGTGC	CCATCGGG
Db	213	GC	AGGAAGC	ATAGTTTGCT	CCATTTGCTT	CTTCTTGGCT	
QY	282	TT	GGGAGT	ACGTC	CCCGGTCA	AGTTTC	ACAGCTCAGCGTC
Db	273	TAGG	GAATATG	TCCCGTGTGA	ATGTGTAT	GAGCTG	AGCGTAT
QY	342	GT	ACCTTC	CGCTTCA	AGGAGCGT	TGTG	CAGCCGCCAGCAC

Db 333 ATATCTTCGGTTTAAGAGAGAGCTCGTTAATAGGCATGCCAATGAGATTAATCTCCCTTGA 392
QY 402 GCTTGAATTCAGAGCCGTTCAATGCTCAGTCCCGCCCAATCGGTGCATCATCTATTGG 461
Db 393 ACTTGAATTTGAACCTTTCAATGCAACATTCGCTCGCCCAACTCGTTCATCATCCATTGG 452
QY 462 AAGCGGTGCGAGTTCCTCAACGACACTGCTCCTCAATCATGTTCCGCAACAGGAGTTG 521
Db 453 GAATGGGGTTCAGTTCCTCAATCGTCACTCTCTCAATTAATGTTCCGTAAACAAGAAAG 512
QY 522 CTTGGAGCCCTGTTGGAATTCCTCCGTTGGCCACCGGCACAAGGCGCATGTTATGATGCT 581
Db 513 CATGGAGCCCTTGTGAGTTCCTCCGACTCAACAACATGATGGCCGCTCTATGATGCT 572
QY 582 TAATGATAGATAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCA 641
Db 573 GAATGATCGAATACAGAAATATCCCATACTTCAGGGAGCTTTGGCAAGCAGAGGAGTT 632
QY 642 CTTGTCAAGCTCCCTGCTGACACACCATACTCACAAATTCCTTATTAATTTCAAGAGTG 701
Db 633 CTTTCTTAACCTTCCTCTGGCAACACCATACTCTGAAATTCGAATTTGAATTTCAAGGGAT 692
QY 702 GGGCTTGGAGAAAGGTTGGGTTGATACAGCAGGACATGTTTGGAAATGATCCATCTCCT 761
Db 693 GGGATTTGAAAGGGGATGGGGTGACACAGCAGACAGAGGTTTCAGAAATGGTGCATCTCT 752
QY 762 TCTAGACATCATTCAGGGCCAGACCCCATCTACCTTAGAGAAAATTTCTGGGGAGGATCCC 821
Db 753 TCTGGACATACTCAGGACACCTGATCTCTCTGTTCTGGAGAGCTTTCTAGGAAGGATTC 812
QY 822 CATGATTTTAACTGTTGTGTTATCCCTCATGATACCTTGGTCAAGCTAATGATTT 881
Db 813 TAGGTGTTCAATGTTGATTTTGTCTCCGATGGTTACTTTGGCCAAAGCCAAATGCTT 872
QY 882 AGGCTTCCAGACACAGGAGGACAGTCTGTATATATCTGACCAAGTCCGTCACATAGA 941
Db 873 GGGTCTCCCTGATACTGGTGACAGGTGCTCATCTTCTGATCAAGTACGTGCATTTGA 932
QY 942 AATGAGATGTTCTCCGTTTAAAGAAACAGGGCTTGATGTTTCCCAAGATTCAT 1001
Db 933 AATGAGATGCTCTTAGGATACAGAAAGCAGGACTGGAAGTTATTCAGAAATTCAT 992
QY 1002 TGTACTCGGCTGATACAGATGCAAGGACATCATGCAATCAGGGCTTGAGAGAT 1061
Db 993 TGTAAACAGACTGCTCCGAGCAAGAGGAAACAGTGCACACAGAGTTAGAAAGAGT 1052
QY 1062 TAGTGAACACAGCATACTTACATATTACAGGTTCCCTTCAGAAATGAAATGGGATACT 1121
Db 1053 TAGTGGTACAGAACACGCACACATCTCGGATACCAATTTAGGACTGAAAGGGAATCT 1112
QY 1122 TAAGAAATGATATCAGATTTGATGTGTGSCCATATCTGGAACATTTGCTGAGGATGC 1181
Db 1113 TCGCAAGTGAATCTCAAGGTTTGTGTTCTGSCCATACCTGAGACTTTTGCAGAGGATGC 1172
QY 1182 TGCTGGTGAATTTGCTGCTGAAATFACAGGTTACCTCCAGACTTCATAATTTGGAAGTACAG 1241
Db 1173 ATCAATGAAATTTCTGCGAGTTGAGGGGTGACCAAACTCTCATCATTTGCAACTACAG 1232
QY 1242 TGATGAAATCTTTGTGGCGTCAATGCTATCTTCAAGATGGGAATTTACCCAGTGCACAT 1301
Db 1233 TGATGGAATCTGTTGCTCTTTGTTAGCTAGTAAAGCTAGTGTGATACAGTGTATAT 1292
QY 1302 TGCTCATGCTCTGGAAGAGTAAATGATCCAGATTCAGACATATTTTGGAGAAATTTGGA 1361
Db 1293 TGCTCATGCTTTAGAGAAACCAAGTACCCCGAGTCTGACATTTTACTTGGAGAAACCATGA 1352
QY 1362 TGAGAGTACATTTCTCTCCGAGTTCACTGCTGATATTAATTTCTATGACATGCTGA 1421
Db 1353 AGATAAGTATACATTTTCAAGTCAAGTTCATGTCAGATCTAATTTGCCATGAATAATGCCGA 1412
QY 1422 TTTTATCATCACCAGCACATACCAAGAAATTTGCTGGAGCAAAATACTGTTGGACAGTA 1481

Db 1413 TTTTATCATCACCAGCACATACCAAGAGATTTGCGGGAAGCAGAAACAATGTTGGGCAATA 1472
QY 1482 TGAGAGTCATACTGCTCTTACTCTGCTCGTGTGTGACGAGTTGTCCATGGGATCGATGT 1541
Db 1473 CGAGAGCCACACAGCTTTTCACTATGCTGGTCTTTTACCAGGTGTTTCAATGAATGATGT 1532
QY 1542 CTTTGATCCAAAGTTCATATATAGTCTCTCTCGGAGCTGACATGTCCTATATACCTTTCCACA 1601
Db 1533 CTTTGATCCTAAGTTTAAATATAGTCTCTCCAGGAGCTGATATGACCATATCTTTCCATA 1592
QY 1602 TACCGAAGGCCAAGCGACTCACCTCTCTCATGTTCAATCGAAATTTTCAATTTATGA 1661
Db 1593 TTCTGACAGGAAAGAGACCTCACGCTCTCATGATCAATGAGAACTCTCTTTAG 1652
QY 1662 CCGGAGCAAAACGATGAACACATTTGGGCACTCTGGATGACCGGTCAAAAGCCCATCTCTT 1721
Db 1653 TCGCGAAACAGAAATGATGAGCATGTGTGTTTACTGAGCGACCAATCGAAGCCAATCATCTT 1712
QY 1722 CTCCATGCGAAGCTCTGACAGGCTGAGAAACATTAACAGGGCTGCTGAGCTTTTGCTAA 1781
Db 1713 CTCTATGCGAAGACTTGAAGGCTGAAAACTTGACTGGCTAGTTGAATGCTATGCCAA 1772
QY 1782 GTGCGCTAAGCTGAGGGAGCTGTAAACCTTTGTCTGTTGCCGGTACAAATGATGTCAA 1841
Db 1773 GAATAGCAAGCTTAGAGAGCTTGCAATCTTGTATAGTCTGGTGGCTACATCGATGAA 1832
QY 1842 CAAGTCCAGGACAGGGAAGAGATCGCGGAGATAGAGAGATGCAAGTCAATCAAGAC 1901
Db 1833 TCAGTCCAGGGATAGAGAGGAAATGGCTGAGATACAAAGATGCAAGCTCTGATTGAGCA 1892
QY 1902 CCACAACTTGTTCGGGCAAGTTCGCTGGATCTCTGCGCCAGACAAACAGGGCCCGTAACGG 1961
Db 1893 GTATGATTTACCGGTGAGTTTAGGTGATAGTCTCTCAAAATGAACCGGTGCTCGAATGG 1952
QY 1962 CGAGCTCTATCGCTACATCGCTGATACCCATGCTGCTTTCTGACAGCGGCTTGTATGA 2021
Db 1953 TGAAGCTTACGTTATATCTCGACAGACAAAGGTGTTTGTTCAGGCTGCTTTCTATGA 2012
QY 2022 AGGTTGCGTCTCACCGTCTGTTGAGGCGCATGACCTGTGGGCTTCCTACTTTTCGCAAGCT 2081
Db 2013 AGCATTTGGGCTTACGGTTGTGGAATCAATGACTTGTGCACTTCCCAACGTTTGTACCTG 2072
QY 2082 CCATGGAGCTCCAGCTGATCATAGACATGGCTCTCGGGCTTCCCATTTGACCGCTA 2141
Db 2073 TCATGTTGGAGCCCGCAGAGATTTATCGAAACCGAGTTTCTGGGTTCCCAATTTGACCCATA 2132
QY 2142 CCACCCGAAACAGGCTGTAAATCTGATGGCGGACTTCTTTCGACCGGTGCAAGCAAGACC 2201
Db 2133 TCATCCAGACCAAGTTGCAGCTACCTTGGTCAAGCTTCTTTGAGACTGTAAACCAATCC 2192
QY 2202 AGATCACTGGGTGAATATATCTGGAGCAGGCTCGAGCGCATATACGAGAGTACACATG 2261
Db 2193 AAATCATTTGGTTTAAATCTCTGAAGGAGGCTCAAGCGGAATCTATGAAAGGTACACATG 2252
QY 2262 GAAGATATCTCAGAGAGTTGATGACACTGCGCGGTCTACGTTTCTCGAAGTACT 2321
Db 2253 GAAGAGTATCTCAGAGAGCTGCTTACCTCGCTGGAGTCTATGCAATCTCTGAAACATGT 2312
QY 2322 GTCGAAGCTCGAGAGGCTGGAGAGCAGGCGCTACCTTCAGATGTTTCTACATACATCAAGT 2381
Db 2313 GTCTAAGCTCGAAAGGAGAGAAACACGAGCTTACCTAGAGATGTTTACTCATTTGAAAT 2372
QY 2382 CCGGAGCTGGGAGAGACCGTGGCCGCTTGGCAATTTGA 2417
Db 2373 TCGTGAATTTGGCCAAATCAATCCGCTGGCAACAGA 2408

RESULT 9
ADA71337
ID ADA71337 standard; DNA; 2450 BP.
XX
AC
XX ADA71337;
XX

DT 20-NOV-2003 (first entry)
 XX Rice gene, SEQ ID 4650.
 DE Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 CS *Oryza sativa*.
 XX WO200300898-A1.
 XX PD 03-JAN-2003.
 XX PF 22-JUN-2001; 2001WO-IB001105.
 XX PR 22-JUN-2001; 2001WO-IB001105.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 4660; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 2450 BP; 556 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
 SQ
 Query Match 42.1%; Score 1162; DB 7; Length 2450;
 Best Local Similarity 68.1%; Pred. No. 2.6e-252;
 Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;
 16 CTGAACCGCAACGCGAGCATCCGGACCGCGTCGAGGACACCCCTCCACGCGCACCGCAAC 75
 28 CTGAGCCGCTCCACAGCGCTCAGGAGCGCATCGGCGACTCCCTCTCCGCCACCCCAAT 87
 76 GAGCTCGTGGCCCTCCTCTCCAGTACGTGAACAAGGGAAGGGGATCTCGAGCGGCAC 135
 88 GAGCTCGTGGCGGTCTTACCAGGCTGGTGTAACTCCGAAAGGGAATGCTTCAGGCCAC 147
 136 CACATCTCGAGCGCTCGAGG---TCCAGGCTCGGGGTCCGGCGCTCCCGAG 192
 148 CAGATCATGTCTGAGTACAACACCAATCTCTGAGGCTGATGTGTGAGAAAGCTGAAGGAC 207
 193 GGACCTCTCCGAGCTCCTCCGCTCCGCGAGGAGGCGATCGTCTCGCGCGCTCCGTG 252
 208 GGTGCTTTGAGGATGCTCTGAGGAGTGACAGAGGAGGATGTTATCTCCCATGGGTT 267
 253 GCATCGCGGTGCGCGCGCGCGGAGTTTGGAGTAGCTCCGCGGTCAACGTTCAACGAG 312
 268 GCGCTTGCCATCCGCGCGAGGCGCGGTGTCTGGAGTATGTGAGGCTCAATGTGAGCGAG 327
 313 CTCACGTCGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGGAGCTCTCGAC 372
 328 CTCGCTGTGAGTTGTCAGACATCCCGAGTACTTGCAGTCTCAAGGACAGCTTGTGAA 387
 373 GCGCAGCAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCCGCTTCAATGCTCAGTC 432

Db 388 GAAGGCAACCAACAACAACATTTGTGCTGAGCTGGATTTGAGCCATTCATGCTCTCTC 447
 QY 433 CCAAGCCCAAAATCGGTCAATCTATTGGAACGGGTGTCAGTTCCTCAACCGCACTTG 492
 Db 448 CTTGCTCTCTCTGTGGAAGTCCATTGGCAATGGTGTGCAAGTTCCTCAACGGCATCTG 507
 QY 493 TCTCTAATCATGTTCCGCAAGAGGATTCCTTGGAGCCCTGTTGATTTCTTCCCTGGC 552
 Db 508 TCATCGAAGCTCTTCCATGACAGAGGAGCATGTACCCACTGCTCAACTTCTCTGTCGA 567
 QY 553 CACCGCAACAGGGGCGATGTTATGATGCTTAATGATAGATATCAAAAGCTTGGGGAGGCTT 612
 Db 568 CACAACACTACAGGGCATGACCATGATGTTGAATGACAGAAATCCGCACTCTCAGTGTCTC 627
 QY 613 CAGTCTGTGCTGACCAAGAGCTGAGGAGCATTTGTCAAAGCTCCCTGCTGACACACATAC 672
 Db 628 CAAGGTGCTCTGAGGAAGGCTGAGGAGCATCTTTCTGTGCTTTTTCAGCAGACACCCCTAC 687
 QY 673 TCACATTTGCTTTATAAATTTCAAGAGTGGGCGCTGGCAAGAGGTTGGGGTGATACAGCA 732
 Db 688 TCAGAAATTCACACACAGGTTCCAGGAACCTTGGTCTGGAGAAGGGTGGGGTGACTGTGCC 747
 QY 733 GGACATGTTTTCGAAATGATCCATCTCTCTTAGACATCATTTCAAGCGCCAGACCCATCT 792
 Db 748 AAGCGTCCAGAGGAGCAATTCACCTCTCTTTGGACCTTCTTGGAGCCCTGATCCGTCC 807
 QY 793 ACCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTGTGTTGGTATCCCT 852
 Db 808 ACCCTCGAGAAGTCTCTTGGAAACAATCCCAATGGTGTTCATATGTTGTCATTTGTCCTCCA 867
 QY 853 CATGATCTTTGGTCAAGCTTAATGATATAGCTTGCACAGACACAGGAGGACAGATCGTC 912
 Db 868 CAGGTTACTTCGCGAAGCCCAATGTCTTGGTACCTTGACACTGAGGAGGAGGTTGTC 927
 QY 913 TATATACTGGACCAAGTCCGTGCACTAGAAATAGATGTTCTCCGTTTAAAGAAACAA 972
 Db 928 TACATTTGGACCAAGTCCGTGCTATGAGATGAGATGCTCTTGAAGATCAAGAGCAA 987
 QY 973 GGGCTGATGTTTCCCAAGATCTCATGTTTACCTGCGCTGATACAGATGCAAAAGGA 1032
 Db 988 GGTCTCAATATTACACACCGCATCTTATTGTCAACAGGTTGCTCCCTGATGCAACTGGC 1047
 QY 1033 ACATCATGCAATCAGGCGTTCGAGGATTTAGTGGACACAGCATCTTACATATTACGA 1092
 Db 1048 ACCACTCGGTCAGCGCTTGAGAAGGTCCTTGGCACCGAGGACACCCACATCTACCT 1107
 QY 1093 GTTCCCTTCAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATTTGATGTGTG 1152
 Db 1108 GTGCTTTCAAGACTGAAATGGAAATGTTCCGCAAGTGGATCTCACTTTTGAAGTCTG 1167
 QY 1153 CCAATATCGGAAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGCTGAATTAAGGT 1212
 Db 1168 CCGTACCTCGGAAACATTCACATGATGTCGCGCGCAAGAAATGCTGAGAGCTCCAGGCG 1227
 QY 1213 ACTCAGACTTCCATTAATGGAACTACAGTATGAAATCTTGTGCGCTCATTTGCTATCT 1272
 Db 1228 AATCTGATTTGATCATCGAAATCTACGTGACGGAACCTTTGTTGCTGCTTGTGCA 1287
 QY 1273 TACAAGATGGGAATTAACCAAGTGCACATTTGCTCATGCTCTGGAAGAAAGCTAAGTATCA 1332
 Db 1288 CACAAGATGGGTGTTCACCAATTTGACCATTTGCCATGCGCTTGAGAAACCAAGTACCC 1347
 QY 1333 GATTGACATATTTTGGAGAAATTTGATGAGAGTACCAATTTCTCTGCGGAGTTCAT 1392
 Db 1348 AACTCTGACCTCTACTCGAAGAGTTTGAGGATCACTCACTTCTCATGCGAGTTTCA 1407
 QY 1393 GCTGATATAATTTGCTATGAACAATGCTGATTTTATCATCACAGCACATACCAAGAAAT 1452
 Db 1408 ACTGACTTGTATGAGATGAAACCGCTGACTTCATCATCACAGTACCTTCCAGAGAT 1467
 QY 1453 GCTGGAAGCAAAATPACTTGTGGACAGTATGAGAGTCACTGCTTACTCTGCTGCT 1512

1468 GCCGAAACAGGACACTGTTGGTCAGTATGAGTCTCACATGGCATTACCAATGCTGGT 1527
 1513 CTGTACCGAGTTGTCATGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCCT 1572
 1528 CTGTACCGAGTTGTCATGGATCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCCT 1587
 1573 GGAGCTGACATGTCATATATCTTTCCATACACGAGAGGCAAGCGGACTCACCTCTCTT 1632
 1588 GGTGCGGACATGTCATCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
 1633 CATGGTTCAATCGAAATTTGATTTATGACCGGAGCAAAACGATGACACATTTGGGCAT 1692
 1648 CACCCAGAGATTGAGGAGTTGCTCTACAGCGAAGTTGACAAACAGGACACAGTTTATG 1707
 1693 CTGATGACCGGTCAGAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1752
 1708 CTGAAGGACAGGACAAAGCCCAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1767
 1753 ATACAGGGCTGTGTCGAGCTTTTGTAAAGTGCCTAAGCTGAGGAGCTGTGTAACCTTT 1812
 1768 TTGACTGCTGTGTTGAGCTGTATGTCGCAACCTCGCTGCAAGAGCTGGTAACTTT 1827
 1813 GTGCTGTTCCCGGTTCAATATGTCACAAAGTCCAAAGGACGAGAGATTCGCGAG 1872
 1828 GTGCTGTTCTGTGTCGACCA---TGGCAACCCATCTAAGGACAGGAGGAGCGCTGAG 1884
 1873 ATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
 1885 TTCAAGAGAGATGTTGACCTTTATGAGCAATATACAACTTGAATGGCCCATCCGCTGGATC 1944
 1933 TCTGCCAGACAAACAGGGCCCGTAAAGCGGAGCTCTATCGTACATCGCTGATPACCAT 1992
 1945 TCCGCGGAGATGACCGGTGTCGCAAGGTGAGCTCTACCGTACATCTCGGACACCAAG 2004
 1993 GGTGCTTTTCTGACGCGGCTTGTATGAAGCGTTCGCTCTACCGCTGCTGAGGCGCATG 2052
 2005 GGTGCTTTTGTGACGCGGCTTCTACAGGCAATTCGCTCTCACTGTTGTTGATCCATG 2064
 2053 ACTGTGGGCTTCTACTTCTCGGAGCGCTCCATGGAGTCCAGTGTGATCATAGACAT 2112
 2065 ACTGTGGGCTTCTCGGAGCTTCCGACATTCGCAACCGCTTATGGTGTCCAGTGTGATCATGTAAC 2124
 2113 GGGCTCTCGGCTTCCACATGACCGGCTTACCAACCGGAGCTGTTAATCTGATGGCC 2172
 2125 GGAGTGTCTGGCTTCCACATGACCGGCTTCCAGGAGTCCAGTGTGATCATAGACAT 2184
 2173 GACTTCTTCAACCGGTCGAGGAGGACCGGATCATCTGGTGTGATATATCTGGAGCAGGG 2232
 2185 GAGTTCTTTGAGAGTGCAGGAGGACCGGATCATCTGGAGGAGGAGTCTCGCAGGGCGGT 2244
 2233 CTGACGCGCATATACGAGAGTACATGAGATATATCTACAGAGGTTGATGACACTG 2292
 2245 CTGACGCTATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2304
 2293 GCGGGGCTTACGGTTCTTGAAGTACGTTCTGAAGCTCGAGAGGCTGAGAGGAGGAGGAG 2352
 2305 ACCGGGCTTACGGATCTTGAAGTACGTTCTGAAGCTCGAGAGGCTGAGAGGAGGAGGAG 2364
 2353 TACCTTGAGATGTTTACATATCTGAAGTTCGCGAGCTGCGGAGACCGGCTGCTTGA 2412
 2365 TACCTTGAGATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2424
 2413 ATTGACCAACCGGAGTAG 2430
 2425 GTGAGGGCGAGCCGTCG 2442

RESULT 10
 ADC08208
 ID ADC08208 standard; DNA; 2451 BP.
 XX
 AC
 XX

18-DEC-2003 (first entry)
 Rice DNA sequence Seq ID513 related to grain filling.
 plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 gene; ds; plant.
 Oryza sativa.
 WO2003000905-A2.
 03-JAN-2003.
 21-JUN-2002; 2002WO-IB002450.
 22-JUN-2001; 2001US-0300112P.
 26-SEP-2001; 2001US-0325277P.
 20-DEC-2001; 2001US-0342327P.
 (SYGN) SYNGENTA PARTICIPATIONS AG.
 Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 Glazebrook J, Katagiri F, Krepes J, Provart N, Ricke D;
 WPI; 2003-229341/22.
 P-PSDB; ADC08209.
 New plant genes encoding polypeptides having an activity involved in or
 associated with the synthesis, metabolism or degradation of carbohydrates
 in the plant grain useful in generating plants having improved
 nutritional properties.
 Claim 35; SEQ ID NO 513; 130pp; English.
 This invention, in the area of plant biotechnology, relates to novel
 polynucleotides comprising a nucleotide sequence encoding a protein which
 is involved in or associated with the synthesis, metabolism or
 degradation of carbohydrates in the plant grain and the expression of
 which is up-regulated during grain filling. The plant is selected from
 corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 sugarbeet, wheat, and rice. The invention may be useful for the
 improvement of protein, oil, starch, fibre and moisture content of the
 cereal grains. In addition, carbohydrate levels may be modified to a more
 desirable level using the present invention. The present sequence is a
 DNA sequence encoding a rice protein of the invention. Note: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/publishedpct_sequences.
 Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
 Query Match 42.1%; Score 1162; DB 9; Length 2451;
 Best Local Similarity 68.1%; Pred. No. 2.6e-252;
 Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;
 16 CTGAACCGCAACCGGAGCATCCGGGACCGGCTCGAGGACACCTCCACGCGCAGCGCAAC 75
 28 CTGAGCGGCTTCCACAGGCTCAGGAGCGGATCGGAGCTCTCTCTCGGCGCACCCCAAT 87
 76 GAGCTCGTCCGCTCTCTCTTCCAAAGTACGTGAACAAGGAGGAGGATCTCTGCGAGCGCAC 135
 88 GAGCTCGTCCGCTCTCTTCCAGGCTGTTTAACTCTGGAAGGAGGATGCTTCAGGCGCAC 147
 136 CACATCTTCCGAGCGCTCGACGAGG---TCCAGGGCTCCGGGCTCGCGGCTCGCGGAG 192
 148 CAGATCAATGCTGAGTACCAACACGCAATCTCTGAGGCTGATCTGTGAGAGCTGAAGGAC 207
 193 GGACCTTCTCTCGAGCTCTCTCGCTCCGGGACGAGGAGGAGGATCTGTGCGCGCTTCGTG 252
 208 GGTGCTTTGAGGATGCTCTGAGGAGTGCACAGAGGAGGATGTTATCTCCCATGGGTT 267

QY 253 GCCATGCGGTGCGCGCGCGCGCGGTCTTGGAGTAGCTCCGCGTCAAGCTTCAAGAG 312
Db 268 GCGCTTGCCATCCGCGCGCGCGCGCGGTGCTGGAGTAGTGGAGGTCAATGTGACGAG 327
QY 313 CTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTCTGTCAAC 372
Db 328 CTCGCTGTGAGTTGCTGACAGTCCCGAGTACTTGCAGTTCAGGACAGCTCTGGAA 387
QY 373 GGCAGCAGCAATGATCCCTACGCTCTCGAGCTTGATCTTCGAGCGGTTCAATGCTCAGTTC 432
Db 388 GAAGCAGCAACAAACAACTTTGTGCTGAGCTGGATTTCCAGGCCATTCAATGCCCTCTTC 447
QY 433 CCAGCCCAAAATCGGTCACTCATCTATGGAACGCTGTGCACTTCTCAACCGACGACTTG 492
Db 448 CTTGCTCTTCTGCTGAGTTCATGTCRAATGTCRAATGTCRAATGTCRAATGTCRAATGTC 507
QY 493 TCTCAATCATGTTCCGCAACAGGATGCTTGGAGCCCTCTTGGATTTCTCCGTGTC 552
Db 508 TCAATCGAAGCTCTTCCATGACAAGGAGAGCATGTACCCCACTGCTCAACTTCTCTGTCGA 567
QY 553 CACCGGCAACAGGGGCACTGTATGATGCTTATGATGATGATGATGATGATGATGATGATG 612
Db 568 CACAATCAAGGGGCAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATG 627
QY 613 CAGTCTGTGCTGACCAAGCTGAGGAGCACTGTGCAAGCTCCCTGCTGACACACCATAC 672
Db 628 CAAGGTCTCTGAGGAAGCTGAGGAGCACTTCTGCTCTTTCAGCAGACACCCCTTAC 687
QY 732 TCACAAATGCTTAAATTTCAAGATGCGGCTGAGAGAAAGTTGGGGTGATACAGCA 732
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QY 793 GGACATGTTTGGAAATGATCATCTCTCTCTAGACNTCAATTCAGCGCGCCAGACCATCT 792
Db 748 AAGCGTCTCCAGGAGACCATTCACCTCTCTTTGGACCTTCTTGGGCGCCCTGATCCGTC 807
QY 793 ACCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTGTTGTTGTTATCCCT 852
Db 808 ACCCTAGAGAGTCTTGGACAAATCCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 867
QY 853 CATGATATCTTTGGTCAAGCTAATGATTTAGCTTTGCCAGACACAGGAGGACAGATCGTC 912
Db 868 CACGTTTACTTCGCGCAAGCCAAATGCTTTGGGTTACCTGTGACACTGGAGGGCAGGTTGTC 927
QY 913 TATATCTGGAACCAAGTCCGTGCACTAGAAATGAGTGGTTCTCGGTTTAAAGAAACAA 972
Db 928 TACATTTTGGACCAAGTCCGTGCTATGAGAAATGAGTGCCTTCTGAGGATCAAGCAGCAA 987
QY 973 GGGCTTGATGTTTCCCAAGATTTCTCATTTGTTTACTTGGCTGATACCAAGATGCAAAAGGA 1032
Db 988 GGTCTCAATATTACACCGCATCTTATTTGTCACCAAGTTGCTCTCCCTGATCGACTGGC 1047
QY 1033 ACATCATGCAATCAGCGGTTGAGAGAAATAGTGGAAACAGACATCTTACATATTACGA 1092
Db 1048 ACCACTCGCGTCAAGCTCTTGGAGAGGTCCTTGGCAGCGAGACACACCACTCTACGT 1107
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Db 1108 GTGCTTTTCAGAAATGAAATGGTTCGCAAGTGGATCTCAGCTTTTGAAGTCTGG 1167
QY 1153 CCATATCTGAAACATTTGCTGAGGATGCTGCTGTGAAATTTGCTGTGAAATTTACAAAGT 1212
Db 1168 CGGTACCTTGAACATCTCACTGATGATGTCGCGACGAAATTTGCTGGAGAGCTCCAGGCC 1227
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Db 1228 AATCTGACTTTCATCTCGAAATCTACAGTGAAGGAACTTTGTTGCACTCTTGTCTGCA 1287
QY 1273 TACAAGATGGGAATTAACAGTGCACATTTGCTCATGCTCTCGGAAGAGCTAAGTATCA 1332
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QY 1333 GATTCAGACATATTTTGGAGAAATTCGATGAGAGTACCAATTTCTCTCGCAAGTTCACT 1392
Db 1348 AACTCTGACCTCTACTTGGAAAGATTGGAGTACTACCACTTCTCTATGCCAGTTACA 1407
QY 1393 GCTGATATAAATTTGCTATGAACAATGCTGATTTTATCATCACCGACACATACCAAGAAAT 1452
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QY 1453 GCTGAAAGCAAAATATCTGTTGGAAGATGATGAGTCACTATGCGCTTTACTCTGCTCTGCT 1512
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Db 1708 CTGAGGACAGGAACAGGCCAATCATCTTCCATGCTCTGCTTACCGGTGTCAGAAC 1767
QY 1753 ATAAACAGGCTGCTGGAAGCTTTTGTAACTGCTGCTTAACTGAGGAGCTGCTGTAACCTT 1812
Db 1768 TTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1827
QY 1813 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1872
Db 1828 GTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884
QY 1873 ATAGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
Db 1885 TTCAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1944
QY 1933 TCTGCCAGCAAAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1992
Db 1945 TCCGCGCAGATGAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2004
QY 1993 GGTGCTTCTGCTACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2052
Db 2005 GGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2064
QY 2053 ACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2112
Db 2065 ACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124
QY 2113 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2172
Db 2125 GAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2184
QY 2173 GACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2232
Db 2185 GAGTCTTCTGAGAGTTCAG 2244
QY 2233 CTGACGCGCATATACAGAAAGTACATCGGAAGATATATCTCAGAGAGGTTGATGACATG 2292
Db 2245 CTTCAAGCTATCGAG 2304
QY 2293 GCGCGGCTTACGGTCTGAGAGTACGTTGCTGAGAGTCCGAGAGAGAGAGAGAGAGAGAG 2352
Db 2305 ACCGCGCTTACGGATCTTGGAGTACGTTCTGAAACCTGAGAGAGAGAGAGAGAGAGAG 2364
QY 2353 TACCTTGTGATGCTTCTACATATCTGAAGTTTCGCGAGAGTGGGGAAGACCTGCGCTTGA 2412
Db 2365 TACCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424
QY 2413 ATTGACCAACCGCAGTAG 2430

Db 2425 GTCAGGGCGAGCGTGC 2442

RESULT 11
ADCC7855
ID ADC07855 standard; DNA; 2451 BP.
XX AC ADC07855;
XX DT 18-DEC-2003 (first entry)
DE DE Rice DNA sequence Seq ID:21 related to grain filling.
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.
XX Oryza sativa.
XX OS
XX PN WO200300905-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002WO-IB002450.
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0325277P.
XX 20-DEC-2001; 2001US-0342327P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX WPI; 2001-229341/22.
XX P-PSDB; ADC07856.
XX New plant genes encoding polypeptides having an activity involved in or
XX associated with the synthesis, metabolism or degradation of carbohydrates
XX in the plant grain useful in generating plants having improved
XX nutritional properties.
XX Claim 2; SEQ ID NO 121; 130pp; English.
XX This invention, in the area of plant biotechnology, relates to novel
XX polynucleotides comprising a nucleotide sequence encoding a protein which
XX is involved in or associated with the synthesis, metabolism or
XX degradation of carbohydrates in the plant grain and the expression of
XX which is up-regulated during grain filling. The plant is selected from
XX corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
XX sugarbeet, wheat, and rice. The invention may be useful for the
XX improvement of protein, oil, starch, fibre and moisture content of the
XX cereal grains. In addition, carbohydrate levels may be modified to a more
XX desirable level using the present invention. The present sequence is a
XX DNA sequence encoding a rice protein of the invention. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/publishedpct_sequences.
XX Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
Query Match 42.1%; Score 1162; DB 9; Length 2451;
Best Local Similarity 68.1%; Pred. No. 2.6e-252;
Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;
QY 26 CTGAACCGCAACCGGACATCCGGGACCGGTGAGGACACCCCTCCACGGCGACCGCAAC 75
Db 28 CTGAGCGCGCTCCACAGGCTCAGAGGCGGACCTCCCTCTCCGCGCCACCCCAAT 87
QY 76 GAGCTCGTGGCCCTCTCTCCAGTAGTACGTGAACAGGGGAGGGGATCCTTGACGGCGCAC 135

Db 88 GAGCTCGTGGCCGCTTTACACAGGCTGGTTAACTCGGAAAGGGAATGCTTCAGGCGCCAC 147
QY 136 CACATCTCGACGGCTCGACAGG---TCAGGGGCTCCGGGGTCCGGCGCTCCGCCGAG 192
Db 148 CAGATCAATGCTGAGTACAAACACGCAATCTCTGAGGCTGATCGTGAGAGCTGAAGGAC 207
QY 193 GGACCCCTTCCTGACGCTCTCCGCTCCGGCGAGGAGGATCGTCTCGCGCGCTGCTG 252
Db 208 GGTGCTTTTGAGGATGCTCTGAGGAGTGCAAGAGGGGATGTTATCTCCCATGSGT 267
QY 253 GCCATCGGGTGGCGCGCGCGGGAGTTTGGGAGTAGCTCCGCTCAAGCTTCAAGG 312
Db 268 GCCCTTCGCAATCCGCCCGAGGCCCGGTGCTGGGAGTATGAGGGTCAATGAGAGG 327
QY 313 CTGACGCTCGACGAGCTCAGAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTGAC 372
Db 328 CTGCTGTTGAGTTGCTGACAGTCCCGGAGTACTTGCAGTTTCAAGGACACGCTTGTGAA 387
QY 373 GGCCAGCACAATGATCCCTAGTCTCGAGTTCGAGCTTCGAGCCGTTCAATGTCTCAGTC 432
Db 388 GAAGGCAACCAACCAACTTTGTGCTTGAGCTGATTCGAGCCATTCATGCTCTCTTC 447
QY 433 CCAGCGCCAAATCGGTCTCATCTATTGGAAACGGTGTGACAGTTCCTCAACCGACACTFG 492
Db 448 CTTGCTCTCTCTGTCGAAGTCCATTTGGCAATGCTGTGTCAGTTCCTCAACAGGATCTG 507
QY 493 TCCTCAATCATGTTCCGCAACAGGGATTTGCTTGAGGCCCTGTGTTGGATTTCTCTCGTGGC 552
Db 508 TCATCGAAGCTCTTCCATGACAAGGAGGAGCATGTACCCACTGCTCAACTTCTCTGTCGA 567
QY 553 CACGGGCAACAGGGGATGTTATGATGCTTAACTATGATAACAAGTTGGGAGGCTT 612
Db 568 CACAACTTACAAGGGCATGACCATGATGTTGAATGACAGAAATCCGAGTCTCAGTGTCTC 627
QY 613 CAGTCTGCTGACCAAGCTGAGGAGCACTTGTCAAAAGCTCCCTGCTGACACACCATAC 672
Db 628 CAAGGTGCTCTGAGGAGGCTGAGGAGCACTTCTGCTCTTTCAGCAGACACCCCTTAC 687
QY 673 TCACAATTTGCTTATAAAATTTCAAGAGTGGGGCTGGAGAAAGTTGGGGTGTATACAGA 732
Db 688 TCAGAAATTCACACACAGGTTCCAGGAACTTGGTCTGAGAGAGGGTTGGGGTGACTGCGC 747
QY 733 GGACATGTTTTGGAATGATCCATCTCTCTTAGACATCATTCAGGCGCCAGACCATCT 792
Db 748 AAGCGTTCCAGGAGACCATTCACCTCTTTTGAACCTTCTTGAGGCCCTGATCCGCTCC 807
QY 793 ACCTTAGAATAATTTCTGGGAGGATCCCATGATTTTAACTGTTGTGTGTTATCCCT 852
Db 808 ACCTCGAGAGTCTCTTGAAACAAATCCAAATGTTTCAATGTTGTCATATGTCCTCCA 867
QY 853 CATGGATCTTTGGTCAAGCTAATGATAGGCTTGCAGACACAGGAGGACATCGTC 912
Db 868 CAGGTTACTTCGCGCAAGCAATGTCTGGGTTACCTGCACACTGAGGAGGAGTTGTC 927
QY 913 TATATCTGACCAAGTCCCGTGCACATGAAATGAGATGCTTCCGTTTAAAGAAACAA 972
Db 928 TACATTTTGACCAAGTCCGCTGATGAGAGATGAGATGCTTCTGAGGATCAAGACCAA 987
QY 973 GGGCTTGATGTTTCCCAAGATTTCTATGTTTACTCGGCTGATCCAGATGCAAAAAGGA 1032
Db 988 GGTCTCAATATACACACGATCTTATTTGTCACCAAGTTGCTCTCTGATGCACTGGC 1047
QY 1033 ACATCATGCAATCAGCGGCTTGAGAAATPAGTGGAAACACAGCATATCTTACATATACGA 1092
Db 1048 ACCACCTCGGCTCAGCGCTCTTGAGAGGTCCTTTGGCACCGACACACCCACATCTACGT 1107
QY 1093 GTTCCCTTTCGAATGAAATGGATACTTAAGAAATGGATATCAGATTTGATGCTGG 1152
Db 1108 GTGCTCTTCAGAACTGAAATGGAAATGTTTTCGAAAGTGGATCTCACTGTTTGAAGTCTGG 1167
QY 1153 CCATATCTGGAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGTAATTAACAAGGT 1212

Db 1168 CCGTACCTCGAAACATTCACTGATGATGTCGCGCACGAAATTCCTGGAGAGCTCCAGGCC 1227
Qy 1213 ACTCAGACTTCATTAATTCGGAACCTACAGTGTATGGAATCTTGTGGCGTCACTGCTATCT 1272
Db 1228 AATCTGACTTGTATCATCGAACTACAGTGTATGGAATCTTGTGGCGTCACTGCTATCT 1287
Qy 1273 TACAAGATGGGAATACCCAGTGCACATTTGCTCATGCTCTGGAAGAGCTAAGTATCCA 1332
Db 1288 CACAAGATGGGTATACCCATTTGATCATTTGCCATGCGCTGGAAGAACCAAGTACCCC 1347
Qy 1333 GATTACAGACATATTTGGAAGATTTTCGATGAGAGTACCATTTCTCTGCCAGTTCACT 1392
Db 1348 AACTCTGACTCTACTGGAAGAGTTTGAGGATCACTACCACTTCTCATGCGAGTTTACA 1407
Qy 1393 GCTGATATTAATTCGATGACACATCTGATTTTATCATCACAGCACATACCAAGAAAT 1452
Db 1408 ACTGACTTCAATTCGATGACCAAGTGTGCTTATCATCATCACCAGTACCTTCCAAAGAT 1467
Qy 1453 GTTGAAGCAGAAATCTGTTGACACATGAGTCACTACCTTTACTCTGCTGCTGCT 1512
Db 1468 GCGGNAACAAGACACATGTTGTCAGTATGATCTCATATGSCATTCACATGCTGCTG 1527
Qy 1513 CTGTACCGAGTGTCTCATGGAATGATGCTTCGATCCAAAGTTCAATATAGTCTCTCT 1572
Db 1528 CTGTACCGTGTGTCTCACGATATGATGTTTGTACCCGAAAGTTTAACTGTTCTCGCT 1587
Qy 1573 GGAGCTGACATGCTCATATATCTTTCACATACCGAAGGCCAAGCAGTCACTCTCTT 1632
Db 1588 GGTGCGACATGCTCACTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
Qy 1633 CATGTTTCAATCGAAATTTGATTTATGATCCCGGAGCAAAACGATCAACACATGGGCAT 1692
Db 1648 CACCAGAGATTGAGAGTTGCTCTACAGCAAGTTGACAAACAGGACACATTTATG 1707
Qy 1693 CTGTATGACCGGTCAAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1752
Db 1708 CTGAAGCAGGAAACAAGCCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1767
Qy 1753 ATAAACAGGCTGTGCAAGCTTTTGTAGTCTGAGTCTGAGTCTGAGGAGCTGTTAAACCT 1812
Db 1768 TTGACTGTGCTGTGAGCTGTATGTCGCAACCTCTGCTGCAAGAGCTGTGTTAACCT 1827
Qy 1813 GTCTGTGTCGCGGTACATGATGTCAACAGTCCAAAGCAGCAGGAGAGATCGGGAG 1872
Db 1828 GTGTTGTCTGTGTGACCA--TGGCAACCCATCTAAGACACAGGAGGAGCTGAG 1884
Qy 1873 ATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
Db 1885 TCAAGAGATGTTGACCTTATGAGCAATACAACTTGAATGGCCACATCCGCTGGATC 1944
Qy 1933 TCTGCCACAGCAAAAGGCGCCGTACAGGAGCTCTATCGCTACATCGCTGATACCCAT 1992
Db 1945 TCGCGCAGATGAACCGTGTCCGCAACGTTGAGTCTCTACCGTTACATCTGCAACCAAG 2004
Qy 1993 GGTCCTTTCTGATCAGCGCGCTTGTATGAGCTTCTGCTCTCACCGTCTGTGAGGCCATG 2052
Db 2005 GGTCCTTTCTGAGCGCGCTTCTACAGGCGCTTCTGCTCTCTCTCTCTCTCTCTCTCT 2064
Qy 2053 ACTGTGGCTCTCTACTTTGCGGAGCTGCTCATGAGGCTTCTGAGTATGATGATGATG 2112
Db 2065 ACTGTGGCTCTCTGAGATTTGCAACCGGCTATGTTGTTGTTGTTGTTGTTGTTGTTG 2124
Qy 2113 GGCGTCTCGGGCTTCCCATTTGACCGCTACCCAGGAGCTGTTAATCTGATGGCC 2172
Db 2125 GAGTGTCTGGCTTCCATTTGACCTATACCGAGGTGCAAGGCGCTCTGGCGCTGCTGTT 2184
Qy 2173 GACTTCTTCCAGCGTTCAGCAAGCAAGCCAGATCACTGGGTGATATATCTGAGCAGGG 2232
Db 2185 GAGTCTTTGAGAGTGGCAGGAGAGCCAGCCACTGGACCAAGATCTCGAGGCGGT 2244
Qy 2233 CTGACGCGCATATACAGAGATGACATGATGAGAGATATCTCAGAGAGTTGATGACACTG 2292
Db 2245 CTTACGCTGATCGAGAGAAATACACTGGAAGCTCTACTCTGAGAGGCTGATGACCTC 2304

Qy 2293 GCGGGCTCTACGGTTTCTGGAAGTACGTGTGAGAGCTGAGAGGCTGAGAGCGGC 2352
Db 2305 ACCGGCTCTACGGATTTCTGGAAGTACGTGTGAGAGCTGAGAGGCTGGAACCCGCGC 2364
Qy 2353 TACTTGAATGTTCTACATACCTGGAAGTTCGCGAGCTGCGAGAGCCGTGCGCTTGA 2412
Db 2365 TACTTGAATGTTCTGATGCTTGAAGTTCGCGAGCTGCGAGAGCCGTGCGCTTGA 2424
Qy 2413 ATTGACCAACCGCAGTAG 2430
Db 2425 GTGAGGCGGAGCGCTCG 2442
RESULT 12
ADC68521
ID ADC68521 standard; cDNA; 2754 BP.
XX
AC ADC68521;
XX
DT 18-DEC-2003 (first entry)
XX
S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:13.
XX
Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
KW biosynthetic pathway; plant; gene; ss.
XX
Schedonorus arundinaceus.
XX
W02003040306-A2.
XX
15-MAY-2003.
XX
07-NOV-2002; 2002WO-NZ000239.
PF
07-NOV-2001; 2001US-0337703P.
PR
(GENE-) GENESIS RES & DEV CORP LTD.
(WEIG-) WRIGHTSON SEEDS LTD.
PA
Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;
PI Saulsbury KM, Hall C;
XX
WPI: 2003-441544/41.
DR
P-PSDB; ADC68365.
XX
New polynucleotide encoding polypeptides from Lolium perenne or Festuca
arundinacea, useful for modulating the biosynthesis of lignin, fructan or
tannin in a plant.
XX
Claim 1; SEQ ID NO 13; 240pp; English.
XX
The present invention describes isolated polynucleotides (I) encoding
proteins (II) from Lolium perenne and Festuca arundinacea which are
active in lignin, fructan and tannin biosynthetic pathways. Also
described: (1) an isolated oligonucleotide probe or primer comprising at
least 10 contiguous residues complementary to 10 contiguous residues of
(I); (2) a kit comprising the oligonucleotide probe or primer; (3) a
genetic construct comprising (I); (4) a transgenic plant cell comprising
the genetic construct of (3); (5) a plant or its seed, fruit or progeny
comprising the transgenic plant cell of (4); (6) modulating one or more
of the lignin, fructan or tannin compositions of a plant; (7) producing a
plant having one or more of the lignin, fructan or tannin compositions;
and (8) modifying the activity of (II) involved in a lignin, fructan or
tannin biosynthetic pathway in a plant. (I) can be used for modulating
the biosynthesis of lignin, fructan or tannin in a plant. The present
sequence is used in the exemplification of the present invention.
XX
SQ Sequence 2754 BP; 652 A; 685 C; 684 G; 733 T; 0 U; 0 Other;

Query Match 41.2%; Score 1135.6; DB 9; Length 2754;
Best Local Similarity 67.5%; Pred. NO. 2.5e-246;
Matches 1629; Conservative 0; Mismatches 774; Indels 9; Gaps 2;

QY 7 GCGCCGAGAGTGAACCGCAACGCGAGCATCCCGGATCCGCGAGACACCCCTCCACGCG 66
Db 116 GGTGCGAAGCTGACTGCTCTCCACAGTCTCCGCGAGCGCTTGGTGCACCTTCTCCTCC 175
QY 67 CACCGCAAGAGCTGCTGCGCCCTCTCTCCAGTACGTGAACAGAGAGGCGCATCCCTG 126
Db 176 CATCCCAAGAGCTCAATGCGCTCTCTTCCAGTATGTTCCAGGCGCAAGAGATGCTT 235
QY 127 CAGCGCCACACATCTCTCGAGCGCTCGAGAGGTCCAGGGCTCCGCGGCTCCGCGCTC 186
Db 236 CAGCGCCACAGCTGCTCACTGAGTTCGAAGCATGTTTGGAGTCTG-----ACAAGGAG 289
QY 187 GCGAGGAGCCCTCTCTCGAGCTCTCCGCTCCGCGAGAGGCGATGCTGCTCGCGCG 246
Db 290 AGGTATGCACTTTTCAAGACATCTCCGCTGCTCCGCGAGGAGCAATTTGCTCTCCGCCA 349
QY 247 TTGCTGCGCCATCCGCTGCGCGCGCGCGCGAGTTCGGAGTACGTCGCGCTCAAGTT 306
Db 350 TGGGTTGCACTTGCCATCAGGCCAGCGCTGCTCTGGAGCTACATAGGGTGAATGTT 409
QY 307 CAGGAGCTCAGCGTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAGAGGAGGCTT 366
Db 410 AGCGAGTTGGCGCTTCAGGAGCTTCAAGTCTCCGAGTACCTAGCATTCAGAGAGGAGCTT 469
QY 367 GTCGAGCGCCAGCACATGATCCCTAGCTTCTCGAGCTTGACTTCGAGCGCTCAATGTC 426
Db 470 GTTGATGAGCAGCGCCAGAGAGTTCGCTGAGCTTGATTTGAGCGCTTCAATGCC 529
QY 427 TCAGTCCCGCCAGCGCAATCGGTCTCATCTATGTAAGAAACGGTGTGAGTTCCTCAACCGA 486
Db 530 TCGTTCCCGAGCTTCCATGTCAGTCCATGTAAGAAAGGGGTGAGTTCCTTAACCGT 589
QY 487 CACTGTGCTCAATCATGTTCCGCAACAGGAGTGTCTGGAGCGCCCTGTTGGAATTCCTC 546
Db 590 CACCTGTCTTCAAGCTGTTCCAGGACAGAGAGGAGCTCTACCCACTACTGAACTTCCCTG 649
QY 547 CGTGGCCCGGCGACAGGCGCATGTTATGCTTTATGATAGATACAAAGCTTGGGG 606
Db 650 AAGGCCCATAAACCAAGGCGCAGCAATGATGCTAAAGCAGAGATACGAGCTTCGT 709
QY 607 AGGCTTCAGTGTGTGTCACCAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACA 666
Db 710 GGGCTCCATCAGCCCTTAGAAGGCGAGAGAGTATCTAACAGCATCTTGAAGACACC 769
QY 667 CCATACACAAATTTGCTTATAAATTCAGAGTGGGGCTCGAGAAAGGTTGGGTGAT 726
Db 770 CCGTCTTTGAGTTCAACACAGGTTCCAAGAGCTTGGCTTGGAGAAAGGTTGGGGTGAC 829
QY 727 ACAGCAGGACATGTTTGGAAATGATCCATCTCTCTAGACATCACTCAGGCGCCAGAC 786
Db 830 ACCGTAGCGGTGTACAGGACACCATCCACTCTCTCTGATCTGCTTGAAGCCCTGAT 889
QY 787 CCATCTACCTTAGAGAAATTTCTTGGGAGGATCCCATGATTTTAAACGTTGTTGTGTA 846
Db 890 CCAGCCAGCTTCGAGAAGTTCTTGGAACTATACCGTGAATGTTCAATGCTGTTATCCTG 949
QY 847 TCCCTCATGAGTACTTTGGTCAAGCTAATGATATAGGCTTGCAGACACAGAGAGACAG 906
Db 950 TCTCCACAGGATATTTTCTCAATGTTGGGATACCCCTGATACCGTTCAGGCGGCCAG 1009
QY 907 ATCGTCTATATCTGACCAAGTCCGTGCACTAGAAATGAGATGCTTCCGTTTAAG 966
Db 1010 GTTGTGATCATTTGGATCAGTCCCGTCTTGGAGATGAGATGCTTCTGAGATTAAG 1069
QY 967 AAACAGGCGCTGATGTTTCCCAAGATTTCTCATTTGTTACTCGGCTGATACAGATGCA 1026
Db 1370 CAGCAAGGCTTGACATAACCCCTAAGATCCCTCATTTGACCAAGGTTGTTGCTGATGCT 1129
QY 1327 AAAGGAACATCTGCAATCAGCGGCTTGAGAGAAATTAGTGGAAACACAGCATACTTACATA 1086
Db 1130 GTTGAACACTACATGTGGCCAGCGGCTGGAGAGGTTATTGGGACTGAGCACACTGACATT 1189

QY 1087 TTACGAGTTCCTTTCAGAAATGAAATGGGATCTTAAAGAAATCGATATCAAGATTTGAT 1146
Db 1190 CTTCTGTTTCCATTCAGAACTGAAAGGGATCTCCGTAAGTGATATCTCGTTTIGAT 1249
QY 1147 GTS'GGCCATATCTGGAACATTTGCTGAGGATGCTGCTGGTGAATTCGCTGCTGANTTA 1206
Db 1250 GTCTGGCCATCTCTGGAGACATACCGGAGATGTTGCAACGAACTCATGAGAGAAATG 1309
QY 1207 CAAAGTACTCCAGACTTTCATAATTTGAAATCTACAGTATGAAATCTTGTGCGGCTCATTTG 1266
Db 1310 CAGACCAAGCCTGATCTCTATTATTGGCACTACAGTGAOGTAACTTGTGCGCACCTG 1369
QY 1267 CTATCTTACAGATGGGAATACCCAGTGAACATTTGCTCATGCTCTGGAAGAGCTTAAG 1326
Db 1370 CTCGCGCATTAAGTTGGAGTTTACCAGTGCATATTGCCCCATGCTTTGGAGAAACCAAA 1429
QY 1327 TATCCAGACTCAGACATATTTTGAAGAAATTTGATGAGAGTACCAATTTCTCTGCGCAG 1386
Db 1430 TACCCCACTCAGACATATATTGGAACAAATTCAGAGCCAAATACCAATTTCTCATGCCAG 1489
QY 1387 TTCACTGCTGATATAATGCTATGAACAAATGCTGATTTTATCATCACAGCACATACCAA 1446
Db 1490 TTCCTGCTGACCTTATTGCAATGATCACTGATTTTATCATCACAGCACATTCAG 1549
QY 1447 GAAATGCTGGAAGCAAAATACTGTTGGAAGTATGAGAGTCTACTGCTTTACTCTG 1506
Db 1550 GAAATGCTGGAAGCAAGGACAGCGTGGGCCAGTATGAGTCTTCACATTTGCTTCCACCTC 1609
QY 1507 CTTGCTGTACCGAGTTGTCATGGATCGATGCTTCTGATCCAAAGTTCAATATATAGTC 1566
Db 1610 CTTGATCTCTACCGTGTGTCATGGATGAGTGTGATGCTTCCCAAGTTCAACATTTGTC 1659
QY 1567 TCTCTGAGCTGACATGTCATATATCTTTCCACATACCGAGAGGCCAAGGAGCTCACCC 1626
Db 1670 TCTCTGAGCAGATATGAGGCTTCTACTTCCCATACACTGAACTGAACTGAGAGGCTTACT 1729
QY 1627 TCTCTTATGTTCAATCGAAATTTGATTTATGATCCCGAGGCAAGAGTGAACACAT 1686
Db 1730 GCCTTCCACCTGAAATGGAAGAGCTCTTTTACAGCGATGTTGAGAACTCTGAAACAAAG 1789
QY 1687 GGGCACTGTGATGACCGCTCAAGCCCATCTCTTCTCCATGCGCAAGCTCGACAGGCTG 1746
Db 1790 TTTGATTTAGAGCAAGAAACAGCCGATCATTTCTCAATGGCTCGCTTGAACCGTGTG 1849
QY 1747 AAGAACATAACAGGGCTGTGTCGAGCTTTTGTAGTGCCTAAGCTGAGGAGCTGCTA 1806
Db 1850 AAGAACATACAGGCTTGGTTGAGATGTTCCGTAAGAAATGCTCATCTGAAGGATTTGGCA 1909
QY 1807 AACCTTGTGCTGCTGCGGTGATGATGATGTCAAACAGTCCAGGACAGGAGAGATC 1866
Db 1910 AACCTTGTGATTTGCTGCTGCTGAC---ATGGCAAGAGTCCAGGATAGGGAGGAGCAG 1966
QY 1867 GCGAGATAGAGAGATGATGAATCACTCAAGACCCACAACTTGTTCGGGCGAGTTCCGC 1926
Db 1967 GCTGAGTTCAAAGAGATGATGATCTCTTATGAGGATGACAGCTGAAGGCGCATATCCGG 2026
QY 1927 TGAATCTTCCCGAGCAACAGGCGCCGTAACGCGAGCTCTATCGCTACATCGCTGAT 1986
Db 2027 TGAATCTCAGCTCAGATGAACCGTGTTCGCAATGCGAGTGTACCGCTACATCTGTGAC 2086
QY 1987 ACCATGCTGCTTCTGATCAGCGGCTTCTATGAAGCGTTCCGCTCTCACCGCTGTGAG 2046
Db 2087 ACCAGGCGCATTTGCTCAGCCCGGCTTCTATGAAGCATTTGGCCCTGACTGTTATCGAG 2146
QY 2047 GCCATGACCTTGGGCTTCTCTACTTTTCGGGACCGCTCCATGAGGCTCCAGCTGAGATCATA 2106
Db 2147 GCCATGACATGTTGTTTCGGCAATAGCGACATGCAATGCTGGCCAGCTGAAATCAT 2206
QY 2107 GAGCATGCGGCTCTCGGCTTCCATGACCCGCTACCAACCCGAAACAGGCTGTTAATCTG 2166
Db 2207 GTGGATGCTGCTGCTGTTTGCATCGATCCCTTACCAAGTGAAGGCTGCGAGATATC 2266
QY 2167 ATGGCCGACTTCTTTCGACCGGTCGAAGCAAGCCAGATCACTGGGTGAATATATCTGGA 2226

Db 2267 CTGGTCACTCTCTTGGAGAAATCCAGCGGGATCCAACTCTGGGACAAATGTCGGA 2326
 Qy 2227 GCAGGGCTCAGCGCATATACAGAGAGTACATGAGAAATATCTACAGAGAGTTGATG 2286
 Db 2327 GAGGSCCTGAAGAGAAATTTATGAGAGATACACCTGGAAGCTGTACTTCAGAGAGGCTGATG 2386
 Qy 2287 ACACGTGGCGGGGCTCTACGCTTCTGGAAGTAGCTCTGAAGCTCGAGAGGCTGGAGAG 2346
 Db 2387 ACCCTGACTGGTGATATATGTTCTGGAAGTAGCTGAGCAACCTTGAGAGGCTGAGACT 2446
 Qy 2347 AGGCGCTACCTTTGAGATGTTCTACATCTACTGAAGTTCCGCGAGCTGCGAAGACCGTGCG 2406
 Db 2447 CGCGGTACCTTTGAGATGTTCTACATCTACTGAAGTTCCGCGAGCTGCGAAGTCTGCA 2506
 Qy 2407 CTTCGAAATGAC 2418
 Db 2507 TTGGCTGTCGAC 2518

RESULT 13

ID ABK98516 standard; cDNA; 2829 BP.

XX AC ABK98516;

XX DT 21-OCT-2002 (first entry)

XX DE cDNA sequence encoding perennial ryegrass sucrose synthase.

XX KW Perennial ryegrass; sucrose phosphate synthase; SPS; invertase; INV;
 KW sucrose synthase; SS; sucrose:sucrose 1-fructosyltransferase; SST;
 KW sucrose transporter; ST; fructan:fructan 1-fructosyltransferase; FFT;
 KW sucrose:fructan 6-fructosyltransferase; soluble carbohydrate transport;
 KW SST; soluble carbohydrate metabolism; plant; gene; ss.

XX OS Lolium perenne.

XX PN WO200231130-A1.

XX PD 18-APR-2002.

XX PF 10-OCT-2001; 2001WO-AU001275.

XX PR 10-OCT-2000; 2000AU-00000673.

XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX PI (AGRE-) AGRESEARCH LTD.

XX PS Spargenberg G, Sawbridge Tl, Ong EK, Emmerling M;

XX DR WPI; 2002-444177/47.

XX DR P-PSDB; ABG69063.

XX PT New enzymes and transporter proteins involved in metabolism and/or
 PT transport of soluble carbohydrates, useful as molecular genetic markers,
 PT and in modifying soluble carbohydrate metabolism and/or transport in
 plants.

XX PS Claim 5; Fig 74; 177pp; English.

XX CC The present invention relates to the isolation of polynucleotide
 CC sequences encoding perennial ryegrass enzymes or transporter proteins
 CC selected from sucrose phosphate synthase (SPS), invertase (INV), sucrose
 CC synthase (SS), sucrose transporter (ST), sucrose:sucrose 1-
 CC fructosyltransferase (SST), fructan:fructan 1-fructosyltransferase (FFT),
 CC and sucrose:fructan 6-fructosyltransferase (SST). The nucleic acid
 CC sequences of the invention are useful as molecular genetic markers, to
 CC isolate cDNAs and genes encoding homologous proteins from the same or
 CC other plant species, and for the modification of soluble carbohydrate
 CC metabolism and/or transport in plants. The polypeptide sequences may be
 CC used to immunise animals to produce antibodies with specificity for the
 CC proteins, and these antibodies may then be used to screen cDNA expression

CC libraries to isolate full-length cDNA clones of interest. ABK98425-
 CC ABK98516 represent nucleotide sequences encoding perennial ryegrass
 CC enzymes or transporter proteins involved in the metabolism and/or
 CC transport of soluble carbohydrates

XX SQ Sequence 2829 BP; 697 A; 678 C; 697 G; 757 T; 0 U; 0 Other;

Query Match 41.2%; Score 1134.6; DB 6; Length 2829;
 Best Local Similarity 67.5%; Pred. No. 4.2e-246;
 Matches 1628; Conservative 0; Mismatches 774; Indels 9; Gaps 2;

Qy 7 GCGCCGAGCTGAACCGGACCGAGCATCCGGAGCCGCTCGAGGACACCCCTCCACGCG 66
 Db 102 GCTGCCAAGCTGACTGCTCCACACTCTCCGGAGGCGCTTGTGTCACCTTCTCTCC 161
 Qy 67 CACCGCAACGAGCTGTCGCCCTCTCTCAAGTACGTGAACAAGGGAGGAGCATCTG 126
 Db 162 CATCTTAAGAGCTCATTTGCCCTCTTTCAAGTATGTTTACCAGGGCAAGGAATGCTT 221
 Qy 127 CAGCGCACCATCTCTCGACGCGCTCGAGAGGTCCAGGGCTCCGGGCTCCGCGCTC 186
 Db 222 CAGCGCACCATCTCTCGAGTTCCTGAGTTTGAAGCTT-----GTTTGAAGCTGCA 275
 Qy 187 GCGGAGGACCTTCTCGACGCTCTCCGCTCCGCGCAGGAGGCGCATCGTCTGCCGCG 246
 Db 276 AGATATGCACTCTTGAAGACATTAATCCGTGCTGCTCAGAGAGCAATGTGCTGCC 335
 Qy 247 TTCGTGGCCATCGGGTGGCGCGCGCGGAGTTTGGAGTACCTCGCGGTCAAGCTT 306
 Db 336 TGGGTGCACTGGCCCATCAGGCTAGGCCGCTGCTGGGACTTACATACGGGTGAATGT 395
 Qy 307 CAGGAGCTCAGGCTCGAGCAGCTCAAGTCTCGGAGTACCTCGCTTCAAGGAGGCTT 366
 Db 396 AGCGAGTTGGCTGTGAGGAGCTGACAGTTCCGAGTACCTAGCAFTCAAGGAACAGCTT 455
 Qy 367 GTGAGCGGCGACACAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTCAATGTC 426
 Db 456 GTGATGAGCAGCGCAGCAGCAAGTTTGTGCTTGAGCTTGATTTGAGCGTTTCATGCT 515
 Qy 427 TCAGTCCACGCGCCAAATCGGTCACTATATGGAACGGTGTGAGTCTCTCAACCGA 486
 Db 516 TCGTTCCCGGCTCTTCCATGTCCAAAGTCCATGGAATGGGGTGCAGTCTCTTAACCGT 575
 Qy 487 CACTTGTCTCAATCATGTTCCGACAGGAGTTCCTCGAGCCCTGTTGGATTTCCTC 546
 Db 576 CACTGTCTTCAAGCTGTTCCAGGACAGGAGAGCTCTACCCACTACTGAACTTCTCTG 635
 Qy 547 CGTGGCCACCGGCACAAGGGGCAATGTTATGATGCTTTAATGATAGATACAAAGCTTGG 606
 Db 636 AAAGCCCATTAATAAGGGCACGACATGATGCTAAATGACAGCAATTCAGAGCCCTCGT 695
 Qy 607 AGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACA 666
 Db 696 GGGCTCCAGTCAAGCCCTTAGAAGGCAAGAGATATTTAACGAGCATCCCTCAGGACACC 755
 Qy 667 CATACTCACAATTTGCTTATAAATTTCAAGAGTGGGCTCGAGAAAGGTTGGGTGAT 726
 Db 756 CGTCTCTGAGTTCACCAAGGTTCCAAAGCTTGGCTTGGAGAGAGGTTGGGGCGAC 815
 Qy 727 ACAGCAGGACATGTTTTTGGAAATGATCCATCTCTCTTAGACATCATTCAGGCGCCAGAC 786
 Db 816 ACCGCTAAGCGGTATACAGGACTCCCATCCACTTGTCTTCTTGTACTTCTGAGGCCCTGAT 875
 Qy 787 CCATCTACCTAGCAAAATTTCTGGGAGGATCCCATCATTTTAAAGTCTGTTGGTGA 846
 Db 876 CAGCGAGCTGGAGAGTTCCTTGGAACTATACCAATGATGTTCAATGTTGTTTATCTCG 935
 Qy 847 TCCCTCATGATATCTTTGGTCAAGCTAATGATAGGCTTCGCCAGACACAGGAGACAG 906
 Db 936 TCTCACAGGATATTTTGTCTCAATGCTGTTGGGATACCCCTGATCTACTGTTGGCCAG 995
 Qy 907 ATCGCTATATCTGAGCAAGTCCGCTACCTAGAAAATGAGATGTTCTTCGTTTAAAG 966

XX	SQ	Sequence	2494 BP, 622 A, 599 C, 628 G, 645 T; 0 U; 0 Other;
		Query Match	41.1%; Score 1133; DB 3; Length 2494;
		Best Local Similarity	67.5%; Pred. No. 9.2e-246;
		Matches 1627; Conservative	0; Mismatches 775; Indels 9; Gaps 2;
Qy	7	GCCCGAAGCTGAACGCGCAAGCGGAGCATCGGGACCGCGTGGAGGACACCCCTCCACGCG 66	
Db	27	GCTSCCAAGCTAGCTCGCCTCCACAGTCTCCGGAAGCCTCGGTGCCACCTTCTCGCT 86	
Qy	67	CACGCAACAGCTCGTGCCTCTCTCCAGTACGTGAACAGGGGAGGAGCGCATCTG 126	
Db	87	CATCCCAATGAGTTGATGCACTCTTCTAGGTATGTTAACCGAGGAAAGGGAATC 146	
Qy	127	CAGCGGCACACATCCTCGAGCGCTCGAGAGGTCCAGGCTCCGGGCTCCGGCGCTC 186	
Db	147	CAGGTCACACAGCTGCTTGGGAGTTGATGCTT-----GATCGAAGCTGACAAAGAG 200	
Qy	187	GCGAGGGAACCTTCTCGAGCTCTCGGTCTCGCGGACGAGGCGATCGTGTCTGCGCGC 246	
Db	201	AAATATGCTCCCTTTGAAGACATTTCTCGGCTGCTCAGGAAGCCATTGTGTCTGCGCGC 260	
Qy	247	TTGTGACCATCGGGTGCCTCGCGCGCGCGGAGTTTGGGAGTACGTCCCGCTCAAGTT 306	
Db	261	TGGGTGCACTGGCCATCAGGCCAAGGCTGGTGTCTGGGACTACATTCGGGTGAATGTA 320	
Qy	307	CAGCAGCTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCCGTTTCAAGGAGGAGCTT 366	
Db	321	AGTGAGTTGGCAGTGGAGAGCTCAGTGTCTTCTGAGTACTTGGCTTCAAGGAACAGCTT 380	
Qy	367	GTGAGGGCGCAGACAAATGATTCCTACGTTCTCGAGCTTCACTTCGAGCGGTTCAATGTC 426	
Db	381	GTGTATGGACACACCAACAGCACTTTGTTCTTCTGAGCTTGATTTGAGCCCTTCAATGCC 440	
Qy	427	TCGATCCCAAGCCCAATCGGTATCATCTATTGGAAACGGTGTGACGTTCCTCAACCGA 486	
Db	441	TCCTTCCGCGCGCGTCCATGTCTCCAGTCCATCGGAAATGGGTGACAGTTCTTTAACCGT 500	
Qy	487	CACCTTGCTCAATCATGTTCCGCAACAGGATGTCTTGAGGCCCTGTGTGATTTCTCTC 546	
Db	501	CACCTGTCTCAAGTTGTCTCAGGACAGGAGCGCTTACCCCTTCTGTAACTTCTCTG 560	
Qy	547	CGTGGCCACGGGCACAAAGGGGCATGTTATGATGCTTAATGATGAATACAAAGCTTGGGG 606	
Db	561	AAAGCCCATAAACACAAAGGCGACGCAATGATGCTGAATGACAGAAATTCAGAGGCTTCGT 620	
Qy	607	AGGCTTCAGTCTGTGCTGACAAAGCTGAGGAGCACTGTTCAAAGCTTCTCTGCTGACACA 666	
Db	621	GGGCTCCAAATCATCTCTTAGAAAGGCAAGAAATATCTGATGGGCATTCCTCAAGACAG 680	
Qy	667	CCATCTCAAAATTTGCTTATAATTTCAAGGTGGGGCTTGAGAAAGGTTGGGGTGAT 726	
Db	681	CCCTACTCGGAGTTCAACACAGGTTCCAGAGCTCGGTTTGGAGAGGGTTGGGGTAC 740	
Qy	727	ACAGCAGGACATGTTTGGAAATGATCCATCTCCTCTAGACATCATTCAGGCGCCAGAC 786	
Db	741	TGTGCAAGCGTGTGCTGTGACACCATCCACTTGCTTCTTGACCTTCTTGAGGCCCTGAT 800	
Qy	787	CCATCTACCTTAGAGAAATTTCTGGGAGAGHCCCCATGATTTTAAAGTTTGTGTGTA 846	
Db	801	CCGCGCAACTTGAGAGAGTTTCTTGGAACTATTTCAAATGATGTTCAATGTGTATTCCTG 860	
Qy	847	TCGCTCATGATACTTTTGTTCGAGCTAAATGTAATTAGGCTTGGCAGACACAGGAGGACAG 906	
Db	861	CTTCGCGATGATACCTTTGGCCAAATCCAAATGTGTGTGGGATACCTCTGATATCTGGTGTGAG 920	
Qy	907	ATCGTCTATATACCTGGACCAAGTCGCTGCACTAGAAATGAGATGGTTCTCCGTTTAAAG 966	
Db	921	GTGTGTATATTTGGACCAAGTCGCGCTTTGGAGATGAGATGCTTTTGAGGATCAAG 980	
Qy	967	AAACAAGGCTTGATGTTTCCCCAAGATCTCATTTGTTACTCGGCTGATACAGATGCA 1026	

QY 2107 GAGCATGGCGTCTCGGCTTCCACATGACCCGCTACCAACCCCGACAGGCTGTTAATCTG 2166
 Db |||||
 QY 2118 GTTCATGGGGTCTGTCTGCAATGATCTTTACCAAGTGAAGGCTGCTGATATC 2177
 Db |||||
 QY 2167 ATGCCCACTCTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGA 2256
 Db |||||
 QY 2178 TTGCTCAACTCTTTGAGAAGTGAAGCAGGATTCACCTACTGCGACATATTCACAG 2237
 Db |||||
 QY 2227 GCAGGCTGACGCCATATACGAGATGACATGGAAGATATCTAGAGAGGTTGATG 2286
 Db |||||
 QY 2238 GGAGGCTGACAGAGATTTACGAGAGTACACCTGGAGCTGTACTCTCTGAGAGCTGATG 2297
 Db |||||
 QY 2287 ACCTGCGCGGGTCTACGGTCTTCTGAAGTACGTGTCGAGCTCGAGGCTCGAGACG 2346
 Db |||||
 QY 2298 ACCTGACTGTGATACGGATCTGGAAGTACGTAAGCAACCTTGAGAGCGCGAGACT 2357
 Db |||||
 QY 2347 AGCGCTACCTTGAGATGTTCTACATCTGGAAGTTCGCGAGCTGCGGAAGACCGTGC 2406
 Db |||||
 QY 2358 CGCGGTTACATTSAGATGTTCTATGCTCTGAATACCGCAGCTGSCCAGCGCGCTCCA 2417
 Db |||||
 QY 2407 CTTCGCAATTGA 2417
 Db |||||
 QY 2418 TTGGCTGTGGA 2425

RESULT 15

ADG68423
 ID ADC68423 standard; cDNA; 2714 BP.
 XX
 AC ADC68423;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Lolium perenne fructan biosynthesis protein cDNA SEQ ID NO:133.
 XX
 XW Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
 XW biosynthetic pathway; plant; gene; ss.
 OS Lolium perenne.
 XX
 PN WO2003040306-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-NZ000239.
 XX
 PR 07-NOV-2001; 2001US-0337703P.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIGHT-) WRIGHTSON SEEDS LTD.
 PI Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;
 PI Saulsbury KM, Hall C;
 XX
 DR WPI: 2003-441544/41.
 DR P-PSDB; ADC68459.
 XX
 PT New polynucleotide encoding polypeptides from Lolium perenne or Festuca
 PT arundinacea, useful for modulating the biosynthesis of lignin, fructan or
 PT tannin in a plant.
 XX
 PS Claim 1; SEQ ID NO 133; 240pp; English.
 CC
 CC The present invention describes isolated polynucleotides (I) encoding
 CC proteins (II) from Lolium perenne and Festuca arundinacea which are
 CC active in lignin, fructan and tannin biosynthetic pathways. Also
 CC described: (1) an isolated oligonucleotide probe or primer comprising at
 CC least 10 contiguous residues complementary to 10 contiguous residues of
 CC (I); (2) a kit comprising the oligonucleotide probe or primer; (3) a
 CC genetic construct comprising (I); (4) a transgenic plant cell comprising
 CC the genetic construct of (3); (5) a plant or its seed, fruit or progeny
 CC comprising the transgenic plant cell of (4); (6) modulating one or more

CC of the lignin, fructan or tannin compositions of a plant; (7) producing a
 CC plant having one or more of the lignin, fructan or tannin compositions;
 CC and (8) modifying the activity of (II) involved in a lignin, fructan or
 CC tannin biosynthetic pathway in a plant. (I) can be used for modulating
 CC the biosynthesis of lignin, fructan or tannin in a plant. The present
 CC sequence is used in the exemplification of the present invention.

XX
 SQ Sequence 2714 BP; 656 A; 664 C; 671 G; 723 T; 0 U; 0 Other;

Query Match 41.1%; Score 1133; DB 9; Length 2714;
 Best Local Similarity 67.5%; Pred. No. 9.5e-246;
 Matches 1627; Conservative 0; Mismatches 775; Indels 9; Gaps 2;

QY 7 GCCCGAAGCTGAACCGCAACGAGCATCCGGACCCGCTCGAGGACACCCCTCCACGCG 66
 Db 48 GCTGCCAAGCTGACTCGTCTCCACAGTCTCCGGAGCGCTTGGTGCACCTCTCTCTCC 107
 QY 67 CACGCGAAGGCTCGTCCGCTCTCTCCCAAGTACGTGAACAGGGGGAAGGCAATCTCTG 126
 Db 108 CATCTTAAGAGCTCATTTGCCCCCTCTTTTCAAGTATGTTCAACGAGGCAAGGAATGCTT 167
 QY 127 CAGCGCACCAATCTCTCGACGCGCTCCAGAGGTCCAGGGCTCCGGGCTCCGCGGCTC 186
 Db 168 CAGCGCACCAAGCTCTCACTGAGTTTGAAGCTT-----GTTTGAAGCTCAGAGGNG 221
 QY 187 GCGAGGAGACCTTCTCTCGAGCTCTCCGCTCCGCGAGGAGGAGGATCTCTGCGCGCG 246
 Db 222 AGATATGACCCCTTTGAAGACATTTCTCGTCTGCTCAGGAAGCAATTTGCTGCCCCCA 281
 QY 247 TTCGTGCCCATCGGGTGGCGCCGCGCGGAGTTTGGGAGTACGTCGCGCTCAACGTT 306
 Db 282 TGGGTGACCTGGCCATCAGGCTTAGGCTGGTCTTGGGACTACATACGGGTGAAATGTT 341
 QY 307 CACGAGCTCAGCGTGCAGAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGAGAGAGCTT 366
 Db 342 AGCGAGTTGGCTGTTGAGGAGCTGACAGTTTCCGAGTACCTGGCATTCAGAGACAGCTT 401
 QY 367 GTCGAGCGCCAGACACATGATCCCTAGCTTCTCGAGCTTGAATTCGAGCCGCTCAATGTC 426
 Db 402 GTTGAAGAGCAGCGCCAGCAGCAAGTTTGTGCTTGAGCTTGTATTTGAGCTTTCAATGCC 461
 QY 427 TCAGTCCCGCCGCGCCAAATCGGTGATCATCTATTGGAACGCTGTCAGTCTTCAACCGA 486
 Db 462 TCCTTCCAGCTCTTCCATGTTCCAGTCCATTTGGAATGAGGCTGCGAGTTCTTAAACCGT 521
 QY 487 CACTTGTCTCAATCATATGTTCCGCAACAGGAGTGTCTTTGAGGCCCTTGTGGATTTCTC 546
 Db 522 CACTGTCTTCCAAGCTGTTCCAGGACAGGAGGCTCTACCCACTACTGAATCTCTG 581
 QY 547 CGTGGCCACCGGCACAGGGGGCATGTTATGATGCTTAAATGATAGATACAAAGCTTGGGG 606
 Db 582 AAAGCCCATTAACCAACAGGCGCACGCAATGATGCTAAACGACCGAATTCAGAGCTTCGT 641
 QY 607 AGGCTTCAGTCTGTCTGACCAAGCTGAGGAGCAGCTTGTCAAAGCTCCCTGCTGACACA 666
 Db 642 GGGCTCCAATCAGCCCTTAGAAGGCGAAGAGATATCTAAGAGCATCTCTTGAAGACACC 701
 QY 667 CCNATCTCACAATTTGCTTATAAATTTCAAGAGTGGGGCTCGAGAAAGGTGTTGGGGTGAT 726
 Db 702 CCCTGCTCTGAGTTCAACCAACAGCTTCCCAAGAGCTTGGCTTGGAGAGGGTGGGGGAC 761
 QY 727 ACAGCAGGACATGTTTGGAAATGATCCATCTCTCTTAGACATCATTCAGGCGCCAGAC 786
 Db 762 ACCGCTAAGCGGTGTACAGGACACCATCTCTCTTGTGATCTTACTTGGGCGCCCTGAT 821
 QY 787 CCATCTACCTACAGAAATTTCTTGGGAGGATCCCATGATTTTTTAACGTTGTGTTGTA 846
 Db 822 CCAGCAGCTTGGAGAGTTTCTTGGAACTTATACCAGTATGATGTTTCAATGTTTATCTG 881
 QY 847 TCCCTCTCATGGTACTTGTCTCAAGCTAATGATATTAGGCTTGGCAGACACAGGAGGACAG 906
 Db 882 TCTCCACAGGATATTTGCTCAATCCAGTGTCTGGATACCTCTGATCTACTGTTGGGCCAG 941

Qy	907	ATCGTCTTATATAC	TGGAGCAAGTCGGTGCAC	TAGAAATGAGATGGTTCTCCGTTTAAAG	966
Db	942	GTTCTGTACATCTTTGGATCAAGTCGGTCTTTGGAGAAATGAGATGCTTCTGAGGATTAAG	1001		
Qy	967	AAACAAGGGCTTGATGTTTCCC	AAAGATTCTCAATGTTACTCGCTGGATGATACAGAGTCA	1026	
Db	1002	CAGCAAGGCTTGACATAACCCCTTAAGATCTCAATGTAC	AGGCTGTTGCTGTGATGCT	1061	
Qy	1027	AAAGGAACATCATCGCAATCAGCGGCTTTGAGAGAAATTAGTGGAAACACAGCATATCTTACATA	1086		
Db	1062	GTTGGAACTACATGTGGCCAGCGGCTGGAGAAAGTTATTGGACTGAGCACATGACATTT	1121		
Qy	1087	TTACGAGTTCCCTTCAGAAATGAAATGGGATACCTTAAGAAATGGATATCAAGATTGAT	1146		
Db	1122	CTCCGTGTTCCATTCAGAACTGAGAGGGGATCCCTCGTAAAGTGGATCTCTCGTTTGTAT	1181		
Qy	1147	GTTGGGCATATCTGGAACCAATTTGCTGAGAGTCTGCTGGTGAATTTGCTGCTGAATT	1206		
Db	1182	GTTCTGGGCAATCTTGGAGACATACCCGAGATGTTGCCAAACGAATCTCATGAGAGAAATG	1241		
Qy	1207	CAAGGTACTCCAGACTTCATAATTTGGAACCTTACAGTGTAGGAAATCTTGTGGGGTCAATG	1266		
Db	1242	CAGACCAAGCCTGATCTCAATATTGGCAACTACAGTGAAGTAACTTTGTGCGCCACTCTG	1301		
Qy	1267	CTATCTTAAAGATGGGAAATTAACCGATGCAACATTTGCTCATGCTCTGGAAGAAAGACTAAG	1326		
Db	1302	CTTGGCGATTAAGTTTSSGAGTTACCCAGTGCACCAATTTCCCATGCTTTGGAGAAAAA	1361		
Qy	1327	TATCCAGATTCAGACATNTTTGGAAGAAATTCGATGAGAGTAGTACCAATTTCTCTCTGCCAG	1386		
Db	1362	TACCCCAACTCAGACATNTATTGGACAATTTGACAGCCAAATACCAATTTCTCATGCCAG	1421		
Qy	1387	TTCACTGCTGATATPAATTTGGTATTGAAACAATGCTGATTTTATCATCACCAGACATACCAA	1446		
Db	1422	TTCACTGCTGACCTTATTGCCATGAATCACTGATTTTCACTATCAACCAGCATTTCCAG	1481		
Qy	1447	GAATTTGCTGGAGCAAAAATATCTTTGGACAGTATGAGAGTCAATGTCCTTTACTCTG	1506		
Db	1482	GAATTTGCTGGAGCAAGGACAGCTGGGCCAGTATGAGTCTCACATTTGCTTTCACGCTC	1541		
Qy	1507	CGTGGTCTGTACCGAGTTGTCATGGGATCGATGTCTTCCATCCAAAGTTCAATATAGTC	1566		
Db	1542	CGTGATCTTACCGTGTGTGCCATGGGATTTGAGGTGTTCGATCCCAAGTTCAACATGTC	1601		
Qy	1567	TCTCTGGAGCTGACATGTCCATATATCTTTCCACATACCGAGAGGCCAAGCGACTCAAC	1626		
Db	1602	TCTCTGGAGCAGATATGATGTCTACTTCCCATCACTGAATCTGACAGAGGCTTACT	1661		
Qy	1627	TCTCTTCAATGGTCAATTCGAAAAATTTGATTTATGACCCGAGCAAAAACGATGAACACATTT	1686		
Db	1662	GCCTTCACGCTGAAAATTGAAGAGCTCCTTTACAGTGATGTTGAGAACTCTGAACACAAG	1721		
Qy	1687	GGGCACTGTGATGACCGGTCAAGGCCATCTCTTCTCCATGSCAAGACTCGACAGGGTG	1746		
Db	1722	TTTGTATTGAGGACAAGAACAGGCTTATCATCTCTCAATGGCTCGTCTGTGACCGGTG	1781		
Qy	1747	AAGAACAATAACAGGCTGGTTCGAAGCTTTTGTCTAAGTGCCTTAAGCTGAGGGAGCTGTTA	1806		
Db	1782	AAGAACATGACAGGCTTGGTTGAGATGTTTGGTAGAACTCTCATCTGAAGGATTTTGGCA	1841		
Qy	1807	AACTTTGTCTGTTCTCGTTCGGGTCAATGATGTCAACAAGTCCAAGGACAGGGAGAGATC	1866		
Db	1842	AACCTTTGTGTTGTCTGTTGACCATG---GCAAGGAGTCCAAGGATAGGGAGGAGCAG	1898		
Qy	1867	GCAGGATAGAGAGATGCAATGAACTCATCAAGACCCAACACTTTGTTTCGGGCAAGTTCCGC	1926		
Db	1899	GCTGAGTTCAAAAGGATGTACGTCTCATTTGAGAGGTACAAGCTGGAGGGCCATATCCCG	1958		
Qy	1927	TGGATCTCTGCCAGACAAAACAGGGCCCGTAAACGGGAGCTCTTATCGTACATCGCTGAT	1986		
Db	1959	TGGATCTAGCTAGATGAACCGGTGTTCCGATATGAGAGTTGTACCGCTACATTTGTGAC	2018		
Qy	1987	ACCATGGTCTTTCTGTACAGCGGGCCCTTGTATGAAGCGTTTCGGTCTCAACCGTCGTTGAG	2046		

Db	2019	ACCAAGGGCGCATTTGTTTCAGCCTGCATTCTATGAAGCATTTGGCCTGACTGTTGTCGAG	2078
Qy	2047	GCCATGACCTGTGGGCTTCCCTATTTTCGGACGCTCCATGCGAGGTCACGCTGAGATCATTA	2106
Db	2079	GCCATGACATGTGTTTGCCCAAAATAGCGACATGCCATGTTGGCCACGCTGAATCATTT	2138
Qy	2107	GAGCATGGCCTCTCGGGCTTCCACATTCAGCCCGTACCACCCCAAGCAGGCTGTTAATCTG	2166
Db	2139	GTGAAVGGTGTCTGGTTTGACATCGATCCTTACCAAGTGCAGAGCTGCAGATATC	2198
Qy	2167	ATGCCGCACTTCTTCGACCGGTCAAGCAAGACCCAGATCATCTGGGTGAATATATCTGGA	2226
Db	2199	CTGCTCAACTTCTTTTGAGAAATCCACGGCAGATCCAACTTACTTGGGACAAAATGTCGGAA	2258
Qy	2227	GCAGGGCTCAGCGGCATATACGAGAGAGTACACATGGAAGATATATCTACGAGAGGTTGATG	2286
Db	2259	GGTGGCCTGAAGAGAAATTTATGAGAAATACACCTGGAAGCTGTACTCAGAGAGGCTGATG	2318
Qy	2287	ACACTGGCCGGGCTCTAAGTTTCTGGAGTAGTAGTCTCGAAGCTCCGAGGCTGGAGAGCG	2346
Db	2319	ACCTTGACTGGTGTATGTTGTTTCTGGAAGTATGTAGACACCTTGGAGGCGCTGAGACT	2378
Qy	2347	AGGCGGTACCTTCAGATGTTTCTACATCTGAAAGTTCGGCGAGCTGGCGAAGACCGTGCCG	2406
Db	2379	CGCGGTACTCTCAGATGTTCTAAGCTCTGAAGTACCGCAGCCTGGCTGCTCAGATTCCA	2438
Qy	2407	CTTGCAATTGA	2417
Db	2439	TTGGCGGTGCA	2449

Search completed: May 25, 2004, 16:03:57
Job time : 702.519 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3397.5	80.6	309	1	SUS2_PEA	Q24301 pisum sativ
2	3158	74.9	766	1	SUSY_BETVU	Q42652 beta vulgar
3	3105.5	73.6	805	1	SUS2_ARATH	Q00917 arabidopsis
4	3005	71.3	320	1	SUS2_TULGE	Q41607 tulipa gesn
5	2993.5	71.0	802	1	SUS1_MAIZE	P04712 zea mays (m
6	2985	70.8	816	1	SUS2_MAIZE	P49036 zea mays (m
7	2983.5	70.7	805	1	SUSY_PHAAU	Q01390 phaseolus a
8	2983.5	70.7	805	1	SUSY_SOYBN	P13708 glycine max
9	2983.5	70.7	805	1	SUS1_ORYSA	P30298 oryza sativ
10	2982	70.7	805	1	SUS1_TULGE	Q41608 tulipa gesn
11	2974	70.5	816	1	SUS2_ORYSA	P31924 oryza sativ
12	2948	69.9	816	1	SUS2_ORYSA	Q43009 oryza sativ
13	2944.5	69.8	805	1	SUS1_SOLITU	P10691 solanum tub
14	2944.5	69.8	805	1	SUSY_LYCES	P49037 lycopersico
15	2941.5	69.8	806	1	SUSY_VICFA	P31926 vicia faba
16	2931.5	69.5	805	1	SUSY_MEDSA	O65026 medicago sa
17	2925.5	69.4	805	1	SUS2_SCHLU	P49039 solanum tub
18	2922	69.3	816	1	SUS2_HORVU	P31923 hordeum vul
19	2910.5	69.0	808	1	SUS1_DAUCA	P49035 gaucuss caro
20	2899	68.7	807	1	SUS1_HORVU	P31922 hordeum vul
21	2861.5	67.9	801	1	SUS2_DAUCA	O49845 gaucuss caro
22	2855.5	67.7	806	1	SUS1_ARATH	P49040 arabidopsis
23	2844.5	67.5	803	1	SUSY_ALNGL	P49034 alnus glutin
24	587.5	13.9	218	1	SUSY_SACOF	P31925 saccharum o
25	450	10.7	1056	1	SPS SPIOL	P31928 spinacia ol
26	445	10.6	1059	1	SPS VICFA	Q43876 vicia faba
27	444	10.5	1068	1	SPS MAIZE	P31927 zea mays (m
28	441.5	10.5	1045	1	SPS BETVU	P49031 beta vulgar
29	436.5	10.4	1053	1	SPS SOLITU	Q43845 solanum tub
30	425	10.1	1054	1	SPS1_CRAPL	O04932 craterostig
31	414	9.8	1057	1	SPS1_CITON	O22060 citrus unsh
32	408.5	9.7	1081	1	SPS2_CITON	O04933 craterostig
33	351	8.3	1049	1	SPS GRAYA	Q43802 oryza sativ


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QY 112 KBELVDQNDPYVLELDFEPFNVSVPNRNASSIGNGHQVFLNRHLSSTMFNRDCLEPL 171
DB 122 KBELVEGKNDNIILELDFEPFNASPRFTRSSIGNGVQFLNRHLSSTMFNRKDCLEPL 181
QY 172 LDFLRGHRKHGMMLNDRIQSLGRLOSVLTKAEHLKSLPADTPYQYAYKFOEWGLEK 231
DB 182 LDFLRVHTYKGHMLNDRIQSLKQSLVAEDHLSKLPDLYSEYEYELQGTGFER 241
QY 232 GMDGTAGHVLEMHLLDIIQAPDPTLSEKFLGRIPMFNVVVVSPHGVFGQANVLGLPD 291
DB 242 GMDGTAARVLEMHLLDIIQAPDPTLSEKFLGRIPMFNVVVVSPHGVFGQANVLGLPD 301
QY 292 TGGQIVYILDQVRALENEMVRLKXGLOVSPKILIVTRLIPDAKTSCKNORLERISGTQ 351
DB 302 TGGQIVYILDQVRALENEMVRLKXGLOVSPKILIVTRLIPDAKTSCKNORLERISGTQ 361
QY 352 HTYILRVFPERNENGILKXWISRDVWPYLETFAEDAAAGELAELOQTTPDPIIGNYSDGNL 411
DB 362 YTHILLRVPRSEKGLRKWISRDVWPYLETFAEDVASEIAELAELOQYDPDPIIGNYSDGNL 421
QY 412 VASLLSKYKGIOTCNIAHALEKTYKPSDIPFKNFDKVFHSCQFTADIAMNADFIIT 471
DB 422 VASLLAYKMGVTOCTIAHALEKTYKPSDIPFKNFDKVFHSCQFTADIAMNADFIIT 481
QY 472 STYQIATAGSKNTVGOYESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTKA 531
DB 482 STYQIATAGSKNTVGOYESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTKA 541
QY 532 KRILTSIHGSIENLIYDPQNDHIGLDDRSKPIFSMARLDRVKNITGLVAFKACAKL 591
DB 542 KRILTSIHGSIENLIYDPQNDHIGLDDRSKPIFSMARLDRVKNITGLVAFKACAKL 601
QY 592 RELVNLVVVAGVNDVKNKSDREIEKXKHGELIKTHNLPGQFVWISQATNRAENGELYR 651
DB 602 RELVNLVVVAGVNDVKNKSDREIEKXKHGELIKTHNLPGQFVWISQATNRAENGELYR 661
QY 652 YIADTHGAFVQPALYFAFGLTVEAMTCGLPTPATLHGGPAEIIHGVSGFHDIVHPQ 711
DB 662 YIADTHGAFVQPALYFAFGLTVEAMTCGLPTPATLHGGPAEIIHGVSGFHDIVHPQ 721
QY 712 AVNLMAFDFFDRCKQDPDHWNVISGAGLQRIYKWTWKIYSERLMTLAGVYGFVKYVSKLE 771
DB 722 ASELLVDFORCKEDENHNKVSDDGLQRIYKWTWKIYSERLMTLAGVYGFVKYVSKLE 781
QY 772 RLETRYLEXFIYLLKPRELAKTVPILA 797
DB 782 RLETRYLEXFIYLLKPRELANSVPIA 807

RESULT 2
ID SUSY BETVU STANDARD; PRT; 766 AA.
AC Q42652;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)
DE (fragment).
DE SS1.
GN Beta vulgaris (sugar beet).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161914;
RN [1.
RP SEQUENCE FROM N.A.
RC TISSUE=Tap root;
RX MEDLINE=96270366; PubMed=8639746;
RA Hesse H., Willmitzer L.;
RT "Expression analysis of a sucrose synthase gene from sugar beet (Beta
RL vulgaris L.).";
RL Plant Mol. Biol. 30:863-872(1996).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and

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CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- TISSUE SPECIFICITY: Expressed most predominantly in tap root.
CC -!- SIMILARITY: Belongs to the glucosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X81974; CAAS7499.1; -.
CC PIR; S71493; S71493.
CC InterPro; IPR001296; Glyco trans 1.
CC InterPro; IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC TRANSFERASE; Glycosyltransferase.
CC NON TER 1
CC SEQUENCE 766 AA; 87240 MW; 407803ECD8EC4A82 CRC64;
CC -----
CC Query Match 74.9%; Score 3158; DB 1; Length 766;
CC Best Local Similarity 79.2%; Pred. No. 9.7e-203;
CC Matches 595; Conservative 73; Mismatches 81; Indels 2; Gaps 2;
QY 51 GGRALAEAGFDLVRSAQEAIVLPFPFAIAVPRPGVWYVVRVNVHLSVEQLTVSEYLR 110
DB 3 GKQILSDGFPSEVLRSQAQEAIVVPFPFAIAVPRPGVWYVVRVNVHLSVEQLTVSEYLR 62
QY 111 EKDELVDQNDPYVLELDFEPFNVSVPNRNASSIGNGHQVFLNRHLSSTMFNRDCLEP 170
DB 63 EKDELVDGKADHYVLELDFEPFNESVPRTRSSIGNGVQFLNRHLSSTMFNRKDCLEP 122
QY 171 LLDLFLGRHGRKHGMMLNDRIQSLGRLOSVLTKAEHLKSLPADTPYQYAYKFOEWGLE 230
DB 123 LLDLFLRVHGRKHGMMLNDRIQSLGRLOSVAEDHLSKLPDLYSEYEYELQGTGFER 182
QY 231 KMGDGTAGHVLEMHLLDIIQAPDPTLSEKFLGRIPMFNVVVVSPHGVFGQANVLGLP 290
DB 183 KMGDGTAEARVLEMHLLDIIQAPDPTLSEKFLGRIPMFNVVVVSPHGVFGQANVLGLP 242
QY 291 DTGQIVYILDQVRALENEMVRLKXGLOVSPKILIVTRLIPDAKTSCKNORLERISGT 350
DB 243 DTGQIVYILDQVRSLHEHMLQRIKXGLOVTPRILIVSRILIPDAKTSCKNORLERISGT 302
QY 351 QHTYILRVFPERNENGILKXWISRDVWPYLETFAEDAAAGELAELOQTTPDPIIGNYSDGN 410
DB 303 EHASILRVPRSEKGLRKWISRDVWPYLETFAEDVASEIAELAELOQYDPDPIIGNYSDGN 362
QY 411 LVASLLSKYKGIOTCNIAHALEKTYKPSDIPFKNFDKVFHSCQFTADIAMNADFIIT 470
DB 363 IVASLLSKYKGIOTCNIAHALEKTYKPSDIPFKNFDKVFHSCQFTADIAMNADFIIT 422
QY 471 TSYQIATAGSKNTVGOYESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTKA 530
DB 423 TSYQIATAGSKNTVGOYESHTAFTLPGLYRVVHGIDVDFPKFNIVSPGADMSIYFPHTKA 482
QY 531 -AKRLTSIHGSIENLIYDPQNDHIGLDDRSKPIFSMARLDRVKNITGLVAFKACAKA 589
DB 483 DVTCLTSIHGSIENLIYDPQNDHIGLDDRSKPIFSMARLDRVKNITGLVAFKACAKA 542
QY 590 KRELNLVVVAGVNDVKNKSDREIEKXKHGELIKTHNLPGQFVWISQATNRAENGEL 649
DB 543 KRELNLVVVAGVNDVKNKSDREIEKXKHGELIKTHNLPGQFVWISQATNRAENGEL 602
QY 650 YRIADTHGAFVQPALYFAFGLTVEAMTCGLPTPATLHGGPAEIIHGVSGFHDIVHP 709
DB 603 YRICDKGGIFAPAFYFAFGLTVEAMTCGLPTPATLHGGPAEIIHGVSGFHDIVHP 662
QY 710 EQAVNLMAFDFFDRCKQDPDHWNVISGAGLQRIYKWTWKIYSERLMTLAGVYGFVKYVSK 769

```


RC STRAIN-cv. Apeldoorn;
RA Bolk P.A., de Boer A.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X96939; CAA65640.1; -;
CC InterPro; IPR001296; Glyco_trans_1.
CC InterPro; IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC Trnstrase; Glycosyltransferase; Multigene family.
CC SEQUENCE 820 AA; 93015 MW; AA75AF88D74A0EED CRC64;
CC -----
CC Query Match 71.3%; Score 3005; DB 1; Length 820;
CC Best Local Similarity 69.7%; Pred. No. 1.7e-192;
CC Matches 556; Conservative 118; Mismatches 122; Indels 2; Gaps 2;
CC -----
CC QY 3 HASGRVDETLHAHRELVALSKYVNGKGIQPHHILDALDEVQSGGR-ALAEQFEL 61
CC DB 10 HSVRELTDTLSAHKNELLASRFVQKQXQLPHQLITEYEAIVPAADREKLKDGVE 69
CC QY 62 DVLRSQAQEAIVLPFVAIAVRPRPGVWYVYRVNVHLSVEQLTVSYSLPKELVPGQEN 121
CC DB 70 DVLKAAQEAIVLPFVAIAVRPRPGVWYVYRVNVHLSVEQLTVSYSLPKELVPGQEN 129
CC QY 122 DPLVLELDEPPNVSPRPNRSSISNGVQFLENHLSIMFRNDCLEPLDLRLGRHK 181
CC DB 130 SNFTLELDEPPNVSPRPNRSSISNGVQFLENHLSIMFRNDCLEPLDLRLGRHK 189
CC QY 182 GHVWMLNDRIQSLGRQSVLTAEELSLKLPADTPYSQAFKFEWGLKGMGDTAGHVL 241
CC DB 190 GTSWMLNDRIQSLGRQSVLTAEELSLKLPADTPYSQAFKFEWGLKGMGDTAGHVL 249
CC QY 242 EMHLLDLDIQAQPPSTLEKFLGRIPMIFNVVWVSPHGYFGQANVLGLPDTGCGQIVYILD 301
CC DB 250 ENHLLDLDIQAQPPSTLEKFLGRIPMIFNVVWVSPHGYFGQANVLGLPDTGCGQIVYILD 309
CC QY 302 QYRALENEMVLRLKKGDLVSPKILIVTRLIIDPAKGTSCNORLERISGTOHTVILSVPER 361
CC DB 310 QYRALENEMVLRLKKGDLVSPKILIVTRLIIDPAKGTSCNORLERISGTOHTVILSVPER 369
CC QY 362 NENGILKWKISRDVWVPLETAEADAAGELAAELQGTPTDPIIGNYSDGNLIVASLLSYKMG 421
CC DB 370 TENGILKWKISRDVWVPLETAEADAAGELAAELQGTPTDPIIGNYSDGNLIVASLLSYKMG 429
CC QY 422 ITQCNTAHLEKTKYPSDILFWKPFDEKHFSCQFTADIIAMNAPAFITSTVQETIAGSK 481
CC DB 430 VTQCTTAHALEKTKYPSDILFWKPFDEKHFSCQFTADIIAMNAPAFITSTVQETIAGSK 489
CC QY 482 NTWGVYESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLGSI 541
CC DB 490 JTWGVYESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLGSI 549
CC QY 542 ENLIYDPEQNDHIGHLDRSKPILFSMARLORVKNITGLVEAFKACAKRELNLVWVVA 601
CC DB 550 EELLYSAESTYKFGKDKTKIIFLSMARLDRVKNWMTGLVELYAKNDRLKELNLVWVVC 609
CC QY 602 GYNDVNVKSDREBIAETKQHELIKTHNLFGQFRWISAQNRNARNGELVYIADTGAFV 661
CC DB 610 G-DHAKASKDLERQAEKWKMSLYTEEKYLDGHTIRWISAQNRNARNGELVYIADTGAFV 668

QY 662 QPALYEAFGLTVTEAMTQGLPTFATLHGGAETIIHGVSGFHDIPYHPEQAVNLMADEED 721
DB 669 QKAFTEAFGLTVTEAMTQGLPTFATLHGGAETIIHGVSGFHDIPYHPEQAVNLMADEED 728
QY 722 RQKQDPDHWNVISGAGLQRIYKTYKYSERIMTLAGVYGFVKYYSKLERLTRYRYLEM 781
DB 729 KSKQDQTHDAISNGGLKRIYKTYKYSERIMTLAGVYGFVKYYSKLERLTRYRYLEM 788
QY 782 FYLKERELAKTVPLAID 799
DB 789 FYALKYRNLAQSVPLAID 806
CC -----
CC RESULT 5
CC SUSI_MAIZE STANDARD; PRT; 802 AA.
CC ID SUSI_MAIZE STANDARD; PRT; 802 AA.
CC AC P04712;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1)
CC DE (Shrunken-1).
CC GN SH-1.
CC OS Zea mays (Maize).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CC OX NCBI_TaxID=4577;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA Merr W., Frommer W.-B., Maas C., Starlinger P.;
CC RT "Structure of the sucrose synthase gene on chromosome 9 of Zea mays
CC L";
CC RT EMBO J. 4:1373-1380 (1985).
CC CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways. Most active in the sink
CC tissues where it is responsible for the breakdown of the arriving
CC sucrose.
CC CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X02400; CAA26247.1; -;
CC EMBL; X02382; CAA26229.1; -;
CC PIR; S07184; YUZMS.
CC MaizeDB; 13861; -;
CC InterPro; IPR001296; Glyco_trans_1.
CC InterPro; IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC Trnstrase; Glycosyltransferase; Multigene family.
CC SEQUENCE 802 AA; 91731 MW; BF1BBE60598B680A CRC64;
CC -----
CC Query Match 71.0%; Score 2993.5; DB 1; Length 802;
CC Best Local Similarity 70.0%; Pred. No. 9.5e-192;
CC Matches 558; Conservative 105; Mismatches 131; Indels 3; Gaps 2;
CC -----
CC QY 3 HASGRVDETLHAHRELVALSKYVNGKGIQPHHILDALDEVQSGGRALAEQFEL 62
CC DB 9 HSLRERLGLATFSSHPNELIALFSYVHQKGMQLQRLHQLAEFDALFDSKDKYA--PFED 66
CC QY 63 VLRSQAQEAIVLPFVAIAVRPRPGVWYVYRVNVHLSVEQLTVSYSLPKELVPGQEN 122
CC DB 67 ILRAAQEAIVLPFVAIAVRPRPGVWYVYRVNVHLSVEQLTVSYSLPKELVPGQEN 126

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QY 123 EYVLELDPEFPNVSVPNRSSISGNVGQVFLNRHLSSIMFNDRDCLPLDPLGRHKG 182
DB 127 NFVLELDPEFPNVSFPNRSKSGISGNVGQVFLNRHLSSKLFQDKESLYPLNLFKAHNYK 186
QY 183 HVMMLNDRIQSLGRQSVLTAKAEHLISKUPADTPYQFAYKQFQEWGLKMGWGTAGHVL 242
DB 187 TTWMLNDRIQSLGRQSVLTAKAEHLISKUPADTPYSEFNHRFQELGLEKMGWGTAKRVLD 246
QY 243 MHLHLLDITCAPDPSLTLEKFLGRIPLMFNVVVVSPHGYFQANVGLPDTGGQVILVDQ 302
DB 247 TLHLHLLDLEAPDPSLTLEKFLGRIPLMFNVVVVSPHGYFQANVGLPDTGGQVILVDQ 306
QY 303 VRALENMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRVFERN 362
DB 307 VRALENMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRVFERN 366
QY 363 ENGILKWSIRFQVWPVPLETFAEDAAAGEIAELQGTPTFIIGNYSDGNLVASLLSYKMG 422
DB 367 ENGILKWSIRFQVWPVPLETFAEDAAAGEIAELQGTPTFIIGNYSDGNLVASLLSYKMG 426
QY 423 TQCNIAHALEKTYKYPDSDFWKNFDEKHYHSCOPTADIIAMNADFIITSTYQEIAGSKN 482
DB 427 TQCNIAHALEKTYKYPDSDFWKNFDEKHYHSCOPTADIIAMNADFIITSTYQEIAGSKN 486
QY 483 TVQYVESHATFTPLGLYRVVHGIDVPDKENIVSPGADMSIYPPEHTEKAKRLTSLHGSIE 542
DB 487 TVQYVESHATFTPLGLYRVVHGIDVPDKENIVSPGADMSIYPPEHTEKAKRLTSLHGSIE 546
QY 543 NLIYDPEQNDHGHLDKRSKPIFLSFMARLDVRNKTITGLVEAFKAKRLNELNVVAVG 602
DB 547 ELIYDSENSEHSEKFLVKDKKPIIFSMARLDVRNKTITGLVEAFKAKRLNELNVVAVG 606
QY 603 YNDVNSKDEEELAEKHEMLIKTHNLFCQFRWISACTWRANGELYRYIADTHGAFVQ 662
DB 607 -DHGKSKDEEELAEKHEMLIKTHNLFCQFRWISACTWRANGELYRYIADTHGAFVQ 665
QY 663 PALYAFGLTVVEMTTCGLTFTLHGGPAEITBHGVSFGPHIDYHPQAVNLMADFPOR 722
DB 666 PALYAFGLTVVEMTTCGLTFTLHGGPAEITBHGVSFGPHIDYHPQAVNLMADFPOR 725
QY 723 CXODPDHWNISGAGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTY 782
DB 726 CXADPSYDWEISQGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTY 785
QY 783 YILKPELAKTVPLAID 799
DB 786 YALKYRSLASQVPLSPD 802

RESULT 6
SUS2_MAIZE STANDARD; PRT; 816 AA.
AC P49036;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2).
GN SUS1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94159796; PubMed=8115551;
RA Huang X.-F., Nguyen-Quoc B., Chourey P.S., Yelle S.;
RT "Complete nucleotide sequence of the maize (Zea mays L.) sucrose
synthase 2 cDNA.";
RL Plant Physiol. 104:293-294 (1994).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22;
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RA Nguyen-Quoc B., Huang X.-P., Krivitzky M., Yelle S., Lecharny A.;
RL Submitted (XX-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PHOSPHORYLATION.
RC TISSUE=Leaf;
RX MEDLINE=97037743; PubMed=8883390;
RA Huber S.C., Huber J.L., Liao P.-C., Gage D.A., McMichael R.W. Jr.,
Chourey P.S., Hannah L.C., Koch X.;
RT "Phosphorylation of serine-15 of maize leaf sucrose synthase.
Occurrence in vivo and possible regulatory significance.";
RL Plant Physiol. 112:793-802 (1996).
CC -/- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
fructose for various metabolic pathways.
CC -/- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -/- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
sucrose synthase subfamily.
CC -----
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CC -----
DR EMBL; L22296; AAA33514.1; --
DR EMBL; L33244; AAA33515.1; --
DR MaizeDB; L3861; --
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR00368; Sucrose synth.
DR Pfam; PF00534; Glycos transf 1.
DR Pfam; PF00862; Sucrose synth 1.
DR TRANSFAS; Glycosyltransferase; Multigene family; Phosphorylation.
FT MOD_RES 15 15 PHOSPHORYLATION.
SQ SEQUENCE 816 AA; 92939 MW; E4DF863BE7AFC4C8 CRC64;

Query Match 70.8%; Score 2985; DB 1; Length 816;
Best Local Similarity 69.8%; Pred. No. 3.6e-191;
Matches 559; Conservative 106; Mismatches 128; Indels 8; Gaps 3;

QY 3 HASGREDVETLHAHRLVALLSKYVNGKGLQPHHL-----DALDEVQSGGRALAE 58
DB 14 HSVREIRGDSLSAHPNELVAVFTRLNKLGKMLQPHQIIAEYNNAIPEAE---REKLKDG 70

QY 59 PFLDYLSAQEAIVLPFPAIVANPRGMYVYVNVHLSVEQLTVSEYLRPKELVDG 118
DB 71 AFDVLEAAQEAIVIPPPVVALAIPRPGMYVYVNVSELAVEELRVPEYLQFKEQLVEE 130

QY 119 QHNDPYVLELDFEPFNVSVPNRSSISGNVGQVFLNRHLSSIMFNDRDCLPLDPLGRH 178
DB 131 GPNVNFVLELDFEPFNVSFPNRSKSGISGNVGQVFLNRHLSSKLFQDKESLYPLNLFKAH 190

QY 179 RHKGHVMMLNDRIQSLGRQSVLTAKAEHLISKUPADTPYQFAYKQFQEWGLKMGWGTAG 238
DB 191 NYKQWMTWMLNDRIQSLGRQSVLTAKAEHLISKUPADTPYSEFNHRFQELGLEKMGWGTAG 250

QY 239 HVLEMIHLDDIQAQDPSLTLEKFLGRIPLMFNVVVVSPHGYFQANVGLPDTGGQVILV 298
DB 251 RAQETIHLHLLDLEAPDPSLTLEKFLGRIPLMFNVVVVSPHGYFQANVGLPDTGGQVILV 310

QY 299 ILDOVRALENMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRV 358
DB 311 ILDOVRALENMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRV 370

QY 359 PFRNENGILKWSIRFQVWPVPLETFAEDAAAGEIAELQGTPTFIIGNYSDGNLVASLLSY 418
DB 371 PFRNENGILKWSIRFQVWPVPLETFAEDAAAGEIAELQGTPTFIIGNYSDGNLVASLLSY 430

QY 419 KMGITQCNIAHALEKTYKYPDSDFWKNFDEKHYHSCOPTADIIAMNADFIITSTYQEI 478
DB 431 KMGVTHCTIAHALEKTYKYPDSDFWKNFDEKHYHSCOPTADIIAMNADFIITSTYQEI 490

QY 479 GSKNTVQGVESHATFTPLGLYRVVHGIDVPDKENIVSPGADMSIYPPEHTEKAKRLTSLH 538
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Db 491 GSKTVGQYSEHMAFTMPGLYVWVGIDVDFPKFNVSPGADLSIYFPYTESHKRLTSLH 550
QY 539 GSIEINLYDPEONDESHIGLDORSKPLFSMARLDKVNKNTGLVFAFAKAKRLRLNVLV 598
Db 551 PEIEELYSQTEHKKFVLDNRKELIFSMARLDKVNKNTGLVLYGKRLQELNVLV 610
QY 599 VVAGYNDVNVKSDREIEAIEKHELIKTHNIFGQFRWISAOQNRARNGELYRYIADTHG 658
Db 611 VVCG-DHGNFSKDEQAEKMFOLIEQYNLNGHIRWISAOQNRVRNGELYRYICDTKG 669
QY 659 AFVQALYAFGLTYVEAMTCGLPTATLHGGPAEIIIEHGVSGFHDPYHPGQAVNLMAD 718
Db 670 AFVQAFYAFGLTYVEAMTCGLPTATYAYGPAEIIIEHGVSGYHDPYQGDKASALLVD 729
QY 719 FEDRCKQDDHWNISGAGLQRIYKYTWKYSERLMTLAGVYGFYKYSKLERLETRRY 778
Db 730 FDKQCAEFSHWSKISQSGLRLEEKYTWKLYSERLMTLAGVYGFYKYSNLERRETRY 789
QY 779 LEMFYIKPRELAKTVPLAID 799
Db 790 LEMLYAKYRTMASTVPLAVE 810

RESULT 7
SUSY PHAAU
ID SUSY PHAAU STANDARD; PRT; 805 AA.
AC Q01390;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase).
GN SS1.
OS Phaseolus aureus (mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCB_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 517-537.
RA Arai M., Mori H., Imaseki H.;
RT "Expression of the gene for sucrose synthase during growth of mung
RT bean seedlings.";
RL Plant Cell Physiol. 33:503-506 (1992).
RC
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMEL; D10266; BAA01108.1; -
CC InterPro: IPR001296; Glyco trans 1.
CC InterPro: IPR000368; Sucrose synth.
CC Pfam: PF00534; Glycos_transf_1; 1.
CC Pfam: PF00862; Sucrose_synth; 1.
CC Transferrase; Glycosyltransferase.
CC SEQUENCE 805 AA; 92092 MW; A39683CPDF54EF4A CRC64;

Query Match 70.7%; Score 2983.5; DB 1; Length 805;
Best Local Similarity 69.9%; Pred. No. 4.5e-191;
Matches 557; Conservative 112; Mismatches 127; Indels 1; Gaps 1;

QY 3 HASEGRVEDTLHAHRNELVALLSKYKNGKILQPHHILDALDEVQSGGRLAEGPFLD 62
Db 10 HSLRLRLTSLSANRNEILLASRIEKGKGIHQHVIAFEFEIPEESQKLDGAFGE 69

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QY 63 VLSAQEAIVLPPFVAIAVRPQVWVYRVNVHLSVOLTSEYLRPFKEELVDGQND 122
Db 70 VLSAQEAIVLPPFVAIAVRPQVWVYRVNVHLSVOLTSEYLRPFKEELVDGSSNG 129
QY 123 FVLELDFFPNVSVPRNRSISGNGVQFLNPHLSIMPRNEDCLEPLDLGLRGRHKG 182
Db 130 NFVLELDFFPEFTASFPPTLINKSIGNGVQFLNPHLSAKLPHDKESLHPLLEFLRLHVK 189
QY 183 HVVMLNDRIQSLGRQLSVLTAKBEHLKSLPADTPPYQFAYKFOEWGLEKMGDGTAGHVLE 242
Db 190 KTLMLNDRQNPDALQHLVLRKAEYLGTVPEPPYSAFEHKEFOEIGLERGWDNAERVLE 249
QY 243 MHLLLDITQADPSTLEKPLGRIPMIFNVVSVPHGYFGQANVLGPDTPGQGVYILDQ 302
Db 250 SIQLLDLLEAPDPCLETFLGRIPMVFNVILSPHYFAQDNVLYGPDTPGQGVYILDQ 309
QY 303 VRALENEMVLRLKQGLDVSPLIVTRILPDAGKTSQNRLEISQITQITVILRVFPRN 362
Db 310 VRALENEMHLRIKQGLDIVPRILITRLIPDAVGTTCQRLKVKFTEHSHLRLVFPRT 369
QY 363 ENGILKKNISRFDPVWPEYLETFAADAGEIAAELOQTDPDFIIGNYSDGNIVASLLSYOMGI 422
Db 370 ENGIVKKNISRFEPVWPEYLETFAADAGEIAAELOQTDPDFIIGNYSDGNIVASLLAKLGV 429
QY 423 TQCNIAHALEKTYKPSDIDFMKNFDEKHYHSCFTADITAMNNADFTITSTYQELAGSKN 482
Db 430 TQCNIAHALEKTYKPSDIDFMKNFDEKHYHSCFTADITAMNNADFTITSTYQELAGSKD 489
QY 483 TVGOYESHATAFTLPLGLYRVVHGDVDFPKFNVSPGADMSIYFPHTKAKRLTSLHSGSIE 542
Db 490 TVGOYESHATAFTLPLGLYRVVHGDVDFPKFNVSPGADQTIYFPHTSRLTSFHEIE 549
QY 543 NLIYDEQNDHGHLDLDRSKPLFSMARLDKVNITGLVFAFAKAKRLNVLVWVAG 602
Db 550 ELLYSVSENEEHICVLKDRSKPIFTMARLDKVNITGLVFAFAKAKRLNVLVWVAG 609
QY 603 YNDVNSKOREEIAEIKHELIKTHNIFGQFRWISAOQNRARNGELYRYIADTHGAFVQ 662
Db 610 -DRRKESKOLEEAKEMKMYSLIETKLGQFQFNWISSQNRVRNGELYRYIADTHGAFVQ 666
QY 663 PALYEAFTLVVEMTCGLPTATLHGGPAEIIIEHGVSGFHDPYHPGQAVNLMADFFDR 722
Db 669 PAVYEAFTLVVEMTCGLPTATLHGGPAEIIIEHGVSGFHDPYHPGQAVNLMADFFDR 728
QY 723 CKQDPHWNISGAGLQRIYKYTWKYSERLMTLAGVYGFYKYSKLERLETRRYLEMF 782
Db 729 VKVDPDHWKISQGLQRIEKEYTWQYSQRLTLTGLVYGFYKYSNLERRETRYLEMF 788
QY 783 YILKPRELAKTVPLAID 799
Db 789 YALKYKLAESVPLAVE 805

RESULT 8
SUSY SOYBN
ID SUSY SOYBN STANDARD; PRT; 805 AA.
AC P13708; O22624;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)
DE (Modulin-100).
DE SS.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCB_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Hobbit; TISSUE=Root nodules;
RA Zhang X.-Q., Verma D.P.S., Patil S., Arredondo-Peter R., Miao G.-H.,

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